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| (54) Title: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN <i>ESCHERICHIA COLI</i>  |  |  |   |
| (57) Abstract  |  |  |   |
| <p>The sequences of nucleic acids encoding proteins required for <i>E. coli</i> proliferation are disclosed. The nucleic acids can be used to express proteins or portions thereof, to obtain antibodies capable of specifically binding to the expressed proteins, and to use those expressed proteins as a screen to isolate candidate molecules for rational drug discovery programs. The nucleic acids can also be used to screen for homologous genes that are required for proliferation in microorganisms other than <i>E. coli</i>. The nucleic acids can also be used to design expression vectors and secretion vectors. The nucleic acids of the present invention can also be used in various assay systems to screen for proliferation required genes in other organisms as well as to screen for antimicrobial agents.</p> |  |  |   |

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**Description**

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## GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN

*ESCHERICHIA COLI*BACKGROUND OF THE INVENTION

Since the discovery of penicillin, the use of antibiotics to treat the ravages of bacterial infections has saved millions of lives. With the advent of these "miracle drugs," for a time it was popularly believed that humanity might, once and for all, be saved from the scourge of bacterial infections. In fact, during the 1980s and early 1990s, many large pharmaceutical companies cut back or eliminated antibiotics research and development. They believed that infectious disease caused by bacteria finally had been conquered and that markets for new drugs were limited. Unfortunately, this belief was overly optimistic.

The tide is beginning to turn in favor of the bacteria as reports of drug resistant bacteria become more frequent. The United States Centers for Disease Control announced that one of the most powerful known antibiotics, vancomycin, was unable to treat an infection of the common *Staphylococcus aureus* (staph). This organism is commonly found in our environment and is responsible for many nosocomial infections. The import of this announcement becomes clear when one considers that vancomycin was used for years to treat infections caused by stubborn strains of bacteria, like staph. In short, the bacteria are becoming resistant to our most powerful antibiotics. If this trend continues, it is conceivable that we will return to a time when what are presently considered minor bacterial infections are fatal diseases.

There are a number of causes for the predicament in which practitioners of medical arts find themselves. Over-prescription and improper prescription habits by some physicians have caused an indiscriminate increase in the availability of antibiotics to the public. The patient is also partly responsible, for even in instances where an antibiotic is the appropriate treatment, patients will often improperly use the drug, the result being yet another population of bacteria that is resistant, in whole or in part, to traditional antibiotics.

The bacterial scourges that have haunted humanity remain, in spite of the development of modern scientific practices to deal with the diseases that they cause. Drug resistant bacteria are now advancing on the health of humanity. A new generation of antibiotics to once again deal with the pending health threat that bacteria present is required.

Discovery of New Antibiotics

As more and more bacterial strains become resistant to the panel of available antibiotics, new compounds are required. In the past, practitioners of pharmacology would have to rely upon traditional methods of drug discovery to generate novel, safe and efficacious compounds for the treatment of disease. Traditional drug discovery methods involve blindly testing potential drug candidate-molecules, often selected at random, in the hope that one might prove to be an effective treatment for some disease. The process is painstaking and laborious, with no guarantee of success. Today, the average cost to discover and develop a new drug is nearly US \$500 million, and the average time is 15 years from laboratory to patient. Improving this process, even incrementally, would represent a huge advance in the generation of novel antimicrobial agents.



Newly emerging practices in drug discovery utilize a number of biochemical techniques to provide for directed approaches to creating new drugs, rather than discovering them at random. For example, gene sequences and proteins encoded thereby that are required for the proliferation of an organism make for excellent targets since exposure of bacteria to compounds active against these targets would result in the inactivation of the organism. Once a target is identified, biochemical analysis of that target can be used to discover or to design molecules that interact with and alter the functions of the target. Using physical and computational techniques, to analyze structural and biochemical targets in order to derive compounds that interact with a target is called rational drug design and offers great future potential. Thus, emerging drug discovery practices use molecular modeling techniques, combinatorial chemistry approaches, and other means to produce and screen and/or design large numbers of candidate compounds.

Nevertheless, while this approach to drug discovery is clearly the way of the future, problems remain. For example, the initial step of identifying molecular targets for investigation can be an extremely time consuming task. It may also be difficult to design molecules that interact with the target by using computer modeling techniques. Furthermore, in cases where the function of the target is not known or is poorly understood, it may be difficult to design assays to detect molecules that interact with and alter the functions of the target. To improve the rate of novel drug discovery and development, methods of identifying important molecular targets in pathogenic microorganisms and methods for identifying molecules that interact with and alter the functions of such molecular targets are urgently required.

*Escherichia coli* represents an excellent model system to understand bacterial biochemistry and physiology. The estimated 4288 genes scattered along the  $4.6 \times 10^6$  base pairs of the *Escherichia coli* (*E. coli*) chromosome offer tremendous promise for the understanding of bacterial biochemical processes. In turn, this knowledge will assist in the development of new tools for the diagnosis and treatment of bacteria-caused human disease. The entire *E. coli* genome has been sequenced, and this body of information holds a tremendous potential for application to the discovery and development of new antibiotic compounds. Yet, in spite of this accomplishment, the general functions or roles of many of these genes are still unknown. For example, the total number of proliferation-required genes contained within the *E. coli* genome is unknown, but has been variously estimated at around 200 to 700 (Armstrong, K.A. and Fan, D.P. Essential Genes in the *metB-malB* Region of *Escherichia coli* K12, 1975, J. Bacteriol. 126: 48-55).

Novel, safe and effective antimicrobial compounds are needed in view of the rapid rise of antibiotic resistant microorganisms. However, prior to this invention, the characterization of even a single bacterial gene was a painstaking process, requiring years of effort. Accordingly, there is an urgent need for more novel methods to identify and characterize bacterial genomic sequences that encode gene products required for proliferation and for methods to identify molecules that interact with and alter the functions of such genes and gene products.

#### SUMMARY OF THE INVENTION

One embodiment of the present invention is a purified or isolated nucleic acid sequence consisting essentially of one of SEQ ID NOs: 1-81, 405-485, wherein said nucleic acid inhibits microorganism proliferation. The nucleic acid sequence may be complementary to at least a portion of a coding sequence of a gene whose expression is required for

microorganism proliferation. The nucleic acid sequence may comprise a fragment of one of SEQ ID NOs: 1-81, 405-485, said fragment selected from the group consisting of fragments comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 1-81, 405-485. The nucleic acid sequence may be complementary to a coding sequence of a gene whose expression is required for microorganism proliferation.

Another embodiment of the present invention is a vector comprising a promoter operably linked to a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs: 1-81, 405-485. The promoter may be active in an organism selected from the group consisting of *Escherichia coli*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species.

Another embodiment of the present invention is a host cell containing the vectors described above.

Another embodiment of the present invention is a purified or isolated nucleic acid consisting essentially of the coding sequence of one of SEQ ID NOs: 82-88, 90-242. One aspect of this embodiment is a fragment of the nucleic acid comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 82-88, 90-242.

Another embodiment of the present invention is a vector comprising a promoter operably linked to the nucleic acids of the preceding embodiment.

Another aspect of the present invention is a purified or isolated nucleic acid comprising a nucleic acid sequence complementary to at least a portion of an intragenic sequence, intergenic sequence, sequences spanning at least a portion of two or more genes, 5' noncoding region, or 3' noncoding region within an operon encoding a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs: 243-357, 359-398.

Another embodiment of the present invention is a purified or isolated nucleic acid comprising a nucleic acid having at least 70% homology to a sequence selected from the group consisting of SEQ ID NOs 1-81, 405-485, 82-88, 90-242 or the sequences complementary thereto as determined using BLASTN version 2.0 with the default parameters. The nucleic acid may be from an organism selected from the group consisting of *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, and *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species.

Another embodiment of the present invention is a purified or isolated nucleic acid consisting essentially of a nucleic acid encoding a polypeptide having a sequence selected from the group consisting of SEQ ID NOs.: 243-357, 359-398.

Another embodiment of the present invention is a vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide having a sequence selected from the group consisting of SEQ ID NOs.: 243-357, 359-398.

Another embodiment of the present invention is a host cell containing the vector of the preceding embodiment.

Another embodiment of the present invention is purified or isolated polypeptide comprising the sequence of one of SEQ ID NOs: 243-357, 359-398.

Another embodiment of the present invention is purified or isolated polypeptide comprising a fragment of one of the polypeptides of SEQ ID NOs. 243-357, 359-398, said fragment selected from the group consisting of fragments comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of one of the polypeptides of SEQ ID NOs.: 243-357, 359-398.

Another embodiment of the present invention is an antibody capable of specifically binding the polypeptide of the preceding embodiment.

Another embodiment of the present invention is method of producing a polypeptide, comprising introducing a vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide having a sequence selected from the group consisting of SEQ ID NOs. 243-357, 359-398 into a cell. The method may further comprise the step of isolating said protein.

Another embodiment of the present invention is a method of inhibiting proliferation comprising inhibiting the activity or reducing the amount of a polypeptide having a sequence selected from the group consisting of SEQ ID NOs. 243-357, 359-398 or inhibiting the activity or reducing the amount of a nucleic acid encoding said polypeptide.

Another embodiment of the present invention is method for identifying compounds which influence the activity of a polypeptide required for proliferation comprising:

contacting a polypeptide comprising a sequence selected from the group consisting of 243-357, 359-398 with a candidate compound; and

determining whether said compound influences the activity of said polypeptide.

The activity may be an enzymatic activity. The activity may be a carbon compound catabolism activity. The activity may be a biosynthetic activity. The activity may be a transporter activity. The activity may be a transcriptional activity. The activity may be a DNA replication activity. The activity may be a cell division activity.

Another embodiment of the present invention is a compound identified using the above method.

Another embodiment of the present invention is method for assaying compounds for the ability to reduce the activity or level of a polypeptide required for proliferation, comprising:

providing a target, wherein said target comprises the coding sequence of a sequence selected from the group consisting of SEQ ID NOs. 82-88, 90-242;

contacting said target with a candidate compound; and  
measuring an activity of said target.

The target may be a messenger RNA molecule transcribed from a coding region of one of SEQ ID. NOs.: 82-88, 90-242 and said activity is translation of said messenger RNA. The target may be a coding region of one of SEQ ID. NOs. 82-88, 90-242 and said activity is transcription of said messenger RNA.

Another embodiment of the present invention is a compound identified using the method above.

Another embodiment of the present invention is a method for identifying compounds which reduce the activity or level of a gene product required for cell proliferation comprising the steps of:

expressing an antisense nucleic acid against a nucleic acid encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell;

contacting said sensitized cell with a compound; and

determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

The cell may be selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells. The cell may be an *E. coli* cell. The cell may be from an organism selected from the group consisting of *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, and *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species. The antisense nucleic acid may be transcribed from an inducible promoter. The method may, further comprise the step of contacting said cell with a concentration of inducer which induces said antisense nucleic acid to a sublethal level. The sub-lethal concentration of said inducer may be such that growth inhibition is 8% or more. The inducer may be isopropyl-1-thio- $\beta$ -D-galactoside. The growth inhibition may be measured by monitoring optical density of a culture growth solution. The gene product may be a polypeptide. The gene product may be an RNA. The gene product may comprise a polypeptide having a sequence selected from the group consisting of SEQ ID NOs.: 243-357, 359-398.

Another embodiment of the present invention is a compound identified using the method above.

Another embodiment of the present invention is a method for inhibiting cellular proliferation comprising introducing a compound with activity against a gene corresponding to one of SEQ ID NOs.: 82-88, 90-242 or with activity against the product of said gene into a population of cells expressing a gene. The compound may be an antisense oligonucleotide comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-81, 405-485, or a proliferation-inhibiting portion thereof. The proliferation inhibiting portion of one of SEQ ID NOs. 1-81, 405-485

5 may be a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 1-81, 405-485. The compound may be a triple helix oligonucleotide.

5 Another embodiment of the present invention is a preparation comprising an effective concentration of an antisense oligonucleotide comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-81, 405-485, or a proliferation-inhibiting portion thereof in a pharmaceutically acceptable carrier. The proliferation-inhibiting portion  
10 of one of SEQ ID NOs. 1-81, 405-485 may comprise at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 1-81, 405-485.

15 Another embodiment of the present invention is a method for inhibiting the expression of a gene in an operon required for proliferation comprising contacting a cell in a cell population with an antisense nucleic acid, said cell expressing a gene corresponding to one of SEQ ID NOs.: 82-88, 90-242, wherein said antisense nucleic acid comprises at least a proliferation-inhibiting portion of said operon in an antisense orientation that is effective in inhibiting expression of said gene. The antisense nucleic acid may be complementary to a sequence of a gene comprising one or more of SEQ ID NOs.: 82-88, 90-242. The antisense nucleic acid may be a sequence of one of SEQ ID NOs.: 1-81,  
20 405-485, or a portion thereof. The cell may be contacted with said antisense nucleic acid by introducing a plasmid which expresses said antisense nucleic acid into said cell population. The cell may be contacted with said antisense nucleic acid by introducing a phage which expresses said antisense nucleic acid into said cell population. The cell may be contacted with said antisense nucleic acid by introducing a sequence encoding said antisense nucleic acid into the chromosome of said cell into said cell population. The cell may be contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population. The cell may be contacted  
25 with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme is complementary to said antisense oligonucleotide. The cell may be contacted with said antisense nucleic acid by introducing a liposome comprising said antisense oligonucleotide into said cell. The cell may be contacted with said antisense nucleic acid by electroporation. The antisense nucleic acid may be a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 82-88, 90-  
30 242. The antisense nucleic acid may be an oligonucleotide.

35 Another embodiment of the present invention is a method for identifying bacterial strains comprising the steps of:

40 providing a sample containing a bacterial species; and

30 identifying a bacterial species using a species specific probe having a sequence selected from the group consisting of SEQ ID NOs. 1-81, 405-485, 82-88, 90-242.

45 Another embodiment of the present invention is a method for identifying a gene in a microorganism required for proliferation comprising:

- 50 (a) identifying an inhibitory nucleic acid which inhibits the activity of a gene or gene product required for proliferation in a first microorganism;
- 35 (b) contacting a second microorganism with said inhibitory nucleic acid;

5 (c) determining whether said inhibitory nucleic acid from said first microorganism inhibits proliferation of said second microorganism; and

(d) identifying the gene in said second microorganism which is inhibited by said inhibitory nucleic acid.

Another embodiment of the present invention is a method for assaying a compound for the ability to inhibit proliferation of a microorganism comprising:

10 (a) identifying a gene or gene product required for proliferation in a first microorganism;

(b) identifying a homolog of said gene or gene product in a second microorganism;

(c) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said second microorganism;

15 (d) contacting said second microorganism with a proliferation-inhibiting amount of said inhibitory nucleic acid, thus sensitizing said second microorganism;

(e) contacting the sensitized microorganism of step (d) with a compound; and

20 (f) determining whether said compound inhibits proliferation of said sensitized microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized microorganism.

15 The step of identifying a gene involved in proliferation in a first microorganism may comprise:

25 introducing a nucleic acid comprising a random genomic fragment from said first microorganism operably linked to a promoter wherein said random genomic fragment is in the antisense orientation; and

30 comparing the proliferation of said first microorganism transcribing a first level of said random genomic fragment to the proliferation of said first microorganism transcribing a lower level of said random genomic fragment, wherein a difference in proliferation indicates that said random genomic fragment comprises a gene involved in proliferation.

35 The step of identifying a homolog of said gene in a second microorganism may comprise identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a database using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the default parameters. The step of identifying a homolog of said gene in a second microorganism may comprise identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide by identifying nucleic acids which hybridize to said first gene. The step of identifying a homolog of said gene in a second microorganism may comprise expressing a nucleic acid which inhibits the proliferation of said first microorganism in said second microorganism. The inhibitory nucleic acid may be an antisense nucleic acid. The inhibitory nucleic acid may comprise an antisense nucleic acid to a portion of said homolog. The inhibitory nucleic acid may comprise an antisense nucleic acid to a portion of the operon encoding said homolog. The step of contacting the second microorganism with a proliferation-inhibiting amount of said nucleic acid sequence may comprise directly contacting said second microorganism with said nucleic acid. The step of contacting the second microorganism with a proliferation-inhibiting amount of said nucleic acid sequence may comprise expressing an antisense nucleic acid to said homolog in said second microorganism.

Another embodiment of the present invention is a compound identified using the method above.

Another embodiment of the present invention is a method of assaying a compound for the ability to inhibit proliferation comprising:

- (a) identifying an inhibitory nucleic acid sequence which inhibits the activity of a gene or gene product required for proliferation in a first microorganism;
- (b) contacting a second microorganism with a proliferation-inhibiting amount of said inhibitory nucleic acid, thus sensitizing said second microorganism;
- (c) contacting the proliferation-inhibited microorganism of step (b) with a compound; and
- (d) determining whether said compound inhibits proliferation of said sensitized second microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized second microorganism.

The inhibitory nucleic acid may be an antisense nucleic acid which inhibits the proliferation of said first microorganism. The inhibitory nucleic acid may comprise a portion of an antisense nucleic acid which inhibits the proliferation of said first microorganism. The inhibitory nucleic acid may comprise an antisense molecule against the entire coding region of the gene involved in proliferation of the first microorganism. The inhibitory nucleic acid may comprise an antisense nucleic acid to a portion of the operon encoding the gene involved in proliferation of the first microorganism.

Another embodiment of the present invention is a compound identified using the method above.

Another embodiment of the present invention is a method for assaying compounds for activity against a biological pathway required for proliferation comprising:

- sensitizing a cell by expressing an antisense nucleic acid against a nucleic acid encoding a gene product required for proliferation in a cell to reduce the activity or amount of said gene product;
- contacting the sensitized cell with a compound; and
- determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

The cell may be selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells. The cell may be an *E. coli* cell. The cell may be an organism selected from the group consisting of *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, and *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species. The antisense nucleic acid may be transcribed from an inducible promoter. The method may further comprise contacting the cell with an agent which induces expression of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is expressed at a sublethal level. The sublethal level of said antisense nucleic acid

5 may inhibit proliferation by 8% or more. The agent may be isopropyl-1-thio- $\beta$ -D-galactoside (IPTG). The inhibition of proliferation may be measured by monitoring the optical density of a liquid culture. The gene product may comprise a polypeptide having a sequence selected from the group consisting of SEQ ID NOs: 243-357, 359-398.

Another embodiment of the present invention is a compound identified using the method above.

10 5 Another embodiment of the present invention is a method for assaying a compound for the ability to inhibit cellular proliferation comprising:

contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell;

15 contacting said cell with said compound; and

10 determining whether said compound reduces proliferation to a greater extent than said compound reduces proliferation of cells which have not been contacted with said agent.

20 The agent which reduces the activity or level of a gene product required for proliferation of said cell may comprise an antisense nucleic acid to a gene or operon required for proliferation. The agent which reduces the activity or level of a gene product required for proliferation of said cell may comprise an antibiotic. The cell may contain a temperature sensitive mutation which reduces the activity or level of said gene product required for proliferation of said cell. The antisense nucleic acid may be directed against the same functional domain of said gene product required for proliferation of said cell to which said antisense nucleic acid is directed. The antisense nucleic acid may be directed against a different functional domain of said gene product required for proliferation of said cell than the functional domain to which said antisense nucleic acid is directed.

20 Another embodiment of the present invention is a compound identified using the method above.

30 Another embodiment of the present invention is a method for identifying the pathway in which a proliferation-required nucleic acid or its gene product lies comprising:

expressing a sublethal level of an antisense nucleic acid directed against said proliferation-required nucleic acid in a cell;

35 25 contacting said cell with an antibiotic, wherein the a biological pathway on which said antibiotic acts is known; and

determining whether said cell has a substantially greater sensitivity to said antibiotic than a cell which does not express said sublethal level of said antisense nucleic acid.

40 30 Another embodiment of the present invention is a method for determining the pathway on which a test compound acts comprising:

45 (a) expressing a sublethal level of an antisense nucleic acid directed against a proliferation-required nucleic acid in a cell, wherein the biological pathway in which said proliferation-required nucleic acid lies is known,

(b) contacting said cell with said test compound; and

35 (c) determining whether said cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said antisense nucleic acid.



The method may further comprise:

(d) expressing a sublethal level of a second antisense nucleic acid directed against a second proliferation-required nucleic acid in said cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

(e) determining whether said cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said second antisense nucleic acid.

Another embodiment of the present invention is a purified or isolated nucleic acid consisting essentially of one of SEQ ID NOs: 358, 399-402.

Another embodiment of the present invention is a purified or isolated nucleic acid comprising a sequence selected from the group consisting of 1-81, 405-485, 82-88, 90-242, 358, 399-402.

Another embodiment of the present invention is a compound which interacts with the gene or gene product of a nucleic acid comprising a sequence of one of SEQ ID NOs: 82-88, 90-242 to inhibit proliferation.

Another embodiment of the present invention compound which interacts with a polypeptide comprising one of SEQ ID NOs. 243-357, 359-398 to inhibit proliferation.

Another embodiment of the present invention is a compound which interacts with a nucleic acid comprising one of SEQ ID NOs: 358, 399-402 to inhibit proliferation.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is an IPTG dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing either an antisense clone to the *E. coli* ribosomal protein rplW (AS-rplW) which is required for protein synthesis and essential cell proliferation, or an antisense clone to the *elaD* (AS-*elaD*) gene which is not known to be involved in protein synthesis and which is also essential for proliferation.

Figure 2A is a tetracycline dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing antisense to rplW(AS-rplW) in the presence of 0, 20 or 50  $\mu$ M IPTG.

Figure 2B is a tetracycline dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing antisense to *elaD* (AS-*elaD*) in the presence of 0, 20 or 50  $\mu$ M IPTG.

Figure 3 is a graph showing the fold increase in tetracycline sensitivity of *E. coli* transfected with antisense clones to essential ribosomal proteins L23 (AS-rplW) and L7/L12 and L10 (AS-rplLrplJ). Antisense clones to genes known not to be involved in protein synthesis (atpB/E(AS-atpB/E), *visC* (AS-*visC*, *elaD* (AS-*elaD*), *yohH* (AS-*yohH*) are much less sensitive to tetracycline.

#### Definitions

By "biological pathway" is meant any discrete cell function or process that is carried out by a gene product or a subset of gene products. Biological pathways include enzymatic, biochemical and metabolic pathways as well as pathways involved in the production of cellular structures such cell walls. Biological pathways that are usually required for proliferation of microorganisms include, but are not limited to, cell division, DNA synthesis & replication,

RNA synthesis (transcription), protein synthesis (translation), protein processing, protein transport, fatty acid biosynthesis, cell wall synthesis, cell membrane synthesis & maintenance, etc.

By "inhibit activity against a gene or gene product" is meant having the ability to interfere with the function of a gene or gene product in such a way as to decrease expression of the gene or to reduce the level or activity of a product of the gene. Agents which have activity against a gene include agents that inhibit transcription of the gene and agents that inhibit translation of the mRNA transcribed from the gene. In microorganisms, agents which have activity against a gene can act to decrease expression of the operon in which the gene resides or alter the processing of operon RNA such as to reduce the level or activity of the gene product. The gene product can be a non-translated RNA such as ribosomal RNA, a translated RNA (mRNA) or the protein product resulting from translation of the gene mRNA. Of particular utility to the present invention are anti-sense RNAs that have activities against the operons or genes to which they specifically hybridize.

By "activity against a gene product" is meant having the ability to inhibit the function or to reduce the level or activity of the gene product in a cell.

By "activity against a protein" is meant having the ability to inhibit the function or to reduce the level or activity of the protein in a cell.

By "activity against nucleic acid" is meant having the ability to inhibit the function or to reduce the level or activity of the nucleic acid in a cell.

As used herein, "sublethal" means a concentration of an agent below the concentration required to inhibit all cell growth.

#### DETAILED DESCRIPTION OF THE INVENTION

The present invention describes a group of *E. coli* genes and gene families required for growth and/or proliferation. A proliferation-required gene or gene family is one where, in the absence of a gene transcript and/or gene product, growth or viability of the microorganism is reduced or eliminated. Thus, as used herein the terminology "proliferation-required" or "required for proliferation" encompasses sequences where the absence of a gene transcript and/or gene product completely eliminates cell growth as well as sequences where the absence of a gene transcript and/or gene product merely reduces cell growth. These proliferation-required genes can be used as potential targets for the generation of new antimicrobial agents. To achieve that goal, the present invention also encompasses novel assays for analyzing proliferation-required genes and for identifying compounds which interact with the gene products of the proliferation-required genes. In addition, the present invention contemplates the expression of genes and the purification of the proteins encoded by the nucleic acid sequences identified as required proliferation genes and reported herein. The purified proteins can be used to generate reagents and screen small molecule libraries or other candidate compound libraries for compounds that can be further developed to yield novel antimicrobial compounds. The present invention also describes methods for identification of homologous genes in organisms other than *E. coli*.

The present invention utilizes a novel method to identify proliferation-required *E. coli* sequences. Generally, a library of nucleic acid sequences from a given source are subcloned or otherwise inserted into an inducible expression

vector, thus forming an expression library. Although the insert nucleic acids may be derived from the chromosome of the organism into which the expression vector is to be introduced, because the insert is not in its natural chromosomal location, the insert nucleic acid is an exogenous nucleic acid for the purposes of the discussion herein. The term expression is defined as the production of an RNA molecule from a gene, gene fragment, genomic fragment, or operon. Expression can also be used to refer to the process of peptide or polypeptide synthesis. An expression vector is defined as a vehicle by which a ribonucleic acid (RNA) sequence is transcribed from a nucleic acid sequence carried within the expression vehicle. The expression vector can also contain features that permit translation of a protein product from the transcribed RNA message expressed from the exogenous nucleic acid sequence carried by the expression vector. Accordingly, an expression vector can produce an RNA molecule as its sole product or the expression vector can produce a RNA molecule that is ultimately translated into a protein product.

Once generated, the expression library containing the exogenous nucleic acid sequences is introduced into an *E. coli* population to search for genes that are required for bacterial proliferation. Because the library molecules are foreign to the population of *E. coli*, the expression vectors and the nucleic acid segments contained therein are considered exogenous nucleic acid.

Expression of the exogenous nucleic acid fragments in the test population of *E. coli* containing the expression vector library is then activated. Activation of the expression vectors consists of subjecting the cells containing the vectors to conditions that result in the expression of the exogenous nucleic acid sequences carried by the expression vector library. The test population of *E. coli* cells is then assayed to determine the effect of expressing the exogenous nucleic acid fragments on the test population of cells. Those expression vectors that, upon activation and expression, negatively impact the growth of the *E. coli* screen population were identified, isolated, and purified for further study.

A variety of assays are contemplated to identify nucleic acid sequences that negatively impact growth upon expression. In one embodiment, growth in *E. coli* cultures expressing exogenous nucleic acid sequences and growth in cultures not expressing these sequences is compared. Growth measurements are assayed by examining the extent of growth by measuring optical densities. Alternatively, enzymatic assays can be used to measure bacterial growth rates to identify exogenous nucleic acid sequences of interest. Colony size, colony morphology, and cell morphology are additional factors used to evaluate growth of the host cells. Those cultures that failed to grow or grow with reduced efficiency under expression conditions are identified as containing an expression vector encoding a nucleic acid fragment that negatively affects a proliferation-required gene.

Once exogenous nucleic acid sequences of interest are identified, they are analyzed. The first step of the analysis is to acquire the nucleic acid sequence of the nucleic acid fragment of interest. To achieve this end, the insert in those expression vectors identified as containing a sequence of interest is sequenced, using standard techniques well known in the art. The next step of the process is to determine the source of the nucleic acid sequence.

Determination of sequence source is achieved by comparing the obtained sequence data with known sequences in various genetic databases. The sequences identified are used to probe these gene databases. The result of this

procedure is a list of exogenous nucleic acid sequences corresponding to a list that includes novel bacterial genes required for proliferation as well as genes previously identified as required for proliferation.

The number of DNA and protein sequences available in database systems has been growing exponentially for years. For example, at the end of 1998, the complete sequences of *Caenorhabditis elegans*, *Saccharomyces cerevisiae* and nineteen bacterial genomes, including *E. coli* were available. This sequence information is stored in a number of databanks, such as GenBank (the National Center for Biotechnology Information (NCBI)), and is publicly available for searching.

A variety of computer programs are available to assist in the analysis of the sequences stored within these databases. FastA, (W. R. Pearson (1990) "Rapid and Sensitive Sequence Comparison with FASTP and FASTA" Methods in Enzymology 183:63- 98), Sequence Retrieval System (SRS), (Etzold & Argos, SRS an indexing and retrieval tool for flat file data libraries. Comput. Appl. Biosci. 9:49-57, 1993) are two examples of computer programs that can be used to analyze sequences of interest. In one embodiment of the present invention, the BLAST family of computer programs, which includes BLASTN version 2.0 with the default parameters, or BLASTX version 2.0 with the default parameters, is used to analyze nucleic acid sequences.

BLAST, an acronym for "Basic Local Alignment Search Tool," is a family of programs for database similarity searching. The BLAST family of programs includes: BLASTN, a nucleotide sequence database searching program, BLASTX, a protein database searching program where the input is a nucleic acid sequence; and BLASTP, a protein database searching program. BLAST programs embody a fast algorithm for sequence matching, rigorous statistical methods for judging the significance of matches, and various options for tailoring the program for special situations. Assistance in using the program can be obtained by e-mail at [blast@ncbi.nlm.nih.gov](mailto:blast@ncbi.nlm.nih.gov).

Bacterial genes are often transcribed in polycistronic groups. These groups comprise operons, which are a collection of genes and intergenic sequences. The genes of an operon are co-transcribed and are often related functionally. Given the nature of the screening protocol, it is possible that the identified exogenous nucleic acid sequence corresponds to a gene or portion thereof with or without adjacent noncoding sequences, an intragenic sequence (i.e. a sequence within a gene), an intergenic sequence (i.e. a sequence between genes), a sequence spanning at least a portion of two or more genes, a 5' noncoding region or a 3' noncoding region located upstream or downstream from the actual sequence that is required for bacterial proliferation. Accordingly, determining which of the genes that are encoded within the operons are individually required for proliferation is often desirable.

In one embodiment of the present invention, an operon is dissected to determine which gene or genes are required for proliferation. For example, the RegulonDB DataBase described by Huerta et al. (*Wucl. Acids Res.* 26:55-59, 1998), which may also be found on the website [http://www.cifn.unam.mx/Computational\\_Biology/regulondb/](http://www.cifn.unam.mx/Computational_Biology/regulondb/), may be used to identify the boundaries of operons encoded within microbial genomes. A number of techniques that are well known in the art can be used to dissect the operon. In one aspect of this embodiment, gene disruption by homologous recombination is used to individually inactivate the genes of an operon that is thought to contain a gene required for proliferation.

Several gene disruption techniques have been described for the replacement of a functional gene with a mutated, non-functional (null) allele. These techniques generally involve the use of homologous recombination. The

method described by Link et al. (J. Bacteriol 1997 179:6228; incorporated herein by reference in its entirety) serves as an excellent example of these methods as applicable to disruption of genes in *E. coli*. This technique uses crossover PCR to create a null allele with an in-frame deletion of the coding region of a target gene. The null allele is constructed in such a way that sequences adjacent to the wild type gene (ca. 500 bp) are retained. These homologous sequences surrounding the deletion null allele provide targets for homologous recombination so that the wild type gene on the *E. coli* chromosome can be replaced by the constructed null allele.

The crossover PCR amplification product is subcloned into the vector pK03, the features of which include a chloramphenicol resistance gene, the counter-selectable marker *sacB*, and a temperature sensitive autonomous replication function. Following transformation of an *E. coli* cell population with such a vector, selection for cells that have undergone homologous recombination of the vector into the chromosome is achieved by growth on chloramphenicol at the non-permissive temperature of 43°C. Under these conditions, autonomous replication of the plasmid cannot occur and cell are resistant to chloramphenicol only if the chloramphenicol resistance gene has been integrated into the chromosome. Usually a single crossover event is responsible for this integration event such that the *E. coli* chromosome now contains a tandem duplication of the target gene consisting of one wild type allele and one deletion null allele separated by vector sequence.

This new *E. coli* strain containing the tandem duplication can be maintained at permissive temperatures in the presence of drug selection (chloramphenicol). Subsequently, cells of this new strain are cultured at the permissive temperature 30°C without drug selection. Under these conditions, the chromosome of some of the cells within the population will have undergone an internal homologous recombination event resulting in removal of the plasmid sequences. Subsequent culturing of the strain in growth medium lacking chloramphenicol but containing sucrose is used to select for such recombinative resolutions. In the presence of the counter-selectable marker *sacB*, sucrose is rendered into a toxic metabolite. Thus, cells that survive this counter-selection have lost both the plasmid sequences from the chromosome and the autonomously replicating plasmid that results as a byproduct of recombinative resolution.

There are two possible outcomes of the above recombinative resolution via homologous recombination. Either the wild type copy of the targeted gene is retained on the chromosome or the mutated null allele is retained on the chromosome. In the case of an essential gene, a single copy of the null allele would be lethal and such cells should not be obtained by the above procedure when applied to essential genes. In the case of a non-essential gene, roughly equal numbers of cells containing null alleles and cells containing wild type alleles should be obtained. Thus, the method serves as a test for essentiality of the targeted gene: when applied to essential genes, only cells with a wild type allele on the chromosome will be obtained.

Other techniques have also been described for the creation of disruption mutations in *E. coli*. For example, Link et al. also describe inserting an in-frame sequence tag concomitantly with an in-frame deletion in order to simplify analysis of recombinants obtained. Further, Link et al. describe disruption of genes with a drug resistance marker such as a kanamycin resistance gene. Arigoni et al., (Arigoni, F. et al. A Genome-based Approach for the

5 Identification of Essential Bacterial Genes, Nature Biotechnology 16: 851-856, the disclosure of which is incorporated herein by reference in its entirety) describe the use of gene disruption combined with engineering a second copy of a test gene such that the expression of the gene is regulated by and inducible promoter such as the arabinose promoter to test the essentiality of the gene. Many of these techniques result in the insertion of large fragments of DNA into the gene of interest, such as a drug selection marker. An advantage of the technique described by Link et al. is that it does not rely on an insertion into the gene to cause a functional defect, but rather results in the precise removal of the coding region. This insures the lack of polar effects on the expression of genes downstream from the target gene.

10 Recombinant DNA techniques can be used to express the entire coding sequences of the gene identified as required for proliferation, or portions thereof. The over-expressed proteins can be used as reagents for further study. The identified exogenous sequences are isolated, purified, and cloned into a suitable expression vector using methods well known in the art. If desired, the nucleic acids can contain the sequences encoding a signal peptide to facilitate secretion of the expressed protein.

15 Expression of fragments of the bacterial genes identified as required for proliferation is also contemplated by the present invention. The fragments of the identified genes can encode a polypeptide comprising at least 5, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 75, or more than 75 consecutive amino acids of a gene complementary to one of the identified sequences of the present invention. The nucleic acids inserted into the expression vectors can also contain sequences upstream and downstream of the coding sequence.

20 When expressing the coding sequence of an entire gene identified as required for bacterial proliferation or a fragment thereof, the nucleic acid sequence to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The expression vector can be any of the bacterial, insect, yeast, or mammalian expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon usage and codon bias of the sequence can be optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, et al., U.S. Patent No. 5,082,767, incorporated herein by this reference. Fusion protein expression systems are also contemplated by the present invention.

25 Following expression of the protein encoded by the identified exogenous nucleic acid sequence, the protein is purified. Protein purification techniques are well known in the art. Proteins encoded and expressed from identified exogenous nucleic acid sequences can be partially purified using precipitation techniques, such as precipitation with polyethylene glycol. Chromatographic methods usable with the present invention can include ion-exchange chromatography, gel filtration, use of hydroxyapatite columns, immobilized reactive dyes, chromatofocusing, and use of high-performance liquid chromatography. Electrophoretic methods such one-dimensional gel electrophoresis, high-resolution two-dimensional polyacrylamide electrophoresis, isoelectric focusing, and others are contemplated as purification methods.

Also, affinity chromatographic methods, comprising antibody columns, ligand presenting columns and other affinity chromatographic matrices are contemplated as purification methods in the present invention.

The purified proteins produced from the gene coding sequences identified as required for proliferation can be used in a variety of protocols to generate useful antimicrobial reagents. In one embodiment of the present invention, antibodies are generated against the proteins expressed from the identified exogenous nucleic acid sequences. Both monoclonal and polyclonal antibodies can be generated against the expressed proteins. Methods for generating monoclonal and polyclonal antibodies are well known in the art. Also, antibody fragment preparations prepared from the produced antibodies discussed above are contemplated.

Another application for the purified proteins of the present invention is to screen small molecule libraries for candidate compounds active against the various target proteins of the present invention. Advances in the field of combinatorial chemistry provide methods, well known in the art, to produce large numbers of candidate compounds that can have a binding, or otherwise inhibitory effect on a target protein. Accordingly, the screening of small molecule libraries for compounds with binding affinity or inhibitory activity for a target protein produced from an identified gene sequence is contemplated by the present invention.

The present invention further contemplates utility against a variety of other pathogenic organisms in addition to *E. coli*. For example, the invention has utility in identifying genes required for proliferation in prokaryotes and eukaryotes. For example, the invention has utility with protists, such as *Plasmodium* spp.; plants; animals, such as *Entamoeba* spp. and *Contracaecum* spp; and fungi including *Candida* spp., (e.g., *Candida albicans*), *Saccharomyces cerevisiae*, *Cryptococcus neoformans*, and *Aspergillus fumigatus*. In one embodiment of the present invention, monera, specifically bacteria are probed in search of novel gene sequences required for proliferation. This embodiment is particularly important given the rise of drug resistant bacteria.

The numbers of bacterial species that are becoming resistant to existing antibiotics are growing. A partial list of these organisms includes: *Staphylococcus* spp., such as *S. aureus*; *Enterococcus* spp., such as *E. faecalis*; *Pseudomonas* spp., such as *P. aeruginosa*; *Clostridium* spp., such as *C. botulinum*; *Haemophilus* spp., such as *H. influenzae*; *Enterobacter* spp., such as *E. cloacae*; *Vibrio* spp., such as *V. cholera*; *Moraxella* spp., such as *M. catarrhalis*; *Streptococcus* spp., such as *S. pneumoniae*; *Neisseria* spp., such as *N. gonorrhoeae*; *Mycoplasma* spp., such as *Mycoplasma pneumoniae*; *Salmonella typhimurium*; *Helicobacter pylori*; *Escherichia coli*; and *Mycobacterium tuberculosis*. The sequences identified as required for proliferation in the present invention can be used to probe these and other organisms to identify homologous required proliferation genes contained therein.

In one embodiment of the present invention, the nucleic acid sequences disclosed herein are used to screen genomic libraries generated from bacterial species of interest other than *E. coli*. For example, the genomic library may be from *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium*

5 *tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*,  
10 *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any  
15 of the above species. Standard molecular biology techniques are used to generate genomic libraries from various  
microorganisms. In one aspect, the libraries are generated and bound to nitrocellulose paper. The identified exogenous  
nucleic acid sequences of the present invention can then be used as probes to screen the libraries for homologous  
sequences. The homologous sequences identified can then be used as targets for the identification of new, antimicrobial  
compounds with activity against more than one organism.

For example, the preceding methods may be used to isolate nucleic acids having a sequence with at least  
97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% identity to a nucleic acid sequence  
selected from the group consisting of one of the sequences of SEQ ID NOS. 1-81, 405-485, 82-88, 90-242, fragments  
comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases thereof, and  
the sequences complementary thereto. Identity may be measured using BLASTN version 2.0 with the default  
parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search  
Programs, Nucleic Acid Res. 25: 3389-3402 (1997), the disclosure of which is incorporated herein by reference in its  
entirety). For example, the homologous polynucleotides may have a coding sequence which is a naturally occurring  
allelic variant of one of the coding sequences described herein. Such allelic variants may have a substitution, deletion  
or addition of one or more nucleotides when compared to the nucleic acids of SEQ ID NOS: 1-81, 405-485, 82-88, 90-  
242 or the sequences complementary thereto.

Additionally, the above procedures may be used to isolate nucleic acids which encode polypeptides having at  
least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, or at least 40%  
identity or similarity to a polypeptide having the sequence of one of SEQ ID NOS: 243-357, 359-398 or fragments  
comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof as determined  
using the FASTA version 3.0t78 algorithm with the default parameters. Alternatively, protein identity or similarity  
may be identified using BLASTP with the default parameters, BLASTX with the default parameters, or TBLASTN with  
the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database  
Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997), the disclosure of which is incorporated herein by  
reference in its entirety).

Alternatively, homologous nucleic acids or polypeptides may be identified by searching a database to identify  
sequences having a desired level of homology to a nucleic acid or polypeptide involved in proliferation or an antisense  
nucleic acid to a nucleic acid involved in microbial proliferation. A variety of such databases are available to those  
skilled in the art, including GenBank and GenSeq. In some embodiments, the databases are screened to identify  
nucleic acids or polypeptides having at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, at least  
70%, at least 60%, or at least 50%, at least 40% identity or similarity to a nucleic acid or polypeptide involved in  
proliferation or an antisense nucleic acid involved in proliferation. For example, the database may be screened to  
identify nucleic acids homologous to one of SEQ ID Nos. 1-81, 405-485, 82-88, 90-242 or polypeptides homologous



to SEQ ID NOs. 243-357, 359-398. In some embodiments, the database may be screened to identify homologous nucleic acids or polypeptides from organisms other than *E. coli*, including organisms such as *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species.

In another embodiment, gene expression arrays and microarrays can be employed. Gene expression arrays are high density arrays of DNA samples deposited at specific locations on a glass chip, nylon membrane, or the like. Such arrays can be used by researchers to quantify relative gene expression under different conditions. Gene expression arrays are used by researchers to help identify optimal drug targets, profile new compounds, and determine disease pathways. An example of this technology is found in U.S. Patent No. 5807522, which is hereby incorporated by reference.

It is possible to study the expression of all genes in the genome of a particular microbial organism using a single array. For example, the arrays from Genosys consist of 12 x 24 cm nylon filters containing PCR products corresponding to 4290 ORFs from *E. coli*. 10 ngs of each are spotted every 1.5 mm on the filter. Single stranded labeled cDNAs are prepared for hybridization to the array (no second strand synthesis or amplification step is done) and placed in contact with the filter. Thus the labeled cDNAs are of "antisense" orientation. Quantitative analysis is done by phosphorimager.

Hybridization of cDNA made from a sample of total cell mRNA to such an array followed by detection of binding by one or more of various techniques known to those in the art results in a signal at each location on the array to which cDNA hybridized. The intensity of the hybridization signal obtained at each location in the array thus reflects the amount of mRNA for that specific gene that was present in the sample. Comparing the results obtained for mRNA isolated from cells grown under different conditions thus allows for a comparison of the relative amount of expression of each individual gene during growth under the different conditions.

Gene expression arrays may be used to analyze the total mRNA expression pattern at various time points after induction of an antisense nucleic acid against a proliferation-required gene. Analysis of the expression pattern indicated by hybridization to the array provides information on whether or not the target gene of the antisense nucleic acid is being affected by antisense induction, how quickly the antisense is affecting the target gene, and for later timepoints, what other genes are affected by antisense expression. For example, if the antisense is directed against a gene for ribosomal protein L7/L12 in the 50S subunit, its targeted mRNA may disappear first and then other mRNAs may be observed to increase, decrease or stay the same. Similarly, if the antisense is directed against a different 50S subunit ribosomal protein mRNA (e.g. L25), that mRNA may disappear first followed by changes in mRNA expression that are similar to those seen with the L7/L12 antisense expression. Thus, the mRNA expression pattern observed

5 with an antisense nucleic acid against a proliferation required gene may identify other proliferation-required nucleic acids in the same pathway as the target of the antisense nucleic acid. In addition, the mRNA expression patterns observed with candidate drug compounds may be compared to those observed with antisense nucleic acids against a proliferation-required nucleic acid. If the mRNA expression pattern observed with the candidate drug compound is similar to that observed with the antisense nucleic acid, the drug compound may be a promising therapeutic candidate. Thus, the assay would be useful in assisting in the selection of candidate drug compounds for use in screening methods such as those described below.

10 In cases where the source of nucleic acid deposited on the array and the source of the nucleic acid being hybridized to the array are from two different organisms, gene expression arrays can identify homologous genes in the two organisms.

15 The present invention also contemplates additional methods for screening other microorganisms for proliferation-required genes. In this embodiment, the conserved portions of sequences identified as proliferation-required can be used to generate degenerate primers for use in the polymerase chain reaction (PCR). The PCR technique is well known in the art. The successful production of a PCR product using degenerate probes generated from the sequences identified herein would indicate the presence of a homologous gene sequence in the species being screened. This homologous gene is then isolated, expressed, and used as a target for candidate antibiotic compounds. In another aspect of this embodiment, the homologous gene is expressed in an autologous organism or in a heterologous organism in such a way as to alter the level or activity of a homologous gene required for proliferation in the autologous or heterologous organism. In still another aspect of this embodiment, the homologous gene or portion is expressed in an antisense orientation in such a way as to alter the level or activity of a nucleic acid required for proliferation of an autologous or heterologous organism.

20 The homologous sequences to proliferation-required genes identified using the techniques described herein may be used to identify proliferation-required genes of organisms other than *E. coli*, to inhibit the proliferation of organisms other than *E. coli* by inhibiting the activity or reducing the amount of the identified homologous nucleic acid or polypeptide in the organism other than *E. coli*, or to identify compounds which inhibit the growth of organisms other than *E. coli* as described below.

25 In another embodiment of the present invention, *E. coli* sequences identified as required for proliferation are transferred to expression vectors capable of function within non-*E. coli* species. As would be appreciated by one of ordinary skill in the art, expression vectors must contain certain elements that are species specific. These elements can include promoter sequences, operator sequences, repressor genes, origins of replication, ribosomal binding sequences, termination sequences, and others. To use the identified exogenous sequences of the present invention, one of ordinary skill in the art would know to use standard molecular biology techniques to isolate vectors containing the sequences of interest from cultured bacterial cells, isolate and purify those sequences, and subclone those sequences into an expression vector adapted for use in the species of bacteria to be screened.

30 Expression vectors for a variety of other species are known in the art. For example, Cao et al. report the expression of steroid receptor fragments in *Staphylococcus aureus*. *J. Steroid Biochem Mol Biol.* 44(1):1-11

(1993). Also, Pla et al. have reported an expression vector that is functional in a number of relevant hosts including: *Salmonella typhimurium*, *Pseudomonas putida*, and *Pseudomonas aeruginosa*. J. Bacteriol. 172(8):4448-55 (1990). These examples demonstrate the existence of molecular biology techniques capable of constructing expression vectors for the species of bacteria of interest to the present invention.

Following the subcloning of the identified nucleic acid sequences into an expression vector functional in the microorganism of interest, the identified nucleic acid sequences are conditionally transcribed to assay for bacterial growth inhibition. Those expression vectors found to contain sequences that, when transcribed, inhibit bacterial growth are compared to the known genomic sequence of the pathogenic microorganism being screened or, if the homologous sequence from the organism being screened is not known, it may be identified and isolated by hybridization to the proliferation-required *E. coli* sequence interest or by amplification using primers based on the proliferation-required *E. coli* sequence of interest as described above.

The antisense sequences from the second organism which are identified as described above may then be operably linked to a promoter, such as an inducible promoter, and introduced into the second organism. The techniques described herein for identifying *E. coli* genes required for proliferation may thus be employed to determine whether the identified sequences from a second organism inhibit the proliferation of the second organism.

Antisense nucleic acids required for the proliferation of organisms other than *E. coli* or the genes corresponding thereto, may also be hybridized to a microarray containing the *E. coli* ORFs to gauge the homology between the *E. coli* sequences and the proliferation-required nucleic acids from other organisms. For example, the proliferation-required nucleic acid may be from *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni* or *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species. The proliferation-required nucleic acids from an organism other than *E. coli* may be hybridized to the array under a variety of conditions which permit hybridization to occur when the probe has different levels of homology to the sequence on the microarray. This would provide an indication of homology across the organisms as well as clues to other possible essential genes in these organisms.

In still another embodiment, the exogenous nucleic acid sequences of the present invention that are identified as required for bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. The antisense sequences can be directed against the proliferation-required genes whose sequence corresponds to the exogenous nucleic acid probes identified here (i.e. the antisense nucleic acid may hybridize to the gene or a portion thereof). Alternatively, antisense therapeutics can be directed against operons in which proliferation-required genes reside (i.e. the antisense nucleic acid may hybridize to any gene in the operon in which the proliferation-required genes reside). Further, antisense

therapeutics can be directed against a proliferation-required gene or portion thereof with or without adjacent noncoding sequences, an intragenic sequence (i.e. a sequence within a gene), an intergenic sequence (i.e. a sequence between genes), a sequence spanning at least a portion of two or more genes, a 5' noncoding region or a 3' noncoding region located upstream or downstream from the actual sequence that is required for bacterial proliferation or an operon containing a proliferation-required gene.

In addition to therapeutic applications, the present invention encompasses the use of nucleic acid sequences complementary to sequences required for proliferation as diagnostic tools. For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical specimens. This utility provides a rapid and dependable method by which to identify the causative agent or agents of a bacterial infection. This utility would provide clinicians the ability to prescribe species specific antimicrobial compounds to treat such infections. In an extension of this utility, antibodies generated against proteins translated from mRNA transcribed from proliferation-required sequences can also be used to screen for specific microorganisms that produce such proteins in a species-specific manner.

The following examples teach the genes of the present invention and a subset of uses for the *E. coli* genes identified as required for proliferation. These examples are illustrative only and are not intended to limit the scope of the present invention.

#### EXAMPLES

The following examples are directed to the identification and exploitation of *E. coli* genes required for proliferation. Methods of gene identification are discussed as well as a variety of methods to utilize the identified sequences.

##### Genes Identified as Required for Proliferation of *E. coli*

Exogenous nucleic acid sequences were cloned into an inducible expression vector and assayed for growth inhibition activity. Example 1 describes the examination of a library of exogenous nucleic acid sequences cloned into IPTG-inducible expression vectors. Upon activation or induction, the expression vectors produced an RNA molecule corresponding to the subcloned exogenous nucleic acid sequences. The RNA product was in an antisense orientation with respect to the *E. coli* genes from which it was originally derived. This antisense RNA then interacted with sense mRNA produced from various *E. coli* genes and interfered with or inhibited the translation of the sense messenger RNA (mRNA) thus preventing protein production from these sense mRNA molecules. In cases where the sense mRNA encoded a protein required for the proliferation, bacterial cells containing an activated expression vector failed to grow or grew at a substantially reduced rate.

#### EXAMPLE 1

##### Inhibition of Bacterial Proliferation after IPTG induction

To study the effects of transcriptional induction in liquid medium, growth curves were carried out by back diluting cultures 1:200 into fresh media with or without 1 mM IPTG and measuring the OD<sub>490</sub> every 30 minutes (min). To

study the effects of transcriptional induction on solid medium,  $10^2$ ,  $10^3$ ,  $10^4$ ,  $10^5$ ,  $10^6$ ,  $10^7$  and  $10^8$  fold dilutions of overnight cultures were prepared. Aliquots of from 0.5 to 3  $\mu$ l of these dilutions were spotted on selective agar plates with or without 1 mM IPTG. After overnight incubation, the plates were compared to assess the sensitivity of the clones to IPTG.

Of the numerous clones tested, some clones were identified as a containing sequence that inhibited *E. coli* growth after IPTG induction. Accordingly, the gene to which the inserted nucleic acid sequence corresponds, or a gene within the operon containing the inserted nucleic acid, may be required for proliferation in *E. coli*.

#### Characterization of Isolated Clones Negatively Affecting *E. coli* Proliferation

Following the identification of those expression vectors that, upon expression, negatively impacted *E. coli* growth or proliferation, the inserts or nucleic acid fragments contained in those expression vectors were isolated for subsequent characterization. Expression vectors of interest were subjected to nucleic acid sequence determination.

#### EXAMPLE 2

##### Nucleic Acid Sequence Determination of Identified Clones Expressing Nucleic Acid Fragments with Detrimental Effects of *E. coli* Proliferation

The nucleotide sequences for the exogenous identified sequences were determined using plasmid DNA isolated using QIAPREP (Qiagen, Valencia, CA) and methods supplied by the manufacturer. The primers used for sequencing the inserts were 5' - TGTTTATCAGACCGCTT - 3' (SEQ ID NO: 403) and 5' - ACAATTCACACAGCCTC - 3' (SEQ ID NO: 404). These sequences flank the polylinker in pLEX58A. Sequence identification numbers (SEQ ID NOs) for the identified inserts are listed in Table I and discussed below.

#### EXAMPLE 3

##### Comparison Of Isolated Sequences to Known Sequences

The nucleic acid sequences of the subcloned fragments obtained from the expression vectors discussed above were compared to known *E. coli* sequences in GenBank using BLAST version 1.4 or version 2.0.8 using the following default parameters: Filtering off, cost to open a gap=5, cost to extend a gap=2, penalty for a mismatch in the blast portion of run=-3, reward for a match in the blast portion of run=1, expectation value (e)=10.0, word size=11, number of one-line descriptions=100, number of alignments to show (B)=100. BLAST is described in Altschul, J Mol Biol. 215:403-10 (1990), the disclosure of which is incorporated herein by reference in its entirety. Expression vectors were found to contain nucleic acid sequences in both the sense and antisense orientations. The presence of known genes, open reading frames, and ribosome binding sites was determined by comparison to public databases holding genetic information and various computer programs such as the Genetics Computer Group programs FRAMES and CODONPREFERENCE. Clones were designated as "antisense" if the cloned fragment was oriented to the promoter such that the RNA transcript produced was complementary to the expressed mRNA from a chromosomal locus. Clones were designated as "sense" if they coded for an RNA fragment that was identical to a portion of a wild type mRNA from a chromosomal locus.

The sequences described in Examples 1-2 that inhibited bacterial proliferation and contained gene fragments in an antisense orientation are listed in Table I. This table lists each identified sequence by: a sequence identification number; a Molecule Number; a gene to which the identified sequence corresponds, listed according to the National Center for Biotechnology Information (NCBI), Blattner (Science 277:1453-1474(1997); also contains the *E. coli* K-12 genome sequence), or Rudd (Micro. and Mol. Rev. 62:985-1019 (1998)), (both papers are hereby incorporated by reference) nomenclatures. The CONTIG numbers for each identified sequence is shown, as well as the location of the first and last base pairs located on the *E. coli* chromosome. A Molecule Number with a "\*" indicates a clone corresponding to an intergenic sequence.

The sequences of the nucleic acid inserts of SEQ ID NOs: 1-81 from U.S. Provisional Patent Application No. 60/117,405 which inhibited proliferation were further analyzed. The reanalyzed sequences corresponding to SEQ ID NOs. 1-81 of U.S. Provisional Patent Application No. 60/117,405 have SEQ ID NOs. 405-485 in the present application.

SEQ ID NOs: 82-242 in U.S. Provisional Patent Application No. 60/117,405 are identical to SEQ ID NOs: 82-242 of the present application with the following exceptions. SEQ ID NO: 148 in the present application is the complementary strand of SEQ ID NO: 148 in U.S. Provisional Patent Application No. 60/117,405. Accordingly, the protein of SEQ ID NO: 308 which is encoded by SEQ ID NO: 148 has also been revised. SEQ ID NO: 163 in the present application is the complementary strand of SEQ ID NO: 163 in U.S. Provisional Patent Application No. 60/117,405. Accordingly, the protein of SEQ ID NO: 323 which is encoded by SEQ ID NO: 163 has also been revised.

The target gene of SEQ ID NOs. 18 and 19 of U.S. Provisional Patent Application No. 60/117,405 (SEQ ID NOs. 18, 19, 422, 423 of the present application) has been revised from *dicF* to *ftsZ* to reflect the fact that these SEQ ID NOs. include natural antisense molecules which inhibit *ftsZ* expression.

The gene products of the nucleic acids of SEQ ID NOs. 198 and 239-242 in U.S. Provisional Patent Application No. 60/117,405 and in the present application (SEQ ID NOs. 358 and 399-402 of the present application) have been revised to reflect the fact that these nucleic acids encode nontranslated tRNAs and rRNAs. Tables I and II have been revised accordingly. The SEQ ID NOs. in Table II were also revised to reflect the fact that SEQ ID NOs: 89 and 402 were identical in U.S. Provisional Patent Application No. 60/117,405.

TABLE I

Identified Clones with Corresponding Genes and Operons

| SEQ ID NO. | Molecule No. | Gene (NCBI)       | Gene (Blattner)   | Gene (Rudd)       | CONTIG   |
|------------|--------------|-------------------|-------------------|-------------------|----------|
| 1, 405     | EcXA001      | <i>yhhQ</i>       | <i>b3471</i>      | <i>yhhQ</i>       | AE000423 |
| 2, 406     | EcXA002      | <i>lepB</i>       | <i>lepB</i>       | <i>lepB</i>       | AE000343 |
| 3, 407     | EcXA003      | <i>f586</i>       | <i>b0955</i>      | <i>ycbZ</i>       | AE000197 |
| 4, 408     | EcXA004      | <i>rpsG, rpsL</i> | <i>b3341</i>      | <i>rpsG, rpsL</i> | AE000410 |
| 5, 409     | EcXA005a     | <i>rplL, rplJ</i> | <i>b3986</i>      | <i>rplL, rplJ</i> | AE000472 |
| 6, 410     | EcXA005b     | <i>rplL</i>       | <i>rplL</i>       | <i>rplL</i>       | AE000472 |
| 7, 411     | EcXA005c     | <i>rplL, rplJ</i> | <i>rplL, rplJ</i> | <i>rplL, rplJ</i> | AE000472 |
| 8, 412     | EcXA005d     | <i>rplL, rplJ</i> | <i>rplL, rplJ</i> | <i>rplL, rplJ</i> | AE000472 |
| 9, 413     | EcXA005e     | <i>rplL</i>       | <i>rplL</i>       | <i>rplL</i>       | AE000472 |

| SEQ ID NO. | Molecule No.             | Gene (NCBI)       | Gene (Blattner)     | Gene (Rudd)         | CONTIG   |
|------------|--------------------------|-------------------|---------------------|---------------------|----------|
| 10, 414    | EcXA005f                 | <i>rplL</i>       | <i>rplL</i>         | <i>rplL</i>         | AE000472 |
| 11, 415    | EcXA005g                 | <i>rplL</i>       | <i>rplL</i>         | <i>rplL</i>         | AE000472 |
| 12, 416    | EcXA006                  | <i>pta</i>        | <i>b2297</i>        | <i>pta</i>          | AE000319 |
| 13, 417    | EcXA007                  | <i>yicP</i>       | <i>b3666</i>        | <i>yicP</i>         | AE000444 |
| 14, 418    | EcXA008a                 | <i>yhaU</i>       | <i>b3127</i>        | <i>yhaU</i>         | AE000394 |
| 15, 419    | EcXA008b                 | <i>yhaU</i>       | <i>yhaU</i>         | <i>yhaU</i>         | AE000394 |
| 16, 420    | EcXA008c                 | <i>yhaU</i>       | <i>yhaU</i>         | <i>yhaU</i>         | AE000394 |
| 17, 421    | EcXA009                  | <i>ydeY</i>       | <i>ydeY</i>         | <i>ydeY</i>         | AE000249 |
| 18, 422    | EcXA010a<br>(natural as) | <i>dicF</i>       | <i>b1575</i>        | <i>dicF</i>         | AE000253 |
| 19, 423    | EcXA010b                 | <i>dicF</i>       | <i>dicF</i>         | <i>dicF</i>         | AE000253 |
| 20, 424    | EcXA011                  | <i>fdnG</i>       | <i>b1474</i>        | <i>fdnG</i>         | AE000244 |
| 21, 425    | EcXA012a                 | <i>fusA</i>       | <i>b3340</i>        | <i>fusA</i>         | AE000410 |
| 22, 426    | EcXA012b                 | <i>fusA</i>       | <i>fusA</i>         | <i>fusA</i>         | AE000410 |
| 23, 427    | EcXA012c                 | <i>fusA</i>       | <i>fusA</i>         | <i>fusA</i>         | AE000410 |
| 24, 428    | EcXA013a                 | <i>o86</i>        | <i>b2562</i>        | <i>yfhL</i>         | AE000342 |
| 25, 429    | EcXA013b                 | <i>o86</i>        | <i>b2562</i>        | <i>yfhL</i>         | AE000342 |
| 26, 430    | EcXA013c                 | <i>o86</i>        | <i>b2562</i>        | <i>yfhL</i>         | AE000342 |
| 27, 431    | EcXA014                  | <i>visC</i>       | <i>b2906</i>        | <i>visC</i>         | AE000374 |
| 28, 432    | EcXA015                  | <i>yfdI</i>       | <i>yfdI</i>         | <i>yfdI</i>         | AE000323 |
| 29, 433    | EcXA016                  | <i>yeaQ</i>       | <i>yeaQ</i>         | <i>yeaQ</i>         | AE000274 |
|            |                          | <i>yeaG</i>       | <i>yeaG</i>         | <i>yeaG</i>         |          |
| 30, 434    | EcXA017a                 | <i>yggE</i>       | <i>b2922</i>        | <i>yggE</i>         | AE000375 |
| 31, 435    | EcXA017b                 | <i>yggE</i>       | <i>yggE</i>         | <i>yggE</i>         | AE000375 |
| 32, 436    | EcXA018a                 | <i>o464</i>       | <i>b2074</i>        | <i>yegM</i>         | AE000297 |
| 33, 437    | EcXA018b                 | <i>o464</i>       | <i>b2074</i>        | <i>yegM</i>         | AE000297 |
| 34, 438    | EcXA019a                 | <i>yehA</i>       | <i>yehA</i>         | <i>yehA</i>         | AE000300 |
|            |                          |                   |                     |                     | AE000299 |
| 35, 439    | EcXA019b                 | <i>o172, yehA</i> | <i>o172, yehA</i>   | <i>o172, yehA</i>   | AE000298 |
| 36, 440    | EcXA020                  | <i>o384, f82</i>  | <i>b1794, b1795</i> | <i>yeaP, yeaQ</i>   | AE000274 |
| 37, 441    | EcXA021a                 | <i>f112</i>       | <i>b0218</i>        | <i>yafU</i>         | AE000130 |
| 38, 442    | EcXA021b                 | <i>f112</i>       | <i>b0218</i>        | <i>yafU</i>         | AE000130 |
| 39, 443    | EcXA022                  | <i>o740</i>       | <i>b1629</i>        | <i>ydgN</i>         | AE000258 |
| 40, 444    | EcXA023a                 | <i>f176, f382</i> | <i>b1504, b1505</i> | <i>ydeS, ydeT</i>   | AE000247 |
| 41, 445    | EcXA023b                 | <i>f176, f382</i> | <i>b1504, b1505</i> | <i>ydeS, ydeT</i>   | AE000247 |
| 42, 446    | EcXA024                  | <i>ygiM, ygiN</i> | <i>b3082</i>        | <i>ygiM, ygiN</i>   | AE000390 |
| 43, 447    | EcXA025                  | <i>02383</i>      | <i>b1878</i>        | <i>yeaJ</i>         | AE000289 |
| 44, 448    | EcXA026                  | <i>o61</i>        | <i>Unpre-dicted</i> | <i>Unpre-dicted</i> | AE000138 |
| 45, 449    | EcXA027a                 | <i>yohH</i>       | <i>yohH</i>         | <i>yohH</i>         | AE000303 |
| 46, 450    | EcXA027b                 | <i>yohH</i>       | <i>yohH</i>         | <i>yohH</i>         | AE000303 |
| 47, 451    | EcXA027c                 | <i>yohH</i>       | <i>yohH</i>         | <i>yohH</i>         | AE000303 |
|            |                          | <i>yohI</i>       | <i>yohI</i>         | <i>yohI</i>         |          |
| 48, 452    | EcXA027d                 | <i>yohH</i>       | <i>yohH</i>         | <i>yohH</i>         | AE000303 |
| 49, 453    | EcXA028                  | <i>f296</i>       | <i>b2305</i>        | <i>yfcI</i>         | AE000319 |
| 50, 454    | EcXA029                  | <i>yjiK</i>       | <i>b4391</i>        | <i>yjiK</i>         | AE000509 |
| 51, 455    | EcXA030                  | <i>vi5A</i>       | <i>b3557</i>        | <i>vi5A</i>         | AE000433 |
| 52, 456    | EcXA031                  | <i>rplE</i>       | <i>B3308</i>        | <i>rplE</i>         | AE000408 |
| 53, 457    | EcXA032a                 | <i>ybgD</i>       | <i>ybgD</i>         | <i>ybgD</i>         | AE000175 |
| 54, 458    | EcXA032b**               | <i>ybgD</i>       | <i>ybgD</i>         | <i>ybgD</i>         | AE000175 |

| SEQ ID NO. | Molecule No. | Gene (NCBI)       | Gene (Blattner)   | Gene (Rudd)       | CONTIG   |
|------------|--------------|-------------------|-------------------|-------------------|----------|
|            |              | <i>gltA</i>       | <i>gltA</i>       | <i>gltA</i>       |          |
| 55,459     | EcXA033a     | <i>f477 (as)</i>  | <i>b3052</i>      | <i>waaE</i>       | AE000387 |
|            |              |                   |                   |                   | AE000386 |
| 56,460     | EcXA033b     | <i>f477</i>       | <i>b3052</i>      | <i>waaE</i>       | AE000387 |
| 57,461     | EcXA034a     | <i>cspA</i>       | <i>b3556</i>      | <i>cspA</i>       | AE000433 |
| 58,462     | EcXA034b     | <i>cspA</i>       | <i>b3556</i>      | <i>cspA</i>       | AE000433 |
| 59,463     | EcXA035      | <i>yhjU</i>       | <i>yhjU</i>       | <i>yhjU</i>       | AE000431 |
| 60,464     | EcXA036      | <i>yqiF</i>       | <i>b3101</i>      | <i>yqiF</i>       | AE000392 |
|            |              | <i>o99</i>        | <i>b3100</i>      | <i>yqiK</i>       |          |
| 61,465     | EcXA037      | <i>ydeH</i>       | <i>b1535</i>      | <i>ydeH</i>       | AE000251 |
| 62,466     | EcXA038      | <i>sieB</i>       | <i>b1353</i>      | <i>sieB</i>       | AE000233 |
| 63,467     | EcXA039      | <i>ybbD</i>       |                   | <i>ybbD</i>       | AE000156 |
| 64,468     | EcXA040      | <i>insB 6</i>     | <i>b3445</i>      | <i>insB 6</i>     | AE000420 |
| 65,469     | EcXA041      | <i>f234</i>       | <i>b1138</i>      | <i>ymfE</i>       | AE000214 |
| 66,470     | EcXA042a     | <i>rplY</i>       | <i>rplY</i>       | <i>rplY</i>       | AE000308 |
| 67,471     | EcXA042b     | <i>rplY</i>       | <i>rplY</i>       | <i>rplY</i>       | AE000308 |
| 68,472     | EcXA043      | <i>ybgB</i>       | <i>ybgB</i>       | <i>ybgB</i>       | AE000176 |
|            |              | <i>cydA</i>       | <i>cydA</i>       | <i>cydA</i>       |          |
| 69,473     | EcXA044      | <i>purB</i>       | <i>b1131</i>      | <i>purB</i>       | AE000213 |
| 70,474     | EcXA045**    | <i>csrA</i>       | <i>csrA</i>       | <i>csrA</i>       | AE000353 |
|            |              | <i>serV</i>       | <i>serV</i>       | <i>serV</i>       |          |
| 71,475     | EcXA046**    | <i>fimE, fimA</i> | <i>b4313</i>      | <i>fimE, fimA</i> | AE000502 |
| 72,476     | EcXA047**    | <i>f96, cspB</i>  | <i>f96, cspB</i>  | <i>cspB, ydIS</i> | AE000252 |
| 73,477     | EcXA048      | <i>yefE</i>       | <i>yefE</i>       | <i>yefE</i>       | AE000294 |
| 74,478     | EcXA049      | <i>yaiC</i>       | <i>b0385</i>      | <i>yaiC</i>       | AE000145 |
| 75,479     | EcXA050      | <i>o467, o222</i> | <i>yaiU, yaiV</i> | <i>yaiU, yaiV</i> | AE000144 |
| 76,480     | EcXA051a     | <i>rplB, rplW</i> | <i>rplB, rplW</i> | <i>rplB, rplW</i> | AE000408 |
| 77,481     | EcXA051b     | <i>rplW</i>       | <i>rplW</i>       | <i>rplW</i>       | AE000408 |
| 78,482     | EcXA052      | <i>infC</i>       | <i>infC</i>       | <i>infC</i>       | AE000267 |
|            |              |                   |                   |                   | AE000266 |
| 79,483     | EcXA053      | <i>gor</i>        | <i>gor</i>        | <i>gor</i>        | AE000426 |
| 80,484     | EcXA054      | <i>rplF</i>       | <i>rplF</i>       | <i>rplF</i>       | AE000408 |
| 81,485     | EcXA055      | <i>rrlG</i>       | <i>rrlG</i>       | <i>rrlG</i>       | AE000345 |

## EXAMPLE 4

Identification of Genes and their Corresponding Operons Affected by Antisense Inhibition

The sequencing of the entire *E. coli* genome is described in Blattner et al., Science 277:1453-1474(1997) the entirety of which is hereby incorporated by reference and the sequence of the genome is listed in GenBank Accession No.U00096, the disclosure of which is incorporated herein by reference in its entirety. The operons to which the proliferation-inhibiting nucleic acids correspond were identified using RegulonDB and information in the literature. The coordinates of the boundaries of these operons on the *E. coli* genome are listed in Table III. Table II lists the molecule numbers of the inserts containing the growth inhibiting nucleic acid fragments, the genes in the operons corresponding to the inserts, the SEQ ID NOs of the genes containing the inserts, the SEQ ID NOs of the proteins encoded by the genes, the start and stop points of the genes on the *E. coli* genome, the orientation of the genes on the genome, whether the operons



are predicted or documented, and the predicted functions of the genes. The identified operons, their putative functions, and whether or not the genes are presently thought to be required for proliferation are discussed below.

Functions for the identified genes were determined by using either Blattner functional class designations or by comparing identified sequence with known sequences in various databases. A variety of biological functions were noted for the genes to which the clones of the present invention correspond. The functions for the genes of interest appear in Table II.

The proteins that are listed in Table II are involved in a wide range of biological functions.

TABLE II  
All Operon Data with Whole Chromosome Coordinates

| GeneSeq ID No. | Gene Prod. Seq ID No. | Mole. No.  | Genes On Operon | Left Coordinate | Right Coordinate | Predicted (P) Or Documented (D) Operon | Blattner functional class of encoded proteins | Predicted functional class of encoded proteins                                 |
|----------------|-----------------------|------------|-----------------|-----------------|------------------|--|---|--|
| 82             | 243                   | EcXA001    | <i>phd</i>      | 3606848         | 3607513          | (P)                                    | Hypothetical ORF, unclassified, unknown       | Hypothetical outer membrane protein  |
| 83             | 244                   |            | <i>dcrB</i>     | 3607532         | 3608143          |  | Hypothetical ORF, unclassified, unknown       | Resistance to phage C1; periplasmic protein perhaps anchored to inner membrane |
| 84             | 245                   | EcXA002    | <i>lepB</i>     | 2702355         | 2703329          | (P)                                    | Transport and binding proteins                | Secretion  |
| 85             | 246                   | EcXA003    | <i>ycbZ</i>     | 1015762         | 1017522          | (P)                                    | Unknown                                       | Protease   |
| 86             | 247                   | EcXA004    | <i>tufA</i>     | 3467782         | 3468966          | (D)                                    | Translation, post-translational modification  | Translation (Elongation factor Tu)   |
| 87             | 248                   |            | <i>fusA</i>     | 3469037         | 3471151          |  | Translation, post-translational modification  | Translation (elongation factor efp)  |
| 88             | 249                   |            | <i>rpsG</i>     | 3471179         | 3471718          |  | Translation, post-translational modification  | Translation  |
| 89             | 402                   | EcXA055    | <i>rpsG</i>     | 2727636         | 2729178          |  | Translation, post-translational modification  | Translation (rRNA)   |
| 90             | 250                   |            | <i>rpsL</i>     | 3471815         | 3471815          |  | Translation, post-translational modification  | Translation  |
| 91             | 251                   | EcXA005a-g | <i>rplJ</i>     | 4177574         | 4178071          | (D)                                    | Translation, post-translational modification  | Translation  |
| 92             | 252                   |            | <i>rplL</i>     | 4178138         | 4178503          |  | Translation, post-translational modification  | Translation  |
| 93             | 253                   | EcXA006    | <i>pta</i>      | 2412767         | 2414911          | (P)                                    | Carbon compound catabolism                    | Carbon compound catabolism   |
| 94             | 254                   | EcXA007    | <i>yicP</i>     | 3841591         | 3843357          | (P)                                    | Hypothetical ORF, unclassified, unknown       | Probable adenine deaminase   |

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|----------------|-----------------------|-------------|------------------------|-----------------|------------------|--|---|--|
| 95             | 255                   | EcXA008a-c  | <i>yhaD</i>            | 3268266         | 3269492          | (P)                                    | Hypothetical ORF, unclassified, unknown       |  |
| 96             | 256                   |             | <i>yhaE</i>            | 3269508         | 3270407          |  | Putative enzymes                              |  |
| 97             | 257                   |             | <i>yhaF</i>            | 3270428         | 3271198          |  | Hypothetical ORF, unclassified, unknown       |  |
| 98             | 258                   |             | <i>yhaU</i>            | 3271214         | 3272548          |  | Carbon compound catabolism                    | Probable integral membrane protein Phthalate permease family |
| 99             | 259                   | EcXA009     | <i>ydeX</i>            | 1599514         | 1601049          | (P)                                    | Putative transport proteins                   |  |
| 100            | 260                   |             | <i>ydeY</i>            | 1601043         | 1602071          |  | Putative transport proteins                   | Putative ABC transporter                                     |
| 101            | 261                   |             | <i>ydeZ</i>            | 1602071         | 1603063          |  | Hypothetical ORF, unclassified, unknown       |  |
| 102            | 262                   |             | <i>yneA</i>            | 1603075         | 1604097          |  | Hypothetical ORF, unclassified, unknown       |  |
| 103            | 263                   |             | <i>yneB</i>            | 1604124         | 1604999          |  | Hypothetical ORF, unclassified, unknown       |  |
| 104            | 264                   |             | <i>yneC</i>            | 1605023         | 1605313          |  | Hypothetical ORF, unclassified, unknown       |  |
| 105            | 265                   | EcXA010a-b  | <i>ftsZ</i>            | 1053305         | 106456           | (P)                                    | Cell processes (incl. Adaptation, protection) | Regulator of cell division                                   |
| 106            | 266                   | EcXA011     | <i>fahG</i>            | 1545425         | 1548472          | (D)                                    | Energy metabolism                             | Anaerobic respiration (formate dehydrogenase)                |
| 107            | 267                   |             | <i>fahH</i>            | 1548485         | 1549369          |  | Energy metabolism                             |  |
| 108            | 268                   | EcXA 012a-c | <i>fahI</i>            | 1549362         | 1550015          |  | Energy metabolism                             |  |
|                |                       |             | Same operon as EcXA004 |                 |                  |  |   |  |
| 109            | 269                   | EcXA013a-c  | <i>yhlZ</i>            | 2697683         | 2697943          | (P)                                    | Hypothetical ORF, unclassified, unknown       | No homologues, no motifs                                     |
| 110            | 270                   | EcXA014     | <i>visC</i>            | 3049135         | 3050337          | (P)                                    | Hypothetical ORF, unclassified, unknown       | Ubiquinone synthesis   |

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|----------------|-----------------------|------------|-----------------|-----------------|------------------|---------------------------------|---|--|
| 111            | 271                   |            | <i>ubiH</i>     | 3050360         | 3051538          | Operon                          | Biosynthesis of cofactors, prosthetic groups and carriers |  |
| 112            | 272                   |            | <i>pepP</i>     | 3051535         | 3052860          |                                 | Translation, post-translational modification              |  |
| 113            | 273                   |            | <i>ygIB</i>     | 3052886         | 3053470          |                                 | Hypothetical ORF, unclassified, unknown                   |  |
| 114            | 274                   | EcXA015    | <i>ydgG</i>     | 2465875         | 2466237          | (P)                             | Hypothetical ORF, unclassified, unknown                   |  |
| 115            | 275                   |            | <i>ydhH</i>     | 2466234         | 2467154          |                                 | Cell structure  | Putative membrane protein                            |
| 116            | 276                   |            | <i>ydl</i>      | 2467151         | 2468482          |                                 | Hypothetical ORF, unclassified, unknown                   |  |
| 117            | 277                   | EcXA016    | <i>yeaQ</i>     | 1877031         | 1877279          | (P)                             | Hypothetical ORF, unclassified, unknown                   | Homologue to transglycosylase associated protein     |
| 118            | 278                   |            | <i>yeaG</i>     | 1877427         | 1877609          | (P)                             | Hypothetical ORF, unclassified, unknown                   | No homologues  |
| 119            | 279                   |            | <i>yeaR</i>     | 1877613         | 1877972          |                                 | Hypothetical ORF, unclassified, unknown                   |  |
| 120            | 280                   | EcXA017a-b | <i>yggE</i>     | 3065360         | 3066100          | (P)                             | Structural proteins                                       | Homologues in multiple bacteria, no motifs           |
| 121            | 281                   | EcXA018a-b | <i>pegM</i>     | 2151891         | 2153285          | (P)                             | Putative transport proteins                               | Transport (multiple transferable resistance)         |
| 122            | 282                   |            | <i>yegU</i>     | 2153285         | 2156407          |                                 | Hypothetical ORF, unclassified, unknown                   |  |
| 123            | 283                   |            | <i>yegO</i>     | 2156408         | 2159485          |                                 | Hypothetical ORF, unclassified, unknown                   |  |
| 124            | 284                   |            | <i>yegB</i>     | 2159486         | 2160901          |                                 | Putative transport proteins                               |  |
| 125            | 285                   | EcXA019a-b | <i>yebA</i>     | 2185400         | 2186434          | (P)                             | Cell structure  | Weak homology to pilin precursor from <i>H. Inf.</i> |

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|----------------|-----------------------|------------|---|-----------------|------------------|--|---|---|
| 126            | 286                   |            | <i>yehB</i>                             | 2186450         | 2188930          |  | Hypothetical ORF, unclassified, unknown Putative chaperones |   |
| 127            | 287                   |            | <i>yehC</i>                             | 2188946         | 2189665          |  |   |   |
| 128            | 288                   |            | <i>yehD</i>                             | 2189700         | 2190242          |  | Cell structure  |   |
|                |                       | EcXA020    | Same operon as EcXA016 (one of the two) |                 |                  |  |   |   |
| 129            | 289                   | EcXA021a-b | <i>patU</i>                             | 238746          | 239084           | (P)                                    | Hypothetical ORF, unclassified, unknown                     | Homologues in <i>H. Inf.</i> and <i>S. Pombe.</i> , no motifs, transmembrane region present |
| 130            | 290                   | EcXA022    | <i>ydgL</i>                             | 1703781         | 1704372          | (P)                                    | Hypothetical ORF, unclassified, unknown                     |   |
| 131            | 291                   |            | <i>ydgM</i>                             | 1704372         | 1704950          |  | Hypothetical ORF, unclassified, unknown                     |   |
| 132            | 292                   |            | <i>ydgN</i>                             | 1704943         | 1707165          |  | Hypothetical ORF, unclassified, unknown                     |   |
| 133            | 293                   |            | <i>ydgO</i>                             | 1707166         | 1708224          |  | Hypothetical ORF, unclassified, unknown                     |   |
| 134            | 294                   |            | <i>ydgP</i>                             | 1708228         | 1708848          |  | Hypothetical ORF, unclassified, unknown                     |   |
| 135            | 295                   |            | <i>ydgQ</i>                             | 1708852         | 1709547          |  | Hypothetical ORF, unclassified, unknown                     |   |
| 136            | 296                   |            | <i>nth</i>                              | 1709547         | 1710182          |  | Transcription, RNA processing and degradation               |   |
| 137            | 297                   | EcXA023a-b | <i>ydeR</i>                             | 1585817         | 1586320          | (P)                                    | Hypothetical ORF, unclassified, unknown                     |   |
| 138            | 298                   |            | <i>ydeS</i>                             | 1586333         | 1586863          |  | Hypothetical ORF, unclassified, unknown                     | fim1-like   |

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|----------------|-----------------------|------------|-----------------|-----------------|------------------|--|---|--|
| 139            | 299                   |            | <i>ydeT</i>     | 1586877         | 1586025          |  | Structural proteins                           | fim-like   |
| 140            | 300                   | EcXA024    | <i>ygiM</i>     | 3231359         | 3231785          | (P)                                    | Hypothetical ORF, unclassified, unknown       | Weak homology to long chain fatty acid coa ligase in <i>Archaeoglobus</i>  |
| 141            | 301                   |            | <i>ygiN</i>     | 3231782         | 3232096          |  | Hypothetical ORF, unclassified, unknown       | Homologues in various bacteria   |
| 142            | 302                   | EcXA025    | <i>yeaJ</i>     | 2042885         | 2050036          | (P)                                    | Hypothetical ORF, unclassified, unknown       | Strong similarity to numerous attaching and effacing proteins and invasins |
| 143            | 303                   | EcXA026    | <i>raeA</i>     | 331001          | 331184           | unpredicted                            |   | nif-like   |
| 144            | 304                   | EcXA027a-d | <i>yohG</i>     | 2225343         | 2226539          | (P)                                    | Putative transport proteins                   |  |
| 145            | 305                   |            | <i>yohH</i>     | 2226569         | 2226859          |  | Hypothetical ORF, unclassified, unknown       | Xylose binding protein-like  |
| 146            | 306                   |            | <i>yohI</i>     | 2227458         | 2228405          | (P)                                    | Putative regulatory protein                   |  |
| 147            | 307                   | EcXA028    | <i>ycfI</i>     | 2420669         | 2421559          | (P)                                    | Hypothetical ORF, unclassified, unknown       | Similar to <i>S. Typhi</i> histidine transport gene                        |
| 148            | 308                   | EcXA029    | <i>yjiK</i>     | 4626424         | 4628091          | (P)                                    | Hypothetical ORF, unclassified, unknown       | Similar to ABC transporter   |
| 149            | 309                   | EcXA030    | <i>yisA</i>     | 3718309         | 3718830          | (P)                                    | Hypothetical ORF, unclassified, unknown       | IS150 ori A  |
| 150            | 310                   |            | <i>yisB</i>     | 3718827         | 3719678          |  | Phage, transposon, or plasmid                 |  |
| 151            | 311                   | EcXA031    | <i>rpmJ</i>     | 3402555         | 3440371          | (D)                                    | Translation, post-translational modification  |  |
| 152            | 312                   |            | <i>pilA</i>     | 3440403         | 3441734          |  | Putative transport proteins                   |  |
| 153            | 313                   |            | <i>rpmO</i>     | 3441742         | 3442176          |  | Translation, post-translational modification  |  |

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|----------------|-----------------------|------------|-----------------|-----------------|------------------|--|---|---|
| 154            | 314                   |            | <i>rpmD</i>     | 3442180         | 3442359          |  | Translation, post-translational modification  |   |
| 155            | 315                   |            | <i>rpsE</i>     | 3442363         | 3442866          |  | Translation, post-translational modification  |   |
| 156            | 316                   |            | <i>rplR</i>     | 3442881         | 3443234          |  | Translation, post-translational modification  |   |
| 157            | 317                   |            | <i>rplF</i>     | 3443244         | 3443777          |  | Translation, post-translational modification  | Translation   |
| 158            | 318                   |            | <i>rpsH</i>     | 3443780         | 3444182          |  | Translation, post-translational modification  |   |
| 159            | 319                   |            | <i>rpsN</i>     | 3444216         | 3444521          |  | Translation, post-translational modification  |   |
| 160            | 320                   |            | <i>rplE</i>     | 3444536         | 3445075          |  | Translation, post-translational modification  | Translation   |
| 161            | 321                   |            | <i>rplX</i>     | 3445090         | 3445404          |  | Translation, post-translational modification  |   |
| 162            | 322                   |            | <i>rplN</i>     | 3445415         | 3445786          |  | Translation, post-translational modification  |   |
| 163            | 323                   | EcXA032a-b | <i>yhgD</i>     | 751452          | 752018           | (P)                                    | translational modification                    | Hypothetical fibrillar protein  |
| 164            | 324                   |            | <i>gltA</i>     | 752408          | 753691           | (D)                                    | Cell processes (incl. Adaptation, protection) |   |
| 165            | 325                   | EcXA033a-b | <i>waaE</i>     | 3192961         | 3194394          | (P)                                    | Energy metabolism<br>Putative enzymes         | Glutamine biosynthesis<br>ADP heptose synthase/<br>autotrophic growth protein |
| 166            | 326                   |            | <i>glnE</i>     | 3194442         | 3197262          |  | Translation, post-translational modification  |   |
| 167            | 327                   |            | <i>ygiF</i>     | 3197305         | 3198608          |  | Hypothetical ORF, unclassified, unknown       |   |
| 168            | 328                   | EcXA034a-b | <i>cspA</i>     | 3717678         | 3717890          | (P)                                    | Cell processes (incl. Adaptation, protection) | RNA chaperonin  |
| 169            | 329                   | EcXA035    | <i>ygiS</i>     | 3694087         | 3695658          | (P)                                    | Translation, post-translational modification  |   |

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|----------------|-----------------------|-----------|---------------------|-----------------|------------------|--|---|--|
| 170            | 330                   |           | <i>yhjT</i>         | 3695658         | 3695846          |  | Hypothetical ORF, unclassified, unknown       |  |
| 171            | 331                   |           | <i>yhjU</i>         | 3695843         | 3697522          |  | Hypothetical ORF, unclassified, unknown       | Regions similar to dehydrogenases, nucleases etc.                |
| 172            | 332                   | EcXA036   | <i>yqjC</i>         | 3246594         | 3246977          | (P)                                    | Hypothetical ORF, unclassified, unknown       |  |
| 173            | 333                   |           | <i>yqjD</i>         | 3247015         | 3247320          |  | Hypothetical ORF, unclassified, unknown       |  |
| 174            | 334                   |           | <i>yqjE</i>         | 3247323         | 3247727          |  | Hypothetical ORF, unclassified, unknown       |  |
| 175            | 335                   |           | <i>yqjK</i>         | 3247717         | 3248016          |  | Similar to mukB from H. Inf.                  |  |
| 176            | 336                   |           | <i>yqjF</i>         | 3248112         | 3248594          | (P)                                    | Hypothetical ORF, unclassified, unknown       | Homologues in many bacteria, blocks: secretion/ATP synthase/lfts |
| 177            | 337                   | EcXA037   | <i>ydeH</i>         | 1620984         | 1621874          | (P)                                    | Hypothetical ORF, unclassified, unknown       | Similar to carbonyl-kinase, oxidase, symporters                  |
| 178            | 338                   | EcXA038   | <i>sieB</i>         | 1416572         | 1417183          | (P)                                    | Phage, transposon, or plasmid                 | Super-infection exclusion factor B-like                          |
| 179            | 339                   |           | <i>rajB (b1354)</i> | 1417192         | 1417368          |  | Hypothetical ORF, unclassified, unknown       |  |
| 180            | 340                   | EcXA039   | <i>thsD</i>         | 522485          | 526765           | (P)                                    | Hypothetical ORF, unclassified, unknown       |  |
| 181            | 341                   |           | <i>ybbC</i>         | 526805          | 527173           |  | Hypothetical ORF, unclassified, unknown       |  |
| 182            | 342                   |           | <i>ybbH</i>         | 527173          | 527883           |  | Hypothetical ORF, unclassified, unknown       | Rhs-like element   |
| 183            | 343                   |           | <i>ybbD</i>         | 527864          | 528124           |  | Hypothetical ORF, unclassified, unknown       | ATP synthase, desaturase   |



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|----------------|-----------------------|------------|-----------------|-----------------|------------------|---------------------------------|---|--|
| 184            | 344                   |            | <i>ybl</i>      | 528163          | 528354           | Operon                          | Hypothetical ORF, unclassified, unknown       |  |
| 185            | 345                   | EcXA040    | <i>insB_6</i>   | 351114          | 351389           | (P)                             | Phage, transposon, or plasmid                 |  |
| 186            | 346                   |            | <i>insA</i>     | 351308          | 3581811          |                                 | Phage, transposon, or plasmid                 |  |
| 187            | 347                   |            | <i>yrbA</i>     | 3580669         | 3581065          |                                 | Hypothetical ORF, unclassified, unknown       |  |
| 188            | 348                   |            | <i>yhbZ</i>     | 3579494         | 3580672          |                                 | Hypothetical ORF, unclassified, unknown       |  |
| 189            | 349                   | EcXA041    | <i>ymiD</i>     | 1196090         | 1196755          | (P)                             | Hypothetical ORF, unclassified, unknown       | No assigned role                               |
| 190            | 350                   |            | <i>ymiE</i>     | 1196756         | 1197460          |                                 | Hypothetical ORF, unclassified, unknown       | No assigned role                               |
| 191            | 351                   | EcXA042a-b | <i>rplY</i>     | 2280537         | 2280821          | (P)                             | Translation, post-translational modification  | Translation                                    |
| 192            | 352                   | EcXA043    | <i>hrsA</i>     | 765207          | 767183           | (P)                             | Translation, post-translational modification  |  |
| 193            | 353                   |            | <i>ybgB</i>     | 767201          | 769834           |                                 | Carbon compound catabolism                    | Unknown  |
| 194            | 354                   |            | <i>cydA</i>     | 770678          | 772249           | (D)                             | Energy metabolism                             | Cytochrome D oxidase                           |
| 195            | 355                   |            | <i>cydB</i>     | 772265          | 773404           |                                 | Energy metabolism                             |  |
| 196            | 356                   | EcXA044    | <i>purB</i>     | 1188839         | 1191209          | (D)                             | Nucleotide biosynthesis and metabolism        | Purine biosynthesis                            |
| 197            | 357                   | EcXA045    | <i>csrA</i>     | 2816983         | 2817168          | (P)                             | Regulatory function                           | Carbon storage regulator (mRNA decay factor)   |
| 198            | 358                   |            | <i>serV</i>     | 2816575         | 2816667          | Unpredicted                     | Translation, post-translational modification  | Translation (tRNA)                             |
| 199            | 359                   | EcXA046    | <i>fimB</i>     | 4538525         | 4539127          | (D)                             | Cell structure                                |  |
| 200            | 360                   |            | <i>fimE</i>     | 4539605         | 4540201          |                                 | Cell structure                                | Fimbriae                                       |
| 201            | 361                   |            | <i>fimA</i>     | 4540683         | 4541231          |                                 | Cell structure                                | Regulator of inversion                         |

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|----------------|-----------------------|-----------|-----------------|-----------------|------------------|--|---|--|
| 202            | 362                   |           | <i>fimI</i>     | 4541188         | 4541835          |  | Cell structure                                |  |
| 203            | 363                   |           | <i>fimC</i>     | 4541872         | 4542597          |  | Cell structure                                |  |
| 204            | 364                   |           | <i>fimD</i>     | 4542665         | 4545301          |  | Cell structure                                |  |
| 205            | 365                   |           | <i>fimF</i>     | 4545311         | 4545841          |  | Cell structure                                |  |
| 206            | 366                   |           | <i>fimG</i>     | 4545854         | 4546357          |  | Cell structure                                |  |
| 207            | 367                   |           | <i>fimH</i>     | 4546377         | 4547279          |  | Cell structure                                |  |
| 208            | 368                   | EcXA047   | <i>ydiP</i>     | 1637054         | 1638684          | (P)                                    | Hypothetical ORF, unclassified, unknown       |  |
| 209            | 369                   |           | <i>ydiQ</i>     | 1637548         | 1638081          |  | Hypothetical ORF, unclassified, unknown       |  |
| 210            | 370                   |           | <i>ydiR</i>     | 1638078         | 1638389          |  | Hypothetical ORF, unclassified, unknown       |  |
| 211            | 371                   |           | <i>ydiS</i>     | 1638394         | 1638684          |  | Hypothetical ORF, unclassified, unknown       | Lysis protein                                  |
| 212            | 372                   |           | <i>cspB</i>     | 1639363         | 1639578          | (P)                                    | Cell processes (incl. Adaptation, protection) |  |
| 213            | 373                   | EcXA048   | <i>yisZ_7</i>   | 2099917         | 2100933          | (P)                                    | Phage, transposon, or plasmid                 |  |
| 214            | 374                   |           | <i>yefJ</i>     | 2100938         | 2101411          |  | Putative enzymes                              |  |
| 215            | 375                   |           | <i>yefI</i>     | 2101413         | 2102531          |  | Hypothetical ORF, unclassified, unknown       |  |
| 216            | 376                   |           | <i>yefH</i>     | 2102516         | 2103106          |  | Putative enzymes                              |  |
| 217            | 377                   |           | <i>yefG</i>     | 2103087         | 2104079          |  | Hypothetical ORF, unclassified, unknown       |  |
| 218            | 378                   |           | <i>ric</i>      | 2104082         | 2105248          |  | Cell structure                                |  |
| 219            | 379                   |           | <i>yefE</i>     | 2105248         | 2106351          |  | Hypothetical ORF, unclassified, unknown       | UDP galacto-pyranase mutase                    |
| 220            | 380                   | EcXA049   | <i>yaiC</i>     | 402927          | 404042           | (P)                                    | Hypothetical ORF, unclassified, unknown       | Unknown  |
| 221            | 381                   | EcXA050   | <i>yaiU</i>     | 392239          | 393642           | (P)                                    | Putative enzymes                              | Putative auto-transporter                      |

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|----------------|-----------------------|------------|-----------------|-----------------|------------------|--|---|--|
| 222            | 382                   |            | <i>yanV</i>     | 393885          | 394353           |  | Hypothetical ORF, unclassified, unknown       | Hypothetical outer membrane protein            |
| 223            | 383                   | EcXA051a-b | <i>rpsQ</i>     | 3445951         | 3446205          | (D)                                    | Translation, post-translational modification  |  |
| 224            | 384                   |            | <i>rpmC</i>     | 3446205         | 3446396          |  | Translation, post-translational modification  |  |
| 225            | 385                   |            | <i>rplP</i>     | 3446396         | 3446806          |  | Translation, post-translational modification  |  |
| 226            | 386                   |            | <i>rpsC</i>     | 3446819         | 3447520          |  | Translation, post-translational modification  |  |
| 227            | 387                   |            | <i>rplV</i>     | 3447538         | 3447870          |  | Translation, post-translational modification  |  |
| 228            | 388                   |            | <i>rpsS</i>     | 3447885         | 3448163          |  | Translation, post-translational modification  |  |
| 229            | 389                   |            | <i>rplB</i>     | 3448180         | 3449001          |  | Translation, post-translational modification  | Translation                                    |
| 230            | 390                   |            | <i>rplW</i>     | 3449019         | 3449321          |  | Translation, post-translational modification  | Translation                                    |
| 231            | 391                   |            | <i>rplD</i>     | 3449318         | 3449923          |  | Translation, post-translational modification  |  |
| 232            | 392                   |            | <i>rplC</i>     | 3449934         | 3450563          |  | Translation, post-translational modification  |  |
| 233            | 393                   |            | <i>rpsJ</i>     | 3450596         | 3450907          |  | Translation, post-translational modification  |  |
| 234            | 394                   | EcXA052    | <i>rplT</i>     | 1797417         | 1797773          | (D)                                    | Translation, post-translational modification  |  |
| 235            | 395                   |            | <i>rpmI</i>     | 1797826         | 1798023          |  | Translation, post-translational modification  |  |
| 236            | 396                   |            | <i>infC</i>     | 1798120         | 1798662          |  | Translation, post-translational modification  | Translation                                    |

| GeneSeq ID No. | Gene Prod. Seq ID No. | Mole. No. | Genes On Operon        | Left Coordinate | Right Coordinate | Predicted (P) Or Documented (D) Operon | Blattner functional class of encoded proteins             | Predicted functional class of encoded proteins |
|----------------|-----------------------|-----------|------------------------|-----------------|------------------|--|---|--|
| 237            | 397                   |           | <i>thrS</i>            | 1798666         | 1800594          |  | Translation, post-translational modification              |  |
| 238            | 398                   | EcXA053   | <i>gor</i>             | 3643929         | 3645281          | (P)                                    | Biosynthesis of cofactors, prosthetic groups and carriers | Glutathione oxidoreductase                     |
|                |                       | EcXA054   | Same operon as EcXA031 |                 |                  |  |   |  |
| 239            | 399                   | EcXA055   | <i>mig</i>             | 2724301         | 2727204          | (D)                                    | Translation, post-translational modification              | Translation (rRNA)                             |
| 240            | 400                   |           | <i>mig</i>             | 2724089         | 2724208          |  | Translation, post-translational modification              | Translation (rRNA)                             |
| 241            | 401                   |           | <i>glfW</i>            | 2727389         | 2727464          |  | Translation, post-translational modification              | Translation (rRNA)                             |
| 242            | 402                   |           | <i>rrsG</i>            | 2727636         | 2729178          |  | Translation, post-translational modification              | Translation (rRNA)                             |

5 Several of the expression vectors contain fragments that correspond to genes of unknown function or if the function is known, it is not known whether the gene is essential. For example, EcXA001, 003, 007, 008, 013, 015, 016, 017, 018, 019, 020, 021, 022, 023, 024, 025, 026, 027, 028, 029, 030, 032, 033, 034, 035, 036, 037, 038, 039, 040, 041, 047, 048, 049 and 050 are all exogenous nucleic acid sequences that correspond to *E. coli* proteins that have no known function or  
10 5 where the function has not been shown to be essential or nonessential.

The present invention reports a number of novel *E. coli* genes and operons that are required for proliferation. From the list clone sequences identified here, each was identified to be a portion of a gene in an operon required for the proliferation of *E. coli*. Cloned sequences corresponding to genes already known to be required for proliferation in *E. coli* include EcXA002, 004, 005, 010, 012, 014, 031, 02, 043, 045, 051, 052, 054, and 055. The remaining identified sequences correspond to *E. coli*  
15 10 genes previously undesignated as required for proliferation in the art.

An interesting observation of the present invention is that there are also several sequence fragments that correspond to *E. coli* genes that are not thought to be required for *E. coli* proliferation. Nevertheless, under the conditions described above, the antisense expression of these gene fragments causes a reduction in cell growth. This result implies that the genes  
20 15 corresponding to the identified sequences are actually required for proliferation. Molecule Nos. corresponding to these genes are EcXA006, 044, 046, and 053.

Following identification of the sequences of interest, these sequences were localized into operons. Since bacterial genes are expressed in a polycistronic manner, the antisense inhibition of a single gene in an operon might effect the expression of all the other genes on the operon or the genes down stream from the single gene identified. In order to determine which of the gene products in an operon are required for proliferation, each of the genes contained within an operon may be analyzed for  
30 20 their effect on viability as described below.

**TABLE III**  
**Open Boundaries**

| Mole. No. | Left<br>Coordinate | Right<br>Coordinate |
|-----------|--------------------|---------------------|
| EcXA001   | 3606848            | 3608143             |
| EcXA002   | 2702355            | 2703329             |
| EcXA003   | 1015782            | 1017522             |
| EcXA004   | 3467782            | 3472189             |
| EcXA005   | 4177574            | 4178503             |
| EcXA006   | 2412767            | 2414911             |
| EcXA007   | 3841591            | 3843357             |
| EcXA008   | 3268266            | 3272548             |
| EcXA009   | 1599514            | 1605313             |
| EcXA010   | 1647406            | 1647458             |
| EcXA011   | 1545425            | 1550015             |
| EcXA012   | 3467782            | 3472189             |
| EcXA013   | 2697683            | 2697943             |
| EcXA014   | 3049135            | 3053470             |
| EcXA015   | 2465875            | 2468482             |
| EcXA016   | 1877031            | 1877972             |
| EcXA017   | 3065360            | 3066100             |
| EcXA018   | 2151891            | 2160901             |
| EcXA019   | 2185400            | 2190242             |
| EcXA020   | 1877031            | 1877972             |
| EcXA021   | 238746             | 239084              |
| EcXA022   | 1703791            | 1710182             |
| EcXA023   | 1585817            | 1588025             |
| EcXA024   | 3231369            | 3232096             |
| EcXA025   | 2042885            | 2050036             |
| EcXA026   | 331001             | 331184              |
| EcXA027c  | 2225343            | 2228405             |
| EcXA028   | 2420669            | 2421559             |
| EcXA029   | 4626424            | 4628091             |
| EcXA030   | 3718309            | 3719678             |
| EcXA031   | 3440255            | 3445786             |
| EcXA032b  | 751452             | 753691              |
| EcXA033   | 3192961            | 3188606             |
| EcXA034   | 3717678            | 3717890             |
| EcXA035   | 3694087            | 3697522             |
| EcXA036   | 3246594            | 3248594             |
| EcXA037   | 1620984            | 1621874             |
| EcXA038   | 1416572            | 1417368             |
| EcXA039   | 522485             | 528354              |
| EcXA040   | 3580669            | 3580672             |
| EcXA041   | 1196090            | 1197460             |
| EcXA042   | 2280537            | 2280821             |

| Mols. No. | Left<br>Coordinate | Right<br>Coordinate |
|-----------|--------------------|---------------------|
| EcXA043   | 765207             | 773404              |
| EcXA044   | 1189839            | 1191209             |
| EcXA045   | 2818575            | 2817168             |
| EcXA046   | 4538525            | 4547279             |
| EcXA047   | 1637054            | 1639578             |
| EcXA048   | 2099917            | 2106351             |
| EcXA049   | 402927             | 404042              |
| EcXA050   | 392239             | 394353              |
| EcXA051   | 3445951            | 3450907             |
| EcXA052   | 1797417            | 1800594             |
| EcXA053   | 3643929            | 3645281             |
| EcXA054   | 3440255            | 3445786             |
| EcXA055   | 2724301            | 2729178             |

## EXAMPLE 5

Identification of Individual Genes within an Operon Required for Proliferation

The following example illustrates a method for determining which gene in an operon is required for proliferation. The clone insert corresponding to Molecule No. EcXA004 possesses nucleic acid sequence homology to the *E. coli* genes *rspG* and *rspL*. This molecule corresponds to an operon containing two additional genes *fusA* and *tufA*. The *rspL* gene is the first gene in the operon. To determine which gene or genes in this operon are required for proliferation, each gene is selectively inactivated using homologous recombination. Gene *rspL* is the first gene to be inactivated.

Deletion inactivation of a chromosomal copy of a gene in *E. coli* can be accomplished by integrative gene replacement. The principle of this method (Hamilton, C. M., et al 1989. *J. Bacteriol.* 171: 4617-4622) is to construct a mutant allele of the targeted gene, introduce that allele into the chromosome using a conditional suicide vector, and then force the removal of the native wild type allele and vector sequences. This will replace the native gene with a desired mutation(s) but leave promoters, operators, etc. intact. Essentiality of a gene is determined either by deduction from genetic analysis or by conditional expression of a wild type copy of the targeted gene (trans complementation).

The first step is to generate a mutant *rspL* allele using PCR amplification. Two sets of PCR primers are chosen to produce a copy of *rspL* with a large central deletion to inactivate the gene. In order to eliminate polar effects, it is desirable to construct a mutant allele comprising an in-frame deletion of most or all of the coding region of the *rspL* gene. Each set of PCR primers is chosen such that a region flanking the gene to be amplified is sufficiently long to allow recombination (typically at least 500 nucleotides on each side of the deletion). The targeted deletion or mutation will be contained within this fragment. To facilitate cloning of the PCR product, the PCR primers may also contain restriction endonuclease sites found in the cloning region of a conditional knockout vector such as pK03 (Link, et al 1997 *J. Bacteriol.* 179 (20): 6228-6237). Suitable sites include NotI, SalI, BamHI and SmaI. The *rspL* gene fragments are produced using standard PCR conditions including, but not limited to, those outlined in the manufacturers directions for the

Hot Start Taq PCR kit (Qiagen, Inc., Valencia, CA). The PCR reactions will produce two fragments that can be fused together. Alternatively, crossover PCR can be used to generate a desired deletion in one step (Ho, S. N., et al 1989. *Gene* 77: 51-59, Horton, R. M., et al 1989. *Gene* 77: 61-68). The mutant allele thus produced is called a "null" allele because it cannot produce a functional gene product.

The mutant allele obtained from PCR amplification is cloned into the multiple cloning site of pK03. Directional cloning of the *rpsL* null allele is not necessary. The pK03 vector has a temperature-sensitive origin of replication derived from pSC101. Therefore, clones are propagated at the permissive temperature of 30°C. The vector also contains two selectable marker genes: one that confers resistance to chloramphenicol and another, the *Bacillus subtilis* *sacB* gene, that allows for counter-selection on sucrose containing growth medium. Clones that contain vector DNA with the null allele inserted are confirmed by restriction endonuclease analysis and DNA sequence analysis of isolated plasmid DNA. The plasmid containing the *rpsL* null allele insert is known as a knockout plasmid.

Once the knockout plasmid has been constructed and its sequence verified, it is transformed into a Rec<sup>+</sup> *E. coli* host cell. Transformation can be by any standard method such as electroporation. In some fraction of the transformed cells, plasmids will integrate into the *E. coli* chromosome by homologous recombination between the *rpsL* null allele in the plasmid and the *rpsL* gene in the chromosome. Transformant colonies in which such an event has occurred are readily selected by growth at the non-permissive temperature of 43°C and in the presence of chloramphenicol. At this temperature, the plasmid will not replicate as an episome and will be lost from cells as they grow and divide. These cells are no longer resistant to chloramphenicol and will not grow when it is present. However, cells in which the knockout plasmid has integrated into the *E. coli* chromosome remain resistant to chloramphenicol and propagate.

Cells containing integrated knock-out plasmids are usually the result of a single crossover event that creates a tandem repeat of the mutant and native wild type alleles of *rpsL* separated by the vector sequences. A consequence of this is that *rpsL* will still be expressed in these cells. In order to determine if the gene is essential for growth, the wild type copy must be removed. This is accomplished by selecting for plasmid excision, a process in which homologous recombination between the two alleles results in looping out of the plasmid sequences. Cells that have undergone such an excision event and have lost plasmid sequences including *sacB* gene are selected for by addition of sucrose to the medium. The *sacB* gene product converts sucrose to a toxic molecule. Thus counter selection with sucrose ensures that plasmid sequences are no longer present in the cell. Loss of plasmid sequences is further confirmed by testing for sensitivity to chloramphenicol (loss of the chloramphenicol resistance gene). The latter test is important because occasionally a mutation in the *sacB* gene can occur resulting in a loss of *sacB* function with no effect on plasmid replication (Link, et. al., 1997 *J. Bacteriol.* 179 (20): 6228-6237). These artifact clones retain plasmid sequences and are therefore still resistant to chloramphenicol.

In the process of plasmid excision, one of the two *rpsL* alleles is lost from the chromosome along with the plasmid DNA. In general, it is equally likely that the null allele or the wild type allele will be lost. Therefore, if the *rpsL*



5 gene is not essential, half of the clones obtained in this experiment will have the wild type allele on the chromosome and half will have the null allele. However, if the *rpsL* gene is essential, cells containing the null allele will not be obtained as a single copy of the null allele would be lethal.

10 5 To determine the essentiality of *rpsL*, a statistically significant number of the resulting clones, at least 20, are analyzed by PCR amplification of the *rpsL* gene. Since the null allele is missing a significant portion of the *rpsL* gene, its PCR product is significantly shorter than that of the wild type gene and the two are readily distinguished by gel electrophoretic analysis. The PCR products may also be subjected to sequence determination for further confirmation by methods well known to those in the art.

15 The above experiment is generally adequate for determining the essentiality of a gene such as *rpsL*. However, it may be necessary or desirable to more directly confirm the essentiality of the gene. There are several methods by which this can be accomplished. In general, these involve three steps: 1) construction of an episome containing a wild type allele, 2) isolation of clones containing a single chromosomal copy of the mutant null allele as described above but in the presence of the episomal wild type allele, and then 3) determining if the cells survive when the expression of the episomal allele is shut off. In this case, the trans copy of wild type *rpsL* is made by PCR cloning of the entire coding region of *rpsL* and inserting it in the sense orientation downstream of an inducible promoter such as the *E. coli lac* promoter. Transcription of this allele of *rpsL* will be induced in the presence of IPTG which inactivates the *lac* repressor. Under IPTG induction *rpsL* protein will be expressed as long as the recombinant gene also possesses a ribosomal binding site, also known as a "Shine-Dalgarno Sequence". The trans copy of *rpsL* is cloned on a plasmid that is compatible with pSC101. Compatible vectors include p15A, pBR322, and the pUC plasmids, among others. Replication of the compatible plasmid will not be temperature-sensitive. The entire process of integrating the null allele of *rpsL* and subsequent plasmid excision is carried out in the presence of IPTG to ensure the expression of functional *rpsL* protein is maintained throughout. After the null *rpsL* allele is confirmed as integrated on the chromosome in place of the wild type *rpsL* allele, then IPTG is withdrawn and expression of functional *rpsL* protein shut off. If the *rpsL* gene is essential, cells will cease to proliferate under these conditions. However, if the *rpsL* gene is not essential, cells will continue to proliferate under these conditions. In this experiment, essentiality is determined by conditional expression of a wild type copy of the gene rather than inability to obtain the intended chromosomal disruption.

40 An advantage of this method over some other gene disruption techniques is that the targeted gene can be deleted or mutated without the introduction of large segments of foreign DNA. Therefore, polar effects on downstream genes are eliminated or minimized. There are methods described to introduce inducible promoters upstream of potential essential bacterial genes. However in such cases, polarity from multiple transcription start points can be a problem. One way of preventing this is to insert a gene disruption cassette that contains strong transcriptional terminators upstream of the integrated inducible promoter (Zhang, Y, and Cronan, J. E. 1996 *J. Bacteriol.* 178 (12): 3614-3620). The described techniques will all be familiar to one of ordinary skill in the art.

5           Following the analysis of the *rpsL* gene, the other genes of the operon are investigated to determine if they are required for proliferation.

#### EXAMPLE 6

##### Expression of the Proteins Encoded by Genes Identified as Required for *E. coli* Proliferation

10           5           The following is provided as one exemplary method to express the proliferation-required proteins encoded by the identified sequences described above. First, the initiation and termination codons for the gene are identified. If desired, methods for improving translation or expression of the protein are well known in the art. For example, if the nucleic acid encoding the polypeptide to be expressed lacks a methionine codon to serve as the initiation site, a strong Shine-Delgarno sequence, or a stop codon, these sequences can be added. Similarly, if the identified nucleic acid sequence lacks a transcription termination signal, this sequence can be added to the construct by, for example, splicing out such a sequence from an appropriate donor sequence. In addition, the coding sequence may be operably linked to a strong promoter or an inducible promoter if desired. The identified nucleic acid sequence or portion thereof encoding the polypeptide to be expressed is obtained by PCR from the bacterial expression vector or genome using oligonucleotide primers complementary to the identified nucleic acid sequence or portion thereof and containing restriction endonuclease sequences for *NcoI* incorporated into the 5' primer and *BglII* at the 5' end of the corresponding 3'-primer, taking care to ensure that the identified nucleic acid sequence is positioned in frame with the termination signal. The purified fragment obtained from the resulting PCR reaction is digested with *NcoI* and *BglII*, purified and ligated to an expression vector.

20           15           The ligated product is transformed into DH5 $\alpha$  or some other *E. coli* strain suitable for the over expression of potential proteins. Transformation protocols are well known in the art. For example, transformation protocols are described in: **Current Protocols in Molecular Biology**, Vol. 1, Unit 1.8, (Ausubel, et al., Eds.) John Wiley & Sons, Inc. (1997). Positive transformants are selected after growing the transformed cells on plates containing 50-100  $\mu$ g/ml Ampicillin (Sigma, St. Louis, Missouri). In one embodiment, the expressed protein is held in the cytoplasm of the host organism. In an alternate embodiment, the expressed protein is released into the culture medium. In still another alternative, the expressed protein can be sequestered in the periplasmic space and liberated therefrom using any one of a number of cell lysis techniques known in the art. For example, the osmotic shock cell lysis method described in Chapter 16 of **Current Protocols in Molecular Biology**, Vol. 2, (Ausubel, et al., Eds.) John Wiley & Sons, Inc. (1997). Each of these procedures can be used to express a proliferation-required protein.

30           20           Expressed proteins, whether in the culture medium or liberated from the periplasmic space or the cytoplasm, are then purified or enriched from the supernatant using conventional techniques such as ammonium sulfate precipitation, standard chromatography, immunoprecipitation, immunochromatography, size exclusion chromatography, ion exchange chromatography, and HPLC. Alternatively, the secreted protein can be in a sufficiently enriched or pure state in the supernatant or growth media of the host to permit it to be used for its intended purpose without further enrichment. The purity of the protein product

5 obtained can be assessed using techniques such as Coomassie or silver staining or using antibodies against the control protein. Coomassie and silver staining techniques are familiar to those skilled in the art.

10 5 Antibodies capable of specifically recognizing the protein of interest can be generated using synthetic peptides using methods well known in the art. See, *Antibodies: A Laboratory Manual*, (Harlow and Lane, Eds.) Cold Spring Harbor Laboratory (1988). For example, 15-mer peptides having a sequence encoded by the appropriate identified gene sequence of interest or portion thereof can be chemically synthesized. The synthetic peptides are injected into mice to generate antibodies to the polypeptide encoded by the identified nucleic acid sequence of interest or portion thereof. Alternatively, samples of the protein expressed from the expression vectors discussed above can be purified and subjected to amino acid sequencing analysis to confirm the identity of the recombinantly expressed protein and subsequently used to raise antibodies. An Example describing in detail the generation of monoclonal and polyclonal antibodies appears in Example 7.

15 10 The protein encoded by the identified nucleic acid sequence of interest or portion thereof can be purified using standard immunochromatography techniques. In such procedures, a solution containing the secreted protein, such as the culture medium or a cell extract, is applied to a column having antibodies against the secreted protein attached to the chromatography matrix. The secreted protein is allowed to bind the immunochromatography column. Thereafter, the column is washed to remove non-specifically bound proteins. The specifically bound secreted protein is then released from the column and recovered using standard techniques. These procedures are well known in the art.

20 15 In an alternative protein purification scheme, the identified nucleic acid sequence of interest or portion thereof can be incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies the coding sequence of the identified nucleic acid sequence of interest or portion thereof is inserted in-frame with the gene encoding the other half of the chimera. The other half of the chimera can be maltose binding protein (MBP) or a nickel binding polypeptide encoding sequence. A chromatography matrix having antibody to MBP or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites can be engineered between the MBP gene or the nickel binding polypeptide and the identified expected gene of interest, or portion thereof. Thus, the two polypeptides of the chimera can be separated from one another by protease digestion.

25 20 One useful expression vector for generating maltose binding protein fusion proteins is pMAL (New England Biolabs), which encodes the *malE* gene. In the pMal protein fusion system, the cloned gene is inserted into a pMal vector downstream from the *malE* gene. This results in the expression of an MBP-fusion protein. The fusion protein is purified by affinity chromatography. These techniques as described are well known to those skilled in the art of molecular biology.

#### EXAMPLE 7

##### Production of an Antibody to an isolated *E. coli* Protein

30 30 Substantially pure protein or polypeptide is isolated from the transformed cells as described in Example 6. The concentration of protein in the final preparation is adjusted, for example, by concentration on a 10,000 molecular weight cut off

5 AMICON filter device (Millipore, Bedford, MA), to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows:

#### Monoclonal Antibody Production by Hybridoma Fusion

10 5 Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature* 256:495 (1975) or any of the well-known derivative methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein or peptides derived therefrom over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as described by Engvall, E., "Enzyme immunoassay ELISA and EMIT," *Meth. Enzymol.* 70:419 (1980), and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. et al. *Basic Methods in Molecular Biology* Elsevier, New York. Section 21-2.

#### 25 Polyclonal Antibody Production by Immunization

30 20 Polyclonal antiserum containing antibodies to heterogeneous epitopes of a single protein or a peptide can be prepared by immunizing suitable animals with the expressed protein or peptides derived therefrom described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than larger molecules and can require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. et al. *J. Clin. Endocrinol. Metab.* 33:988-991 (1971).

35 25 Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. et al., Chap. 19 in: *Handbook of Experimental Immunology* D. Wier (ed) Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, 2d Ed. (Rose and Friedman, Eds.) Amer. Soc. For Microbiol., Washington, D.C. (1980).

45 30 Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to

5 identify the presence of antigen in a biological sample. The antibodies can also be used in therapeutic compositions for killing bacterial cells expressing the protein.

## EXAMPLE 8

### Screening Chemical Libraries

#### A. Protein-Based Assays

10 5 Having isolated and expressed bacterial proteins shown to be required for bacterial proliferation, the present invention further contemplates the use of these expressed proteins in assays to screen libraries of compounds for potential drug candidates. The generation of chemical libraries is well known in the art. For example combinatorial chemistry can be used to generate a library of compounds to be screened in the assays described herein. A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining amino acids in every possible combination to yield peptides of a given length. Millions of chemical compounds theoretically can be synthesized through such combinatorial mixings of chemical building blocks. For example, one commentator observed that the systematic, combinatorial mixing of 100 interchangeable chemical building blocks results in the theoretical synthesis of 100 million tetrameric compounds or 10 billion pentameric compounds. (Gallop et al., "Applications of Combinatorial Technologies to Drug Discovery, Background and Peptide Combinatorial Libraries," *Journal of Medicinal Chemistry*, Vol. 37, No. 9, 1233-1250 (1994). Other chemical libraries known to those in the art may also be used, including natural product libraries.

20 20 Once generated, combinatorial libraries can be screened for compounds that possess desirable biological properties. For example, compounds which may be useful as drugs or to develop drugs would likely have the ability to bind to the target protein identified, expressed and purified as discussed above. Further, if the identified target protein is an enzyme, candidate compounds would likely interfere with the enzymatic properties of the target protein. Any enzyme can be a target protein. For example, the enzymatic function of a target protein can be to serve as a protease, nuclease, phosphatase, dehydrogenase, transporter protein, transcriptional enzyme, and any other type of enzyme known or unknown. Thus, the present invention contemplates using the protein products described above to screen combinatorial chemical libraries.

30 25 Those in the art will appreciate that a number of techniques exist for characterizing target proteins in order to identify molecules useful for the discovery and development of therapeutics. For example, some techniques involve the generation and use of small peptides to probe and analyze target proteins both biochemically and genetically in order to identify and develop drug leads. Such techniques include the methods described in PCT publications No. W09935494, W09819162, W09954728, the disclosures of which are incorporated herein by reference in their entireties.

40 30 In another example, the target protein is a serine protease and the substrate of the enzyme is known. The present example is directed towards the analysis of libraries of compounds to identify compounds that function as inhibitors of the target enzyme. First, a library of small molecules is generated using methods of combinatorial library formation well known in

5 the art. U.S. Patent NOs. 5,463,564 and 5,574, 656, to Agrafiotis, et al., entitled "System and Method of Automatically Generating Chemical Compound with Desired Properties," are two such teachings. Then the library compounds are screened to identify library compounds that possess desired structural and functional properties. U.S. Patent No. 5,684,711 also discusses a method for screening libraries.

10 5 To illustrate the screening process, the combined target and chemical compounds of the library are exposed to and permitted to interact with the purified enzyme. A labeled substrate is added to the incubation. The label on the substrate is such that a detectable signal is emitted from metabolized substrate molecules. The emission of this signal permits one to measure the effect of the combinatorial library compounds on the enzymatic activity of target enzymes. The characteristics of each library compound is encoded so that compounds demonstrating activity against the enzyme can be analyzed and features common to the various compounds identified can be isolated and combined into future iterations of libraries.

15 10 Once a library of compounds is screened, subsequent libraries are generated using those chemical building blocks that possess the features shown in the first round of screen to have activity against the target enzyme. Using this method, subsequent iterations of candidate compounds will possess more and more of those structural and functional features required to inhibit the function of the target enzyme, until a group of enzyme inhibitors with high specificity for the enzyme can be found. These compounds can then be further tested for their safety and efficacy as antibiotics for use in mammals.

20 15 It will be readily appreciated that this particular screening methodology is exemplary only. Other methods are well known to those skilled in the art. For example, a wide variety of screening techniques are known for a large number of naturally-occurring targets when the biochemical function of the target protein is known.

#### 25 B. Cell Based Assays

30 20 Current cell-based assays used to identify or to characterize compounds for drug discovery and development frequently depend on detecting the ability of a test compound to inhibit the activity of a target molecule located within a cell or located on the surface of a cell. Most often such target molecules are proteins such as enzymes, receptors and the like. However, target molecules may also include other molecules such as DNAs, lipids, carbohydrates and RNAs including messenger RNAs, ribosomal RNAs, tRNAs and the like. A number of highly sensitive cell-based assay methods are available to those of skill in the art to detect binding and interaction of test compounds with specific target molecules. However, these methods are generally not highly effective when the test compound binds to or otherwise interacts with its target molecule with moderate or low affinity. In addition, the target molecule may not be readily accessible to a test compound in solution, such as when the target molecule is located inside the cell or within a cellular compartment such as the periplasm of a bacterial cell. Thus, current cell-based assay methods are limited in that they are not effective in identifying or characterizing compounds that interact with their targets with moderate to low affinity or compounds that interact with targets that are not readily accessible.

40 30 Cell-based assay methods of the present invention have substantial advantages over current cell-based assays practiced in the art. These advantages derive from the use of sensitized cells in which the level or activity of a

proliferation-required gene product (the target molecule) has been specifically reduced to the point where the presence or absence of its function becomes a rate-determining step for cellular proliferation. Bacterial, fungal, plant, or animal cells can all be used with the present method. Such sensitized cells become much more sensitive to compounds that are active against the affected target molecule. Thus, cell-based assays of the present invention are capable of detecting compounds exhibiting low or moderate potency against the target molecule of interest because such compounds are substantially more potent on sensitized cells than on non-sensitized cells. The affect may be such that a test compound may be two to several times more potent, at least 10 times more potent or even at least 100 times more potent when tested on the sensitized cells as compared to the non-sensitized cells.

Due in part to the increased appearance of antibiotic resistance in pathogenic microorganisms and to the significant side-effects associated with some currently used antibiotics, novel antibiotics acting at new targets are highly sought after in the art. Yet, another limitation in the current art related to cell-based assays is the problem of identifying hits against the same kinds of target molecules in the same limited set of biological pathways over and over again. This may occur when compounds acting at such new targets are discarded, ignored or fail to be detected because compounds acting at the "old" targets are encountered more frequently and are more potent than compounds acting at the new targets. As a result, the majority of antibiotics in use currently interact with a relatively small number of target molecules within an even more limited set of biological pathways.

The use of sensitized cells of the current invention provides a solution to the above problem in two ways. First, desired compounds acting at a target of interest, whether a new target or a previously known but poorly exploited target, can now be detected above the "noise" of compounds acting at the "old" targets due to the specific and substantial increase in potency of such desired compounds when tested on the sensitized cells of the current invention. Second, the methods used to sensitize cells to compounds acting at a target of interest may also sensitize these cells to compounds acting at other target molecules within the same biological pathway. For example, expression of an antisense molecule to a gene encoding a ribosomal protein is expected to sensitize the cell to compounds acting at that ribosomal protein and may also sensitize the cells to compounds acting at any of the ribosomal components (proteins or rRNA) or even to compounds acting at any target which is part of the protein synthesis pathway. Thus an important advantage of the present invention is the ability to reveal new targets and pathways that were previously not readily accessible to drug discovery methods.

Sensitized cells of the present invention are prepared by reducing the activity or level of a target molecule. The target molecule may be a gene product, such as an RNA or polypeptide produced from the proliferation-required nucleic acids described herein. Alternatively, the target may be a gene product such as an RNA or polypeptide which is produced from a sequence within the same operon as the proliferation-required nucleic acids described herein. In addition, the target may be an RNA or polypeptide in the same biological pathway as the proliferation-required nucleic acids described herein.

5 Such biological pathways include, but are not limited to, enzymatic, biochemical and metabolic pathways as well as pathways involved in the production of cellular structures such the cell wall.

Current methods employed in the arts of medicinal and combinatorial chemistries are able to make use of structure-activity relationship information derived from testing compounds in various biological assays including direct  
10 5 binding assays and cell-based assays. Occasionally compounds are directly identified in such assays that are sufficiently potent to be developed as drugs. More often, initial hit compounds exhibit moderate or low potency. Once a hit compound is identified with low or moderate potency, directed libraries of compounds are synthesized and tested in order to identify more potent leads. Generally these directed libraries are combinatorial chemical libraries consisting of compounds with  
15 structures related to the hit compound but containing systematic variations including additions, subtractions and substitutions of various structural features. When tested for activity against the target molecule, structural features are identified that either alone or in combination with other features enhance or reduce activity. This information is used to design subsequent directed libraries containing compounds with enhanced activity against the target molecule. After one or several iterations of this process, compounds with substantially increased activity against the target molecule are identified and may be further developed as drugs. This process is facilitated by use of the sensitized cells of the present  
20 invention since compounds acting at the selected targets exhibit increased potency in such cell-based assays, thus; more compounds can now be characterized providing more useful information than would be obtained otherwise.

Thus, it is now possible using cell-based assays of the present invention to identify or characterize compounds that previously would not have been readily identified or characterized including compounds that act at targets that previously were not readily exploited using cell-based assays. The process of evolving potent drug leads from initial hit  
30 20 compounds is also substantially improved by the cell-based assays of the present invention because, for the same number of test compounds, more structure-function relationship information is likely to be revealed.

The method of sensitizing a cell entails selecting a suitable gene or operon. A suitable gene or operon is one whose expression is required for the proliferation of the cell to be sensitized. The next step is to introduce into the cells to be sensitized, an antisense RNA capable of hybridizing to the suitable gene or operon or to the RNA encoded by the suitable  
35 25 gene or operon. Introduction of the antisense RNA can be in the form of an expression vector in which antisense RNA is produced under the control of an inducible promoter. The amount of antisense RNA produced is limited by varying the inducer concentration to which the cell is exposed and thereby varying the activity of the promoter driving transcription of the antisense RNA. Thus, cells are sensitized by exposing them to an inducer concentration that results in a sub-lethal level of antisense RNA expression.

30 In one embodiment of the cell-based assays, the identified exogenous *E. coli* nucleotide sequences of the present invention are used to inhibit the production of a proliferation-required protein. Expression vectors producing antisense RNA against identified genes required for proliferation are used to limit the concentration of a proliferation-required protein without severely inhibiting growth. To achieve that goal, a growth inhibition dose curve of inducer is calculated by plotting  
45



5 various doses of inducer against the corresponding growth inhibition caused by the antisense expression. From this curve, various percentages of antisense induced growth inhibition, from 1 to 100% can be determined. If the promoter contained in the expression vector contains a *lac* operator the transcription is regulated by *lac* repressor and expression from the promoter is inducible with IPTG. For example, the highest concentration of the inducer IPTG that does not reduce the growth rate (0% growth inhibition) can be predicted from the curve. Cellular proliferation can be monitored by growth medium turbidity via OD measurements. In another example, the concentration of inducer that reduces growth by 25% can be predicted from the curve. In still another example, a concentration of inducer that reduces growth by 50% can be calculated. Additional parameters such as colony forming units (cfu) can be used to measure cellular viability.

10 5 Cells to be assayed are exposed to the above-determined concentrations of inducer. The presence of the inducer at this sub-lethal concentration reduces the amount of the proliferation required gene product to the lowest amount in the cell that will support growth. Cells grown in the presence of this concentration of inducer are therefore specifically more sensitive to inhibitors of the proliferation-required protein or RNA of interest or to inhibitors of proteins or RNAs in the same biological pathway as the proliferation-required protein or RNA of interest but not to inhibitors of unrelated proteins or RNAs.

15 10 Cells pretreated with sub-inhibitory concentrations of inducer and thus containing a reduced amount of proliferation-required target gene product are then used to screen for compounds that reduce cell growth. The sub-lethal concentration of inducer may be any concentration consistent with the intended use of the assay to identify candidate compounds to which the cells are more sensitive. For example, the sub-lethal concentration of the inducer may be such that growth inhibition is at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60% at least about 75%, or more. Cells which are pre-sensitized using the preceding method are more sensitive to inhibitors of the target protein because these cells contain less target protein to inhibit than wild-type cells.

20 20 In another embodiment of the cell based assays of the present invention, the level or activity of a proliferation required gene product is reduced using a temperature sensitive ...mutation in the proliferation-required sequence and an antisense nucleic acid against the proliferation-required sequence. Growing the cells at an intermediate temperature between the permissive and restrictive temperatures of the temperature sensitive mutant where the mutation is in a proliferation-required gene produces cells with reduced activity of the proliferation-required gene product. The antisense RNA directed against the proliferation-required sequence further reduces the activity of the proliferation required gene product. Drugs that may not have been found using either the temperature sensitive mutation or the antisense nucleic acid alone may be identified by determining whether cells in which expression of the antisense nucleic acid has been induced and which are grown at a temperature between the permissive temperature and the restrictive temperature are substantially more sensitive to a test compound than cells in which expression of the antisense nucleic acid has not been induced and which are grown at a permissive temperature. Also drugs found previously from either the antisense nucleic acid alone or the

5 temperature sensitive mutation alone may have a different sensitivity profile when used in cells combining the two approaches, and that sensitivity profile may indicate a more specific action of the drug in inhibiting one or more activities of the gene product.

10 5 Temperature sensitive mutations may be located at different sites within the gene and correspond to different domains of the protein. For example, the *dnaB* gene of *Escherichia coli* encodes the replication fork DNA helicase. DnaB has several domains, including domains for oligomerization, ATP hydrolysis, DNA binding, interaction with primase, interaction with DnaC, and interaction with DnaA [(Biswas, E.E. and Biswas, S.B. 1999. Mechanism and DnaB helicase of *Escherichia coli*: structural domains involved in ATP hydrolysis, DNA binding, and oligomerization. *Biochem.* 38:10919-10928; Hiasa, H. and Marians, K.J. 1999. Initiation of bidirectional replication at the chromosomal origin is directed by the interaction between helicase and primase. *J. Biol. Chem.* 274:27244-27248; San Martin, C., Rademacher, M., Wolpensinger, B., Engel, A., Miles, C.S., Dixon, N.E., and Carazo, J.M. 1998. Three-dimensional reconstructions from cryoelectron microscopy images reveal an intimate complex between helicase DnaB and its loading partner DnaC. *Structure* 6:501-9; Sutton, M.D., Carr, K.M., Vicente, M., and Kaguni, J.M. 1998. *Escherichia coli* DnaA protein. The N-terminal domain and loading of DnaB helicase at the *E. coli* chromosomal. *J. Biol. Chem.* 273:34255-62.), the disclosures of which are incorporated herein by reference in their entirety]. Temperature sensitive mutations in different domains of DnaB confer different phenotypes at the restrictive temperature, which include either an abrupt stop or slow stop in DNA replication with or without DNA breakdown (Wechsler, J.A. and Gross, J.D. 1971. *Escherichia coli* mutants temperature-sensitive for DNA synthesis. *Mol. Gen. Genetics* 113:273-284, the disclosure of which is incorporated herein by reference in its entirety) and termination of growth or cell death. Combining the use of temperature sensitive mutations in the *dnaB* gene that cause cell death at the restrictive temperature with an antisense to the *dnaB* gene could lead to the discovery of very specific and effective inhibitors of one or a subset of activities exhibited by DnaB.

35 When screening for antimicrobial agents against a gene product required for proliferation, growth inhibition of cells containing a limiting amount of that proliferation-required gene product can be assayed. Growth inhibition can be measured by directly comparing the amount of growth, measured by the optical density of the growth medium, between an experimental sample and a control sample. Alternative methods for assaying cell proliferation include measuring green fluorescent protein (GFP) reporter construct emissions, various enzymatic activity assays, and other methods well known in the art.

40 It will be appreciated that the above method may be performed in solid phase, liquid phase or a combination of the two. For example, cells grown on nutrient agar containing the inducer of the antisense construct may be exposed to compounds spotted onto the agar surface. A compound's effect may be judged from the diameter of the resulting killing zone, the area around the compound application point in which cells do not grow. Multiple compounds may be transferred to agar plates and simultaneously tested using automated and semi-automated equipment including but not restricted to

5 multi-channel pipettes (for example the Beckman Multimek) and multi-channel spotters (for example the Genomic Solutions Flexys). In this way multiple plates and thousands to millions of compounds may be tested per day.

10 5 The compounds may also be tested entirely in liquid phase using microtiter plates as described below. Liquid phase screening may be performed in microtiter plates containing 96, 384, 1536 or more wells per microtiter plate to screen multiple plates and thousands to millions of compounds per day. Automated and semi-automated equipment may be used for addition of reagents (for example cells and compounds) and determination of cell density.

#### EXAMPLE 9

15 The effectiveness of the above cell based assay was validated using constructs expressing antisense RNA to *E. coli* genes *rplL*, *rplJ*, and *rplW* encoding ribosomal proteins L7/L12, L10 and L23 respectively. These proteins are part of the protein synthesis apparatus of the cell and as such are required for proliferation. These constructs were used to test the effect of antisense expression on cell sensitivity to antibiotics known to bind to the ribosome and thereby inhibit protein synthesis. Constructs expressing antisense RNA to several other genes (*elaD*, *visC*, *yohH*, and *aptE/B*), the products of which are not involved in protein synthesis were used for comparison.

20 First expression vectors containing antisense constructs to either *rplW* or to *elaD* were introduced into separate *E. coli* cell populations. Vector introduction is a technique well known to those of ordinary skill in the art. The expression vectors of this example contain IPTG inducible promoters that drive the expression of the antisense RNA in the presence of the inducer. However, those skilled in the art will appreciate that other inducible promoters may also be used. Suitable expression vectors are also well known in the art. The *E. coli* antisense clones encoding ribosomal proteins L7/L12, L10 and L23 were used to test the effect of antisense expression on cell sensitivity to the antibiotics known to bind to these proteins. First, expression vectors containing antisense to either the genes encoding L7/L12 and L10 or L23 were introduced into separate *E. coli* cell populations.

25 The cell populations were exposed to a range of IPTG concentrations in liquid medium to obtain the growth inhibitory dose curve for each clone (Fig. 1). First, seed cultures were grown to a particular turbidity that is measured by the optical density (OD) of the growth solution. The OD of the solution is directly related to the number of bacterial cells contained therein. Subsequently, sixteen 200  $\mu$ l liquid medium cultures were grown in a 96 well microtiter plate at 37 C with a range of IPTG concentrations in duplicate two-fold serial dilutions from 1600  $\mu$ M to 12.5  $\mu$ M (final concentration). Additionally, control cells were grown in duplicate without IPTG. These cultures were started from equal amounts of cells derived from the same initial seed culture of a clone of interest. The cells were grown for up to 15 hours and the extent of growth was determined by measuring the optical density of the cultures at 600 nm. When the control culture reached mid-log phase the percent growth of the control for each of the IPTG containing cultures was plotted against the log concentrations of IPTG to produce a growth inhibitory dose response curve for the IPTG. The concentration of IPTG that inhibits cell growth to 50% ( $IC_{50}$ ) as compared to the 0 mM IPTG control (0% growth inhibition) was then calculated from

the curve. Under these conditions, an amount of antisense RNA was produced that reduced the expression levels of *rplW* and *elaD* to a degree such that growth was inhibited by 50%.

Alternative methods of measuring growth are also contemplated. Examples of these methods include measurements of proteins, the expression of which is engineered into the cells being tested and can readily be measured. Examples of such proteins include green fluorescent protein (GFP) and various enzymes.

Cells were pretreated with the selected concentration of IPTG and then used to test the sensitivity of cell populations to tetracycline, erythromycin and other protein synthesis inhibitors. An example of a tetracycline dose response curve is shown in Figures 2A and 2B for the *rplW* and *elaD* genes, respectively. Cells were grown to log phase and then diluted into media alone or media containing IPTG at concentrations which give 20% and 50% growth inhibition as determined by IPTG dose response curves. After 2.5 hours, the cells were diluted to a final OD600 of 0.002 into 96 well plates containing (1) +/- IPTG at the same concentrations used for the 2.5 hour pre-incubation; and (2) serial two-fold dilutions of tetracycline such that the final concentrations of tetracycline range from 1 µg/ml to 15.6 ng/ml and 0 µg/ml. The 96 well plates were incubated at 37°C and the OD600 was read by a plate reader every 5 minutes for up to 15 hours. For each IPTG concentration and the no IPTG control, tetracycline dose response curves were determined when the control (absence of tetracycline) reached 0.1 OD600. To compare tetracycline sensitivity with and without IPTG, tetracycline IC50s were determined from the dose response curves (Figs. 2A-B). Cells with reduced levels of L23 (*rplW*) showed increased sensitivity to tetracycline (Fig. 2A) as compared to cells with reduced levels of *elaD* (Fig. 2B). Figure 3 shows a summary bar chart in which the ratios of tetracycline IC50s determined in the presence of IPTG which gives 50% growth inhibition versus tetracycline IC50s determined without IPTG (fold increase in tetracycline sensitivity) were plotted. Cells with reduced levels of either L7/L12 (genes *rplL*, *rplJ*) or L23 (*rplW*) showed increased sensitivity to tetracycline (Fig. 3). Cells expressing antisense to genes not known to be involved in protein synthesis (*atpB/E*, *visC*, *elaD*, *yohM*) did not show the same increased sensitivity to tetracycline, validating the specificity of this assay (Fig. 3).

In addition to the above, it has been observed in initial experiments that clones expressing antisense RNA to genes involved in protein synthesis (including genes encoding ribosomal proteins L7/L12 & L10, L7/L12 alone, L22, and L18, as well as genes encoding rRNA and Elongation Factor G) have increased sensitivity to the macrolide, erythromycin, whereas clones expressing antisense to the non-protein synthesis genes *elaD*, *atpB/E* and *visC* do not. Furthermore, the clone expressing antisense to *rplL* and *rplJ* does not show increased sensitivity to nalidixic acid and ofloxacin, antibiotics which do not inhibit protein synthesis.

The results with the ribosomal protein genes *rplL*, *rplJ*, and *rplW* as well as the initial results using various other antisense clones and antibiotics show that limiting the concentration of an antibiotic target makes cells more sensitive to the antimicrobial agents that specifically interact with that protein. The results also show that these cells are sensitized to antimicrobial agents that inhibit the overall function in which the protein target is involved but are not sensitized to antimicrobial agents that inhibit other functions.

5 The cell based assay described above may also be used to identify the biological pathway in which a proliferation-required nucleic acid or its gene product lies. In such methods, cells expressing a sub-lethal level of antisense to a target proliferation-required nucleic acid and control cells in which expression of the antisense has not been induced are contacted with a panel of antibiotics known to act in various pathways. If the antibiotic acts in the pathway in which the target proliferation-required nucleic acid or its gene product lies, cells in which expression of the antisense has been induced will be more sensitive to the antibiotic than cells in which expression of the antisense has not been induced.

10 5 As a control, the results of the assay may be confirmed by contacting a panel of cells expressing antisense nucleic acids to many different proliferation-required genes including the target proliferation-required gene. If the antibiotic is acting specifically, heightened sensitivity to the antibiotic will be observed only in the cells expressing antisense to a target proliferation-required gene (or cells expressing antisense to other proliferation-required genes in the same pathway as the target proliferation-required gene) but will not be observed generally in all cells expressing antisense to proliferation-required genes.

15 10 Similarly, the above method may be used to determine the pathway on which a test antibiotic acts. A panel of cells, each of which expresses antisense to a proliferation-required nucleic acid in a known pathway, is contacted with a compound for which it is desired to determine the pathway on which it acts. The sensitivity of the panel of cells to the test compound is determined in cells in which expression of the antisense has been induced and in control cells in which expression of the antisense has not been induced. If the test antibiotic acts on the pathway on which an antisense nucleic acid acts, cells in which expression of the antisense has been induced will be more sensitive to the antibiotic than cells in which expression of the antisense has not been induced. In addition, control cells in which expression of antisense to proliferation-required genes in other pathways has been induced will not exhibit heightened sensitivity to the antibiotic. In this way, the pathway on which the test antibiotic acts may be determined.

20 20 The Example below provides one method for performing such assays.

#### EXAMPLE 10

##### 25 Identification of the Pathway in which a Proliferation-Required Gene Lies or the Pathway on which an Antibiotic Acts

##### 30 A. Preparation of Bacterial Stocks for Assay

40 To provide a consistent source of cells to screen, frozen stocks of host bacteria containing the desired antisense construct are prepared using standard microbiological techniques. For example, a single clone of the organism can be isolated by streaking out a sample of the original stock onto an agar plate containing nutrients for cell growth and an antibiotic for which the antisense construct contains a gene which confers resistance. After overnight growth an isolated colony is picked from the plate with a sterile needle and transferred to an appropriate liquid growth media containing the antibiotic required for maintenance of the plasmid. The cells are incubated at 30°C to 37°C with vigorous shaking for 4 to

6 hours to yield a culture in exponential growth. Sterile glycerol is added to 15% (volume to volume) and 100 $\mu$ L to 500  $\mu$ L aliquots are distributed into sterile cryotubes, snap frozen in liquid nitrogen, and stored at -80°C for future assays.

**B. Growth of Bacteria for Use in the Assay**

A day prior to an assay, a stock vial is removed from the freezer, rapidly thawed (37°C water bath) and a loop of culture is streaked out on an agar plate containing nutrients for cell growth and an antibiotic to which the antisense construct confers resistance. After overnight growth at 37°C, ten randomly chosen, isolated colonies are transferred from the plate (sterile inoculum loop) to a sterile tube containing 5 mL of LB medium containing the antibiotic to which the antisense vector confers resistance. After vigorous mixing to form a homogeneous cell suspension, the optical density of the suspension is measured at 600 nm (OD600) and if necessary an aliquot of the suspension is diluted into a second tube of 5 mL, sterile, LB medium plus antibiotic to achieve an  $OD_{600} \leq 0.02$  absorbance units. The culture is then incubated at 37° C for 1-2 hrs with shaking until the OD600 reaches OD 0.2 – 0.3. At this point the cells are ready to be used in the assay.

**C. Selection of Media to be Used in Assay**

Two fold dilution series of the inducer are generated in culture media containing the appropriate antibiotic for maintenance of the antisense construct. Several media are tested side by side and three to four wells are used to evaluate the effects of the inducer at each concentration in each media. For example, M9 minimal media, LB broth, TBD broth and Muller-Hinton media may be tested with the inducer IPTG at the following concentrations, 50  $\mu$ M, 100  $\mu$ M, 200  $\mu$ M, 400  $\mu$ M, 600  $\mu$ M, 800  $\mu$ M and 1000  $\mu$ M. Equal volumes of test media-inducer and cells are added to the wells of a 384 well microtiter plate and mixed. The cells are prepared as described above and diluted 1:100 in the appropriate media containing the test antibiotic immediately prior to addition to the microtiter plate wells. For a control, cells are also added to several wells of each media that do not contain inducer, for example 0 M IPTG. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD600 of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of inducer is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in media without inducer. The medium yielding greatest sensitivity to inducer is selected for use in the assays described below.

**D. Measurement of Test Antibiotic Sensitivity in the Absence of Antisense Construct Induction**

Two-fold dilution series of antibiotics of known mechanism of action are generated in the culture media selected for further assay development that has been supplemented with the antibiotic used to maintain the construct. A panel of test antibiotics known to act on different pathways is tested side by side with three to four wells being used to evaluate the effect of a test antibiotic on cell growth at each concentration. Equal volumes of test antibiotic and cells are added to the wells of a 384 well microtiter plate and mixed. Cells are prepared as described above using the media selected for assay development supplemented with the antibiotic required to maintain the antisense construct and are diluted 1:100 in identical media immediately prior to addition to the microtiter plate wells. For a control, cells are also added to several

5 wells that contain the solvent used to dissolve the antibiotics but no antibiotic. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD600 of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of antibiotic is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in media without antibiotic. A plot of percent inhibition against  
10 5 log[antibiotic concentration] allows extrapolation of an IC<sub>50</sub> value for each antibiotic.

E. Measurement of Test Antibiotic Sensitivity in the Presence of Antisense Construct Inducer

15 The culture media selected for use in the assay is supplemented with inducer at concentrations shown to inhibit cell growth by 50 and 80% as described above and the antibiotic used to maintain the construct. Two fold dilution series of the panel of test antibiotics used above are generated in each of these media. Several antibiotics are tested side by side  
20 10 with three to four wells being used to evaluate the effects of an antibiotic on cell growth at each concentration, in each media. Equal volumes of test antibiotic and cells are added to the wells of a 384 well microtiter plate and mixed. Cells are prepared as described above using the media selected for use in the assay supplemented with the antibiotic required to maintain the antisense construct. The cells are diluted 1:100 into two 50 mL aliquots of identical media containing concentrations of inducer that have been shown to inhibit cell growth by 50% and 80 % respectively and incubated at  
25 15 37°C with shaking for 2.5 hours. Immediately prior to addition to the microtiter plate wells, the cultures are adjusted to an appropriate OD<sub>600</sub> (typically 0.002) by dilution into warm (37°C) sterile media supplemented with identical concentrations of the inducer and antibiotic used to maintain the antisense construct. For a control, cells are also added to several wells that contain solvent used to dissolve test antibiotics but which contain no antibiotic. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD600 of the wells over an 18-  
30 20 hour period. The percent inhibition of growth produced by each concentration of antibiotic is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in media without antibiotic. A plot of percent inhibition against log[antibiotic concentration] allows extrapolation of an IC<sub>50</sub> value for each antibiotic.

F. Determining the Specificity of the Test Antibiotics

35 A comparison of the IC<sub>50</sub>s generated by antibiotics of known mechanism of action under antisense induced and non-induced conditions allows the pathway in which a proliferation-required nucleic acid lies to be identified. If cells  
40 25 expressing an antisense nucleic acid against a proliferation-required gene are selectively sensitive to an antibiotic acting via a particular pathway, then the gene against which the antisense acts is involved in the pathway in which the antibiotic acts.

G. Identification of Pathway in which a Test Antibiotic Acts

30 As discussed above, the cell based assay may also be used to determine the pathway against which a test antibiotic acts. In such an analysis, the pathways against which each member of a panel of antisense nucleic acids acts are identified as described above. A panel of cells, each containing an inducible antisense vector against a gene in a known proliferation-required pathway, is contacted with a test antibiotic for which it is desired to determine the pathway  
45 50

on which it acts under inducing an non-inducing conditions. If heightened sensitivity is observed in induced cells expressing antisense against a gene in a particular pathway but not in induced cells expressing antisense against genes in other pathways, then the test antibiotic acts against the pathway for which heightened sensitivity was observed.

One skilled in the art will appreciate that further optimization of the assay conditions, such as the concentration of inducer used to induce antisense expression and/or the growth conditions used for the assay (for example incubation temperature and media components) may further increase the selectivity and/or magnitude of the antibiotic sensitization exhibited.

The following example confirms the effectiveness of the methods described above.

#### EXAMPLE 11

##### Identification of the Pathway in which a Proliferation-Required Gene Lies

Antibiotics of various chemical classes and modes of action were purchased from Sigma Chemicals (St. Louis, MO). Stock solutions were prepared by dissolving each antibiotic in an appropriate aqueous solution based on information provided by the manufacturer. The final working solution of each antibiotic contained no more than 0.2% (w/v) of any organic solvent. To determine their potency against a bacterial strain engineered for expression of an antisense against a proliferation-required 50S ribosomal protein, each antibiotic was serially diluted two or three fold in growth medium supplemented with the appropriate antibiotic for maintenance of the anti-sense construct. At least ten dilutions were prepared for each antibiotic. 25  $\mu$ L aliquots of each dilution were transferred to discrete wells of a 384-well microplate (the assay plate) using a multi-channel pipette. Quadruplicate wells were used for each dilution of an antibiotic under each treatment condition (plus and minus inducer). Each assay plate contained twenty wells for cell growth controls (growth media replacing antibiotic), ten wells for each treatment (plus and minus inducer, in this example IPTG). Assay plates were usually divided into the two treatments: half the plate containing induced cells and an appropriate concentrations of inducer (in this example IPTG) to maintain the state of induction, the other half containing non-induced cells in the absence of IPTG.

Cells for the assay were prepared as follows. Bacterial cells containing a construct, from which expression of antisense nucleic acid against *rplL* and *rplJ*, which encode proliferation-required 50S ribosomal subunit proteins, is inducible in the presence of IPTG, were grown into exponential growth ( $OD_{600}$  0.2 to 0.3) and then diluted 1:100 into fresh media containing either 400  $\mu$ M or 0  $\mu$ M inducer (IPTG). These cultures were incubated at 37° C for 2.5 hr. After a 2.5 hr incubation, induced and non-induced cells were respectively diluted into an assay medium at a final  $OD_{600}$  value of 0.0004. The medium contained an appropriate concentration of the antibiotic for the maintenance of the anti-sense construct. In addition, the medium used to dilute induced cells was supplemented with 800  $\mu$ M IPTG so that addition to the assay plate would result in a final IPTG concentration of 400  $\mu$ M. Induced and non-induced cell suspensions were dispensed (25  $\mu$ L/well) into the appropriate wells of the assay plate as discussed previously. The plate was then loaded into a plate reader, incubated at constant temperature, and cell growth was monitored in each well by the measurement of



light scattering at 595 nm. Growth was monitored every 5 minutes until the cell culture attained a stationary growth phase. For each concentration of antibiotic, a percentage inhibition of growth was calculated at the time point corresponding to mid-exponential growth for the associated control wells (no antibiotic, plus or minus IPTG). For each antibiotic and condition (plus or minus IPTG), a plot of percent inhibition versus log of antibiotic concentration was generated and the IC<sub>50</sub> determined. A comparison of the IC<sub>50</sub> for each antibiotic in the presence and absence of IPTG revealed whether induction of the antisense construct sensitized the cell to the mechanism of action exhibited by the antibiotic. Cells which exhibited a significant (standard statistical analysis) numerical decrease in the IC<sub>50</sub> value in the presence of inducer were considered to have an increased sensitivity to the test antibiotic.

The results are provided in the table below, which lists the classes and names of the antibiotics used in the analysis, the targets of the antibiotics, the IC<sub>50</sub> in the absence of IPTG, the IC<sub>50</sub> in the presence of IPTG, the concentration units for the IC<sub>50</sub>s, the fold increase in IC<sub>50</sub> in the presence of IPTG, and whether increased sensitivity was observed in the presence of IPTG.

**TABLE IV**  
Effect of Expression of Antisense RNA to rplL and rplJ on Antibiotic Sensitivity

| ANTIBIOTIC CLASS / Names                       | TARGET                           | IC50 (IPTG) | IC50 (+IPTG) | Conc. Unit | Fold Increase in Sensitivity | Sensitivity Increased? |
|--|----------------------------------|-------------|--------------|------------|------------------------------|------------------------|
| <b>PROTEIN SYNTHESIS INHIBITOR ANTIBIOTICS</b> |                                  |             |              |            |                              |                        |
| <b>AMINOGLYCOSIDES</b>                         |                                  |             |              |            |                              |                        |
| Gentamicin                                     | 30S ribosome function            | 2715        | 19.19        | ng/ml      | 141                          | Yes                    |
| Streptomycin                                   | 30S ribosome function            | 11280       | 161          | ng/ml      | 70                           | Yes                    |
| Spectinomycin                                  | 30S ribosome function            | 18050       | < 156        | ng/ml      |                              | Yes                    |
| Tobramycin                                     | 30S ribosome function            | 3594        | 70.58        | ng/ml      | 51                           | Yes                    |
| <b>MACROLIDES</b>                              |                                  |             |              |            |                              |                        |
| Erythromycin                                   | 50S ribosome function            | 7467        | 187          | ng/ml      | 40                           | Yes                    |
| <b>AROMATIC POLYKETIDES</b>                    |                                  |             |              |            |                              |                        |
| Tetracycline                                   | 30S ribosome function            | 199.7       | 1.83         | ng/ml      | 109                          | Yes                    |
| Minocycline                                    | 30S ribosome function            | 668.4       | 3.897        | ng/ml      | 172                          | Yes                    |
| Doxycycline                                    | 30S ribosome function            | 413.1       | 27.81        | ng/ml      | 15                           | Yes                    |
| <b>OTHER PROTEIN SYNTHESIS INHIBITORS</b>      |                                  |             |              |            |                              |                        |
| Fusidic acid                                   | Elongation Factor G function     | 59990       | 641          | ng/ml      | 94                           | Yes                    |
| Chloramphenicol                                | 30S ribosome function            | 465.4       | 1.516        | ng/ml      | 307                          | Yes                    |
| Lincomycin                                     | 50S ribosome function            | 47150       | 324.2        | ng/ml      | 145                          | Yes                    |
| <b>OTHER ANTIBIOTIC MECHANISMS</b>             |                                  |             |              |            |                              |                        |
| <b>B-LACTAMS</b>                               |                                  |             |              |            |                              |                        |
| Cefoxitin                                      | Cell wall biosynthesis           | 2782        | 2484         | ng/ml      | 1                            | No                     |
| Cefotaxime                                     | Cell wall biosynthesis           | 24.3        | 24.16        | ng/ml      | 1                            | No                     |
| <b>DNA SYNTHESIS INHIBITORS</b>                |                                  |             |              |            |                              |                        |
| Nalidixic acid                                 | DNA Gyrase activity              | 6973        | 6025         | ng/ml      | 1                            | No                     |
| Ofloxacin                                      | DNA Gyrase activity              | 49.61       | 45.89        | ng/ml      | 1                            | No                     |
| <b>OTHER</b>                                   |                                  |             |              |            |                              |                        |
| Bacitracin                                     | Cell membrane function           | 4077        | 4677         | mg/ml      | 1                            | No                     |
| Trimethoprim                                   | Dihydrofolate Reductase activity | 128.9       | 181.87       | ng/ml      | 1                            | No                     |
| Vancomycin                                     | Cell wall biosynthesis           | 145400      | 72550        | ng/ml      | 2                            | No                     |

5           The above results demonstrate that induction of an antisense RNA to genes encoding 50S ribosomal subunit proteins results in a selective and highly significant sensitization of cells to antibiotics that inhibit ribosomal function and protein synthesis. The above results further demonstrate that induction of an antisense construct to an essential gene sensitizes an organism to compounds that interfere with that gene products' biological role. This sensitization is restricted to compounds that interfere with pathways associated with the targeted gene and its product.

10           Assays utilizing antisense constructs to essential genes can be used to identify compounds that specifically interfere with the activity of multiple targets in a pathway. Such constructs can be used to simultaneously screen a sample against multiple targets in one pathway in one reaction (Combinatorial HTS).

15           Furthermore, as discussed above, panels of antisense construct containing cells may be used to characterize the point of intervention of any compound affecting an essential biological pathway including antibiotics with no known mechanism of action.

20           Another embodiment of the present invention is a method for determining the pathway against which a test antibiotic compound is active in which the activity of target proteins or nucleic acids involved in proliferation-required pathways is reduced by contacting cells with a sublethal concentration of a known antibiotic which acts against the target protein or nucleic acid. In one embodiment, the target protein or nucleic acid is a target protein or nucleic acid corresponding to a proliferation-required nucleic acid identified using the methods described above. The method is similar to those described above for determining which pathway a test antibiotic acts against except that rather than reducing the activity or level of a proliferation-required gene product using a sublethal level of antisense to a proliferation-required nucleic acid, the activity or level of the proliferation-required gene product is reduced using sublethal level of a known antibiotic which acts against the proliferation required gene product.

25           Interactions between drugs which affect the same biological pathway has been described in the literature. For example, Mecillinam (Amdinocillin) binds to and inactivates the penicillin binding protein 2 (PBP2, product of the *mrdA* in *E. coli*). This antibiotic interacts with other antibiotics that inhibit PBP2 as well as antibiotics that inhibit other penicillin binding proteins such as PBP3 [(Gutmann, L., Vincent, S., Billot-Klein, D., Acar, J.F., Mrena, E., and Williamson, R. (1986) Involvement of penicillin-binding protein 2 with other penicillin-binding proteins in lysis of *Escherichia coli* by some beta-lactam antibiotics alone and in synergistic lytic effect of amdinocillin (mecillinam). *Antimicrobial Agents & Chemotherapy*, 30:906-912), the disclosure of which is incorporated herein by reference in its entirety]. Interactions between drugs could, therefore, involve two drugs that inhibit the same target protein or nucleic acid or inhibit different proteins or nucleic acids in the same pathway [(Fukuoka, T., Domon, H., Kakuta, M., Ishii, C., Hirasawa, A., Utsui, Y., Ohya, S., and Yasuda, H. (1997) Combination effect between panipenem and vancomycin on highly methicillin-resistant *Staphylococcus aureus*. *Japan. J. Antibio.* 50:411-419; Smith, C.E., Foleno, B.E., Barrett, J.F., and Froese, M.B. (1997) Assessment of the synergistic interactions of levofloxacin and ampicillin against *Enterococcus faecium* by the checkerboard agar dilution and time-kill methods. *Diagnos. Microbiol. Infect. Disease* 27:85-92; den Hollander, J.G., Horrevorts, A.M., van Goor, M.L.,

Verbrugh, H.A., and Mouton, J.W. (1997) Synergism between tobramycin and ceftazidime against a resistant *Pseudomonas aeruginosa* strain, tested in an in vitro pharmacokinetic model. *Antimicrobial Agents & Chemotherapy*. 41:95-110), the disclosure of all of which are incorporated herein by reference in their entireties).

Two drugs may interact even though they inhibit different targets. For example, the proton pump inhibitor, Omeprazole, and the antibiotic, Amoxycillin, two synergistic compounds acting together, can cure *Helicobacter pylori* infection ([Gabryelewicz, A., Laszewicz, W., Dzieniszewski, J., Ciok, J., Marlicz, K., Bielecki, D., Popiela, T., Legutko, J., Knapik, Z., Poniewierka, E. (1997) Multicenter evaluation of dual-therapy (omeprazole and amoxycillin) for *Helicobacter pylori*-associated duodenal and gastric ulcer (two years of the observation). *J. Physiol. Pharmacol.* 48 Suppl 4:93-105), the disclosure of which is incorporated herein by reference in its entirety].

The growth inhibition from the sublethal concentration of the known antibiotic may be at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, or at least about 75%, or more.

Alternatively, the sublethal concentration of the known antibiotic may be determined by measuring the activity of the target proliferation-required gene product rather than by measuring growth inhibition.

Cells are contacted with a combination of each member of a panel of known antibiotics at a sublethal level and varying concentrations of the test antibiotic. As a control, the cells are contacted with varying concentrations of the test antibiotic alone. The  $IC_{50}$  of the test antibiotic in the presence and absence of the known antibiotic is determined. If the  $IC_{50}$ s in the presence and absence of the known drug are substantially similar, then the test drug and the known drug act on different pathways. If the  $IC_{50}$ s are substantially different, then the test drug and the known drug act on the same pathway.

Another embodiment of the present invention is a method for identifying a candidate compound for use as an antibiotic in which the activity of target proteins or nucleic acids involved in proliferation-required pathways is reduced by contacting cells with a sublethal concentration of a known antibiotic which acts against the target protein or nucleic acid. In one embodiment, the target protein or nucleic acid is a target protein or nucleic acid corresponding to a proliferation-required nucleic acid identified using the methods described above. The method is similar to those described above for identifying candidate compounds for use as antibiotics except that rather than reducing the activity or level of a proliferation-required gene product using a sublethal level of antisense to a proliferation-required nucleic acid, the activity or level of the proliferation-required gene product is reduced using a sublethal level of a known antibiotic which acts against the proliferation required gene product.

The growth inhibition from the sublethal concentration of the known antibiotic may be at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, or at least about 75%, or more.

Alternatively, the sublethal concentration of the known antibiotic may be determined by measuring the activity of the target proliferation-required gene product rather than by measuring growth inhibition.

In order to characterize test compounds of interest, cells are contacted with a panel of known antibiotics at a sublethal level and one or more concentrations of the test compound. As a control, the cells are contacted with the same concentrations of the test compound alone. The  $IC_{50}$  of the test compound in the presence and absence of the known antibiotic is determined. If the  $IC_{50}$  of the test compound is substantially different in the presence and absence of the known drug then the test compound is a good candidate for use as an antibiotic. As discussed above, once a candidate compound is identified using the above methods its structure may be optimized using standard techniques such as combinatorial chemistry.

Representative known antibiotics which may be used in each of the above methods are provided in the table below. However, it will be appreciated that other antibiotics may also be used.

| ANTIBIOTIC                                       | INHIBITS/TARGET  | RESISTANT MUTANTS   |
|--|--|---|
| <b>Inhibitors of Transcription</b>               |  |   |
| Rifamycin, 1959 Rifampicin                       | Inhibits initiation of transcription/ $\beta$ -subunit RNA polymerase, <i>rpoB</i> | <i>rpoB</i> , <i>crp</i> , <i>cyaA</i>                                |
| Rifabutin Rifaximin                              |  |   |
| Streptolydigin                                   | Accelerates transcription chain termination/ $\beta$ -subunit RNA polymerase       | <i>rpoB</i>   |
| Streptovaricin                                   | an acyclic ansamycin, inhibits RNA polymerase                                      | <i>rpoB</i>   |
| Actinomycin D + EDTA                             | Intercalates between 2 successive G-C pairs, <i>rpoB</i> , inhibits RNA synthesis  | <i>pldA</i>   |
| <b>Inhibitors of Nucleic Acid Metabolism</b>     |  |   |
| Quinolones, 1962 Nalidixic acid                  | subunit gyrase and/or topoisomerase IV, <i>gyrA</i>                                |   |
| Oxolinic acid                                    |  | <i>gyrAorB</i> , <i>icd</i> , <i>sloB</i>                             |
| Fluoroquinolones Ciprofloxacin, 1983 Norfloxacin | subunit gyrase, <i>gyrA</i> and/or topoisomerase IV (probable target in Staph)     | <i>gyrA</i><br><i>norA</i> (efflux in Staph)<br><i>hipQ</i>           |
| Coumerins Novobiocin                             | Inhibits ATPase activity of $\beta$ -subunit gyrase, <i>gyrB</i>                   | <i>gyrB</i> , <i>cysB</i> , <i>cysE</i> , <i>nov</i> ,<br><i>ompA</i> |
| Coumermycin                                      | Inhibits ATPase activity of $\beta$ -subunit gyrase, <i>gyrB</i>                   | <i>gyrB</i> , <i>hisW</i>   |
| Albicidin  | DNA synthesis  | <i>tsx</i> (nucleoside channel)                                       |
| Metronidazole                                    | Causes single-strand breaks in DNA   | <i>nar</i>  |
| <b>Inhibitors of Metabolic Pathways</b>          |  |   |
| Sulfonamides, 1932 Sulfanilamide                 | blocks synthesis of dihydrofolate, dihydro-<br>pteroate synthesis, <i>folP</i>     | <i>folP</i> , <i>gpt</i> , <i>pabA</i> , <i>pabB</i> ,<br><i>pabC</i> |
| Trimethoprim, 1962                               | Inhibits dihydrofolate reductase, <i>folA</i>                                      | <i>folA</i> , <i>thyA</i>   |
| Showdomycin                                      | Nucleoside analogue capable of alkylating  | <i>nupC</i> , <i>prp</i>  |

| ANTIBIOTIC                                       | INHIBITS/TARGET   | RESISTANT MUTANTS   |
|--|---|---|
| Thiolactomycin                                   | sulfhydryl groups, inhibitor of thymidylate synthetase<br>type II fatty acid synthase inhibitor   | <i>emrB</i><br><i>fadB</i> , <i>emrB</i> due to gene dosage   |
| Psicofuranine                                    | Adenosine glycoside antibiotic, target is GMP synthetase  | <i>guaA,B</i>   |
| Triclosan  | Inhibits fatty acid synthesis   | <i>fabI (envM)</i>  |
| Diazaborines Isoniazid, Ethionamide              | heterocyclic, contains boron, inhibit fatty acid synthesis, enoyl-ACP reductase, <i>fabI</i>  | <i>fabI (envM)</i>  |
| <b>Inhibitors of Translation</b>                 |   |   |
| Phenylpropanoids                                 |   |   |
| Chloramphenicol, 1947                            | Binds to ribosomal peptidyl transfer center preventing peptide translocation/ binds to S6, L3, L6, L14, L16, L25, L26, L27, but preferentially to L16 | <i>rm</i> , <i>cmlA</i> , <i>marA</i> , <i>ompF</i> , <i>ompR</i>   |
| Tetracyclines, 1948, type II polyketides         | Binding to 30S ribosomal subunit, "A" site on 30S subunit, blocks peptide elongation, strongest binding to S7   | <i>clmA (cmr)</i> , <i>mar</i> , <i>ompF</i>  |
| Minocycline                                      |   |   |
| Doxycycline                                      |   |   |
| Macrolides (type I polyketides)                  |   |   |
| Erythromycin, 1950                               | Binding to 50 S ribosomal subunit, 23S rRNA, blocks peptide translocation, L15, L4, L12   |   |
| Carbomycin, Spiramycin                           |   | <i>rm</i> , <i>rplC</i> , <i>rplD</i> , <i>rplV</i> , <i>mec</i>  |
| etc  |   |   |
| Aminoglycosides Streptomycin, 1944               | Irreversible binding to 30S ribosomal subunit, prevents translation or causes mistranslation of mRNA/16S rRNA   | <i>rpsL</i> , <i>strC,M</i> , <i>ubiF</i><br><i>atpA-E</i> , <i>ecfB</i> ,<br><i>hemAC,D,E,G</i> , <i>topA</i> ,<br><i>rpsC,D,E</i> , <i>rm</i> , <i>spcB</i><br><i>atpA-atpE</i> , <i>cpxA</i> , <i>ecfB</i> ,<br><i>hemA,B,L</i> , <i>topA</i><br><i>ksgA,B,C,D</i> , <i>rplB,K</i> ,<br><i>rpsL,N,M,R</i><br><i>rplF</i> , <i>ubiF</i><br><i>cpxA</i><br><i>rpsL</i> |
| Neomycin   |   |   |
| Spectinomycin Kanamycin                          |   |   |
| Kasugamycin                                      |   |   |
| Gentamicin, 1963                                 |   |   |
| Amikacin   |   |   |
| Paromycin  |   |   |
| Lincosamides                                     |   |   |
| Lincomycin, 1955 Clindamycin                     | Binding to 50 S ribosomal subunit, blocks peptide translocation   | <i>linB</i> , <i>rplN,O</i> , <i>rpsG</i>   |
| Streptogramins Virginiamycin, 1955 Pristinamycin | 2 components, Streptogramins A&B, bind to the 50S ribosomal subunit blocking peptide translocation and peptide bond formation                         |   |
| Synercid: quinupristin /dalfopristin             |   |   |
| Fusidanes  |   |   |
| Fusidic Acid                                     | Inhibition of elongation factor G (EF-G) prevents peptide translocation   | <i>fusA</i>   |
| Kirromycin (Mocimycin)                           | Inhibition of elongation factor TU (EF-Tu), prevents peptide bond formation   | <i>tufA,B</i>   |

| ANTIBIOTIC                                | INHIBITS/TARGET  | RESISTANT MUTANTS  |
|---|--|--|
| Pulvomycin                                | Binds to and inhibits EF-TU  |  |
| Thiopeptin                                | Sulfur-containing antibiotic, inhibits protein synthesis, EF-G   | <i>rplE</i>  |
| Tiamulin                                  | Inhibits protein synthesis   | <i>rplC, rplD</i>  |
| Negamycin                                 | Inhibits termination process of protein synthesis  | <i>prfB</i>  |
| Oxazolidinones Linezolid                  | 23S rRNA   |  |
| Isoniazid                                 |  | <i>pdx</i>   |
| Nitrofurantoin                            | Inhibits protein synthesis, nitroreductases convert nitrofurantoin to highly reactive electrophilic intermediates which attack bacterial ribosomal proteins non-specifically                 | <i>nfnA, B</i>   |
| Pseudomonic Acids Mupirocin (Bactroban)   | Inhibition of isoleucyl tRNA synthetase-used for Staph, topical cream, nasal spray   | <i>ileS</i>  |
| Indolmycin                                | Inhibits tryptophanyl-tRNA synthetase  | <i>trpS</i>  |
| Viomycin                                  |  | <i>rmaA</i> (23S rRNA methyltransferase; mutant has slow growth rate, slow chain elongation rate, and viomycin resistance) |
| Thiopeptides                              | Binds to L11-23S RNA complex   |  |
| Thiostrepton                              | Inhibits GTP hydrolysis by EF-G  |  |
| Micrococin                                | Stimulates GTP hydrolysis by EF-G  |  |
| <b>Inhibitors of Cell Walls/Membranes</b> |  |  |
| <b><math>\beta</math>-lactams</b>         |  |  |
| Penicillin, 1929 Ampicillin               | Inhibition of one or more cell wall transpeptidases, endopeptidases, and glycosidases (PBP's), of the 12 PBPs only 2 are essential: <i>mrdA</i> (PBP2) and <i>ftsI</i> ( <i>pbpB</i> , PBP3) | <i>ampC, ampD, ampE, envZ, galU, hipA, hipQ, ompC, ompF, ompR, ptsI, rfa, tolD, tolE</i>                                   |
| Methicillin, 1960                         |  | <i>tonB</i>  |
| Cephalosporins, 1962                      |  | <i>alaS, argS, crp, cyaA, envB, mrdA, B, mreB, C, D</i>  |
| Mecillinam (amdinocillin)                 | Binds to and inactivates PBP2 ( <i>mrdA</i> )<br>Inactivates PBP3 ( <i>ftsI</i> )  |  |
| Aztreonam (Furazlocillin)                 |  | <i>dppA</i>  |
| Bacilysin, Tetaine                        | Dipeptide, inhib glucosamine synthase  |  |
| Glycopeptides Vancomycin, 1955            | Inhib G+ cell wall syn, binds to terminal D-alanyl-D-alanine of pentapeptide,  |  |
| Polypeptides Bacitracin                   | Prevents dephosphorylation and regeneration of lipid carrier   | <i>rfa</i>   |
| Cyclic lipopeptide Daptomycin, 1980       | Disrupts multiple aspects of membrane  |  |

|    |   |  |   |
|----|---|--|---|
| 5  |   | function, including peptidoglycan synthesis, lipoteichoic acid synthesis, and the bacterial membrane potential   |   |
|    | Cyclic polypeptides Polymixin, 1939               | Surfactant action disrupts cell membrane lipids, binds lipid A moiety of LPS   | <i>pmrA</i>                                   |
| 10 | Fosfomycin, 1969                                  | Analogue of P-enolpyruvate, inhibits 1 <sup>st</sup> step in peptidoglycan synthesis - UDP-N-acetylglucosamine enolpyruvyl transferase, <i>murA</i> . Also acts as immunosuppressant | <i>murA, crp, cysA glpT, hipA, ptsI, whpT</i> |
|    | Cycloserine                                       | Prevents formation of D-ala dimer, inhibits D-ala ligase, <i>ddlA,B</i>  | <i>hipA, cycA</i>                             |
| 15 | Alafosfalin                                       | phosphonodipeptide, cell wall synthesis inhibitor, potentiator of $\beta$ -lactams   | <i>pepA, tpp</i>                              |
|    | <b>Inhibitors of Protein Processing/Transport</b> |  |   |
|    | Globomycin  | Inhibits signal peptidase II (cleaves polipoproteins subsequent to lipid modification, <i>lspA</i> )   | <i>lpp, dnaE</i>                              |
| 20 |   |  |   |

## EXAMPLE 12

Transfer of Exogenous Nucleic Acid Sequences to other Bacterial Species Using the *E. coli* Expression Vectors or Expression Vectors Functional in Bacterial Species other than *E. coli*.

5 The above methods were validated using antisense nucleic acids which inhibit the growth of *E. coli* which were identified using methods similar to those described above. Expression vectors which inhibited growth of *E. coli* upon induction of antisense RNA expression with IPTG were transformed directly into *Enterobacter cloacae*, *Klebsiella pneumoniae* or *Salmonella typhimurium*. The transformed cells were then assayed for growth inhibition according to the method of Example 1. After growth in liquid culture, cells were plated at various serial dilutions and a score determined by calculating the log difference in growth for INDUCED vs. UNINDUCED antisense RNA expression as determined by the maximum 10 fold dilution at which a colony was observed. The results of these experiments are listed below in Table VI. If there was no effect of antisense RNA expression in an organism, the clone is minus in Table VI. In contrast, a positive in Table VI means that at least 10 fold more cells were required to observe a colony on the induced plate than on the non-induced plate under the conditions used and in that organism.

15 Sixteen of the constructs were found to inhibit growth in all the organisms tested upon induction of antisense RNA expression with IPTG. Those skilled in the art will appreciate that a negative result in a heterologous organism does not mean that that organism is missing that gene nor does it mean that the gene is unessential. However, a positive result means that the heterologous organism contains a homologous gene which is required for proliferation of that organism. The homologous gene may be obtained using the methods described herein. Those cells that are inhibited by antisense may be used in cell based assays as described herein for the identification and characterization of compounds in order to



develop antibiotics effective in these organisms. Those skilled in the art will appreciate that an antisense molecule which works in the organism from which it was obtained will not always work in a heterologous organism.

**TABLE VI**  
Sensitivity of Other Microorganisms to Antisense Nucleic Acids That Inhibit Proliferation in *E. coli*

| Mol. No. | <i>S. typhimurium</i> | <i>E. cloacae</i> | <i>K. pneumoniae</i> |
|----------|-----------------------|-------------------|----------------------|
| EcXA001  | +                     | +                 | -                    |
| EcXA004  | -                     | -                 | -                    |
| EcXA005  | +                     | +                 | +                    |
| EcXA006  | -                     | -                 | -                    |
| EcXA007  | -                     | +                 | -                    |
| EcXA008  | +                     | -                 | +                    |
| EcXA010  | +                     | +                 | +                    |
| EcXA011  | -                     | +                 | -                    |
| EcXA012  | -                     | +                 | -                    |
| EcXA013  | +                     | +                 | +                    |
| EcXA014  | +                     | +                 | -                    |
| EcXA015  | -                     | +                 | +                    |
| EcXA016  | +                     | +                 | +                    |
| EcXA017  | +                     | +                 | +                    |
| EcXA018  | +                     | +                 | +                    |
| EcXA019  | +                     | +                 | +                    |
| EcXA020  | +                     | +                 | +                    |
| EcXA021  | +                     | +                 | +                    |
| EcXA023  | +                     | +                 | +                    |
| EcXA024  | +                     | -                 | +                    |
| EcXA025  | -                     | -                 | -                    |
| EcXA026  | +                     | +                 | -                    |
| EcXA027  | +                     | +                 | +                    |
| EcXA028  | +                     | -                 | -                    |
| EcXA029  | -                     | -                 | -                    |

| Mol. No. | <i>S. typhimurium</i> | <i>E. cloacae</i> | <i>K. pneumoniae</i> |
|----------|-----------------------|-------------------|----------------------|
| EcXA030  | +                     | +                 | +                    |
| EcXA031  | +                     | -                 | -                    |
| EcXA032  | +                     | -                 | -                    |
| EcXA033  | +                     | +                 | +                    |
| EcXA034  | +                     | +                 | +                    |
| EcXA035  | -                     | -                 | -                    |
| EcXA036  | +                     | -                 | +                    |
| EcXA037  | -                     | +                 | -                    |
| EcXA038  | +                     | +                 | -                    |
| EcXA039  | +                     | -                 | -                    |
| EcXA041  | +                     | +                 | +                    |
| EcXA042  | -                     | +                 | +                    |
| EcXA044  | -                     | -                 | -                    |
| EcXA045  | -                     | +                 | -                    |
| EcXA046  | -                     | -                 | -                    |
| EcXA047  | +                     | +                 | -                    |
| EcXA048  | -                     | -                 | -                    |
| EcXA049  | +                     | -                 | -                    |
| EcXA050  | -                     | -                 | -                    |
| EcXA051  | +                     | -                 | -                    |
| EcXA052  | +                     | -                 | -                    |
| EcXA053  | +                     | +                 | +                    |
| EcXA054  | -                     | -                 | +                    |
| EcXA055  | +                     | -                 | -                    |

## EXAMPLE 13

Use of Identified Exogenous Nucleic Acid Sequences as Probes

The identified sequence of the present invention can be used as probes to obtain the sequence of additional genes of interest from a second organism. For example, probes to potential bacterial target proteins may be hybridized to nucleic acids from other organisms including other bacteria and higher organisms, to identify homologous sequences. Such

5 hybridization might indicate that the protein encoded by the gene to which the probe corresponds is found in humans and therefore not necessarily a good drug target. Alternatively, the gene can be conserved only in bacteria and therefore would be a good drug target for a broad spectrum antibiotic or antimicrobial.

10 5 Probes derived from the identified nucleic acid sequences of interest or portions thereof can be labeled with detectable labels familiar to those skilled in the art, including radioisotopes and non-radioactive labels, to provide a detectable probe. The detectable probe can be single stranded or double stranded and can be made using techniques known in the art, including *in vitro* transcription, nick translation, or kinase reactions. A nucleic acid sample containing a sequence capable of hybridizing to the labeled probe is contacted with the labeled probe. If the nucleic acid in the sample is double stranded, it can be denatured prior to contacting the probe. In some applications, the nucleic acid sample can be immobilized on a surface such as a nitrocellulose or nylon membrane. The nucleic acid sample can comprise nucleic acids obtained from a variety of sources, including genomic DNA, cDNA libraries, RNA, or tissue samples.

15 10 Procedures used to detect the presence of nucleic acids capable of hybridizing to the detectable probe include well known techniques such as Southern blotting, Northern blotting, dot blotting, colony hybridization, and plaque hybridization. In some applications, the nucleic acid capable of hybridizing to the labeled probe can be cloned into vectors such as expression vectors, sequencing vectors, or *in vitro* transcription vectors to facilitate the characterization and expression of the hybridizing nucleic acids in the sample. For example, such techniques can be used to isolate, purify and clone sequences from a genomic library, made from a variety of bacterial species, which are capable of hybridizing to probes made from the sequences identified in Examples 5 and 6.

#### EXAMPLE 14

##### Preparation of PCR Primers and Amplification of DNA

30 20 The identified *E. coli* genes corresponding directly to or located within the operon of nucleic acid sequences required for proliferation or portions thereof can be used to prepare PCR primers for a variety of applications, including the identification or isolation of homologous sequences from other species, for example *S. typhimurium*, *E. cloacae*, and *Klebsiella pneumoniae*, which contain part or all of the homologous genes. Because homologous genes are related but not identical in sequence, those skilled in the art will often employ degenerate sequence PCR primers. Such degenerate sequence primers are designed based on conserved sequence regions, either known or suspected, such as conserved coding regions. The successful production of a PCR product using degenerate probes generated from the sequences identified herein would indicate the presence of a homologous gene sequence in the species being screened. The PCR primers are at least 10 bases, and preferably at least 20 bases in length. More preferably, the PCR primers are at least 20-30 bases in length. In some embodiments, the PCR primers can be more than 30 bases in length. It is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to Genetic Engineering White, B.A. Ed. in *Methods in Molecular Biology* 67: Humana Press, Totowa 1997. When the entire coding sequence of the target gene is known, the 5' and 3' regions of the target gene

5 can be used as the sequence source for PCR probe generation. In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites.

#### EXAMPLE 15

##### Inverse PCR

15 The technique of inverse polymerase chain reaction can be used to extend the known nucleic acid sequence identified in Examples 5 and 6. The inverse PCR reaction is described generally by Ochman et al., in Ch. 10 of *PCR Technology: Principles and Applications for DNA Amplification*, (Henry A. Erlich, Ed.) W.H. Freeman and Co. (1992). Traditional PCR requires two primers that are used to prime the synthesis of complementary strands of DNA. In inverse PCR, only a core sequence need be known.

20 Using the sequences identified as relevant from the techniques taught in Examples 5 and 6 and applied to other species of bacteria, a subset of exogenous nucleic sequences are identified that correspond to genes or operons that are required for bacterial proliferation. In species for which a genome sequence is not known, the technique of inverse PCR provides a method for obtaining the gene in order to determine the sequence or to place the probe sequences in full context to the target sequence to which the identified exogenous nucleic acid sequence binds.

25 To practice this technique, the genome of the target organism is digested with an appropriate restriction enzyme so as to create fragments of nucleic acid that contain the identified sequence as well as unknown sequences that flank the identified sequence. These fragments are then circularized and become the template for the PCR reaction. PCR primers are designed in accordance with the teachings of Example 15 and directed to the ends of the identified sequence are synthesized. The primers direct nucleic acid synthesis away from the known sequence and toward the unknown sequence contained within the circularized template. After the PCR reaction is complete, the resulting PCR products can be sequenced so as to extend the sequence of the identified gene past the core sequence of the identified exogenous nucleic acid sequence identified. In this manner, the full sequence of each novel gene can be identified. Additionally the sequences of adjacent coding and noncoding regions can be identified.

#### EXAMPLE 16

##### Identification of Genes Required for *Staphylococcus aureus* Proliferation

30 Genes required for proliferation in *Staphylococcus aureus* are identified according to the methods described above.

#### EXAMPLE 17

##### Identification of Genes Required for *Neisseria gonorrhoeae* Proliferation

45 Genes required for proliferation in *Neisseria gonorrhoeae* are identified according to the methods described above.

## EXAMPLE 18

Identification of Genes Required for *Pseudomonas aeruginosa* Proliferation

Genes required for proliferation in *Pseudomonas aeruginosa* are identified according to the methods described above.

## EXAMPLE 19

Identification of Genes Required for *Enterococcus faecalis* Proliferation

Genes required for proliferation in *Enterococcus faecalis* are identified according to the methods described above.

## EXAMPLE 20

Identification of Genes Required for *Haemophilus influenzae* Proliferation

Genes required for proliferation in *Haemophilus influenzae* are identified according to the methods described above.

## EXAMPLE 21

Identification of Genes Required for *Salmonella typhimurium* Proliferation

Genes required for proliferation in *Salmonella typhimurium* are identified according to the methods described above.

## EXAMPLE 22

Identification of Genes Required for *Helicobacter pylori* Proliferation

Genes required for proliferation in *Helicobacter pylori* are identified according to the methods described above.

## EXAMPLE 23

Identification of Genes Required for *Mycoplasma pneumoniae* Proliferation

Genes required for proliferation in *Mycoplasma pneumoniae* are identified according to the methods described

above.

## EXAMPLE 24

Identification of Genes Required for *Plasmodium ovale* Proliferation

Genes required for proliferation in *Plasmodium ovale* are identified according to the methods described above.

## EXAMPLE 25

Identification of Genes Required for *Saccharomyces cerevisiae* Proliferation

Genes required for proliferation in *Saccharomyces cerevisiae* are identified according to the methods described above.

## EXAMPLE 26

Identification of Genes Required for *Entamoeba histolytica* Proliferation

Genes required for proliferation in *Entamoeba histolytica* are identified according to the methods described above.

## EXAMPLE 27

Identification of Genes Required for *Candida albicans* Proliferation

Genes required for proliferation in *Candida albicans* are identified according to the methods described above.

**EXAMPLE 28**Identification of Genes Required for *Klebsiella pneumoniae* Proliferation

Genes required for proliferation in *Klebsiella pneumoniae* are identified according to the methods described above.

**EXAMPLE 29**Identification of Genes Required for *Salmonella typhi* Proliferation

Genes required for proliferation in *Salmonella typhi* are identified according to the methods described above.

**EXAMPLE 30**Identification of Genes Required for *Salmonella paratyphi* Proliferation

Genes required for proliferation in *Salmonella paratyphi* are identified according to the methods described above.

**EXAMPLE 31**Identification of Genes Required for *Salmonella choleraesuis* Proliferation

Genes required for proliferation in *Salmonella choleraesuis* are identified according to the methods described above.

**EXAMPLE 32**Identification of Genes Required for *Staphylococcus epidermis* Proliferation

Genes required for proliferation in *Staphylococcus epidermis* are identified according to the methods described above.

**EXAMPLE 33**Identification of Genes Required for *Mycobacterium tuberculosis* Proliferation

Genes required for proliferation in *Mycobacterium tuberculosis* are identified according to the methods described above.

**EXAMPLE 34**Identification of Genes Required for *Mycobacterium leprae* Proliferation

Genes required for proliferation in *Mycobacterium leprae* are identified according to the methods described above.

**EXAMPLE 35**Identification of Genes Required for *Treponema pallidum* Proliferation

Genes required for proliferation in *Treponema pallidum* are identified according to the methods described above.

**EXAMPLE 36**Identification of Genes Required for *Bacillus anthracis* Proliferation

Genes required for proliferation in *Bacillus anthracis* are identified according to the methods described above.

**EXAMPLE 37**Identification of Genes Required for *Yersinia pestis* Proliferation

Genes required for proliferation in *Yersinia pestis* are identified according to the methods described above.

**EXAMPLE 38**Identification of Genes Required for *Clostridium botulinum* Proliferation

Genes required for proliferation in *Clostridium botulinum* are identified according to the methods described above.

**EXAMPLE 39**Identification of Genes Required for *Campylobacter jejuni* Proliferation

Genes required for proliferation in *Campylobacter jejuni* are identified according to the methods described above.

**EXAMPLE 40**Identification of Genes Required for *Chlamydia trachomatis* Proliferation

Genes required for proliferation in *Chlamydia trachomatis* are identified according to the methods described above.

**Use of Isolated Exogenous Nucleic Acid Fragments as Antisense Antibiotics**

In addition to using the identified sequences to enable screening of molecule libraries to identify compounds useful to identify antibiotics, the sequences themselves can be used as therapeutic agents. Specifically, the identified exogenous sequences in an antisense orientation can be provided to an individual to inhibit the translation of a bacterial target gene.

Generation of Antisense Therapeutics from Identified Exogenous Sequences

The sequences of the present invention can be used as antisense therapeutics for the treatment of bacterial infections or simply for inhibition of bacterial growth *in vitro* or *in vivo*. The therapy exploits the biological process in cells where genes are transcribed into messenger RNA (mRNA) that is then translated into proteins. Antisense RNA technology contemplates the use of antisense oligonucleotides directed against a target gene that will bind to its target and decrease or inhibit the translation of the target mRNA. In one embodiment, antisense oligonucleotides can be used to treat and control a bacterial infection of a cell culture containing a population of desired cells contaminated with bacteria. In another embodiment, the antisense oligonucleotides can be used to treat an organism with a bacterial infection.

Antisense oligonucleotides can be synthesized from any of the sequences of the present invention using methods well known in the art. In a preferred embodiment, antisense oligonucleotides are synthesized using artificial means. Uhlmann & Peymann, Chemical Rev. 90:543-584 (1990) review antisense oligonucleotide technology in detail. Modified or unmodified antisense oligonucleotides can be used as therapeutic agents. Modified antisense oligonucleotides are preferred since it is well known that antisense oligonucleotides are extremely unstable. Modification of the phosphate backbones of the antisense oligonucleotides can be achieved by substituting the internucleotide phosphate residues with methylphosphonates, phosphorothioates, phosphoramidates, and phosphate esters. Nonphosphate internucleotide analogs such as siloxane bridges, carbonate bridges, thioester bridges, as well as many others known in the art. The preparation of certain antisense oligonucleotides with modified internucleotide linkages is described in U.S. Patent No. 5,142,047, hereby incorporated by reference.

Modifications to the nucleoside units of the antisense oligonucleotides are also contemplated. These modifications can increase the half-life and increase cellular rates of uptake for the oligonucleotides *in vivo*. For example,

5  $\alpha$ -anomeric nucleotide units and modified bases such as 1,2-dideoxy-d-ribofuranose, 1,2-dideoxy-1-phenyltrifuranose, and *N*, *N*-ethano-5-methyl-cytosine are contemplated for use in the present invention.

10 5 An additional form of modified antisense molecules is found in peptide nucleic acids. Peptide nucleic acids (PNA) have been developed to hybridize to single and double stranded nucleic acids. PNA are nucleic acid analogs in which the entire deoxyribose-phosphate backbone has been exchanged with a chemically completely different, but structurally homologous, polyamide (peptide) backbone containing 2-aminoethyl glycine units. Unlike DNA, which is highly negatively charged, the PNA backbone is neutral. Therefore, there is much less repulsive energy between complementary strands in a PNA-DNA hybrid than in the comparable DNA-DNA hybrid, and consequently they are much more stable. PNA can hybridize to DNA in either a Watson/Crick or Hoogsteen fashion (Demidov et al., *Proc. Natl. Acad. Sci. U.S.A.* 92:2637-2641, 1995; Egholm, *Nature* 365:566-568, 1993; Nielsen et al., *Science* 254:1497-1500, 1991; Dueholm et al., *New J. Chem.* 21:19-31, 1997).

15 10 Molecules called PNA "clamps" have been synthesized which have two identical PNA sequences joined by a flexible hairpin linker containing three 8-amino-3,6-dioxaoctanoic acid units. When a PNA clamp is mixed with a complementary homapurine or homopyrimidine DNA target sequence, a PNA-DNA-PNA triplex hybrid can form which has been shown to be extremely stable (Bentín et al., *Biochemistry* 35:8863-8869, 1996; Egholm et al., *Nucleic Acids Res.* 23:217-222, 1995; Griffith et al., *J. Am. Chem. Soc.* 117:831-832, 1995).

20 15 The sequence-specific and high affinity duplex and triplex binding of PNA have been extensively described (Nielsen et al., *Science* 254:1497-1500, 1991; Egholm et al., *J. Am. Chem. Soc.* 114:9677-9678, 1992; Egholm et al., *Nature* 365:566-568, 1993; Almarsson et al., *Proc. Natl. Acad. Sci. U.S.A.* 90:9542-9546, 1993; Demidov et al., *Proc. Natl. Acad. Sci. U.S.A.* 92:2637-2641, 1995). They have also been shown to be resistant to nuclease and protease digestion (Demidov et al., *Biochem. Pharm.* 48:1010-1013, 1994). PNA has been used to inhibit gene expression (Harvey et al., *Science* 258:1481-1485, 1992; Nielsen et al., *Nucl. Acids. Res.*, 21:197-200, 1993; Nielsen et al., *Gene* 149:139-145, 1994; Good & Nielsen, *Science*, 95: 2073-2076, 1998; all of which are hereby incorporated by reference), to block restriction enzyme activity (Nielsen et al., *supra.*, 1993), to act as an artificial transcription promoter (Mollegaard, *Proc. Natl. Acad. Sci. U.S.A.* 91:3892-3895, 1994) and as a pseudo restriction endonuclease (Demidov et al., *Nucl. Acids. Res.* 21:2103-2107, 1993). Recently, PNA has also been shown to have antiviral and antitumoral activity mediated through an antisense mechanism (Norton, *Nature Biotechnol.*, 14:615-619, 1996; Hirschman et al., *J. Invest. Med.* 44:347-351, 1996). PNAs have been linked to various peptides in order to promote PNA entry into cells (Basu et al., *Bioconj. Chem.* 8:481-488, 1997; Partridge et al., *Proc. Natl. Acad. Sci. U.S.A.* 92:5592-5596, 1995).

25 30 The antisense oligonucleotides contemplated by the present invention can be administered by direct application of oligonucleotides to a target using standard techniques well known in the art. The antisense oligonucleotides can be generated within the target using a plasmid, or a phage. Alternatively, the antisense nucleic acid may be expressed from a sequence in the chromosome of the target cell. It is further contemplated that contemplated that the antisense oligonucleotide contemplated are incorporated in a ribozyme sequence to enable the antisense to specifically bind and cleave its



5 target mRNA. For technical applications of ribozyme and antisense oligonucleotides see Rossi et al., *Pharmacol. Ther.* 50(2):245-254, (1991), which is hereby incorporated by reference. The present invention also contemplates using a retron to introduce an antisense oligonucleotide to a cell. Retron technology is exemplified by U.S. Patent No. 5,405,775, which is hereby incorporated by reference. Antisense oligonucleotides can also be delivered using liposomes or by electroporation  
10 5 techniques which are well known in the art.

The antisense nucleic acids of the present invention can also be used to design antibiotic compounds comprising nucleic acids which function by intracellular triple helix formation. Triple helix oligonucleotides are used to inhibit transcription from a genome. The sequences identified as required for proliferation in the present invention, or portions thereof, can be used  
15 as templates to inhibit microorganism gene expression in individuals infected with such organisms. Traditionally, homopurine sequences were considered the most useful for triple helix strategies. However, homopyrimidine sequences can also inhibit gene expression. Such homopyrimidine oligonucleotides bind to the major groove at homopurine:homopyrimidine sequences. Thus, both types of sequences based on the sequences of the present invention that are required for proliferation are contemplated for use as antibiotic compound templates.  
20

The antisense oligonucleotides of this example employ the identified sequences of the present invention to induce bacterial cell death or at least bacterial stasis by inhibiting target gene translation. Antisense oligonucleotides containing from about 8 to 40 bases of the sequences of the present invention have sufficient complementarity to form a duplex with the target sequence under physiological conditions.  
25

To kill bacterial cells or inhibit their growth, the antisense oligonucleotides are applied to the bacteria or to the target cells under conditions that facilitate their uptake. These conditions include sufficient incubation times of cells and oligonucleotides so that the antisense oligonucleotides are taken up by the cells. In one embodiment, an incubation period of 7-10 days is sufficient to kill bacteria in a sample. An optimum concentration of antisense oligonucleotides is selected for use.  
30 20

The concentration of antisense oligonucleotides to be used can vary depending on the type of bacteria sought to be controlled, the nature of the antisense oligonucleotide to be used, and the relative toxicity of the antisense oligonucleotide to the desired cells in the treated culture. Antisense oligonucleotides can be introduced to cell samples at a number of different concentrations preferably between  $1 \times 10^{-10} \text{M}$  to  $1 \times 10^{-4} \text{M}$ . Once the minimum concentration that can adequately control gene expression is identified, the optimized dose is translated into a dosage suitable for use *in vivo*. For example, an inhibiting concentration in culture of  $1 \times 10^{-7}$  translates into a dose of approximately 0.6 mg/kg body weight. Levels of oligonucleotide approaching 100 mg/kg body weight or higher may be possible after testing the toxicity of the oligonucleotide in laboratory animals. It is additionally contemplated that cells from the subject are removed, treated with the antisense oligonucleotide, and reintroduced into the subject. This range is merely illustrative and one of skill in the art are able to determine the optimal concentration to be used in a given case.  
35 25  
40  
30  
45

5 After the bacterial cells have been killed or controlled in a desired culture, the desired cell population may be used for other purposes.

#### EXAMPLE 41

10 5 The following example demonstrates the ability of an *E. coli* antisense oligonucleotide to act as a bactericidal or bacteriostatic agent to treat a contaminated cell culture system. The application of the antisense oligonucleotides of the present invention are thought to inhibit the translation of bacterial gene products required for proliferation.

15 10 The antisense oligonucleotide of this example corresponds to a 30 base phosphorothioate modified oligodeoxynucleotide complementary to a nucleic acid involved in proliferation, such as Molecule Number EcXA001. A sense oligodeoxynucleotide complementary to the antisense sequence is synthesized and used as a control. The oligonucleotides are synthesized and purified according to the procedures of Matsukura, et al., Gene 72:343 (1988). The test oligonucleotides are dissolved in a small volume of autoclaved water and added to culture medium to make a 100 micromolar stock solution.

20 15 Human bone marrow cells are obtained from the peripheral blood of two patients and cultured according standard procedures well known in the art. The culture is contaminated with the K-12 strain of *E. coli* and incubated at 37°C overnight to establish bacterial infection.

25 20 The control and antisense oligonucleotide containing solutions are added to the contaminated cultures and monitored for bacterial growth. After a 10 hour incubation of culture and oligonucleotides, samples from the control and experimental cultures are drawn and analyzed for the translation of the target bacterial gene using standard microbiological techniques well known in the art. The target *E. coli* gene is found to be translated in the control culture treated with the control oligonucleotide, however, translation of the target gene in the experimental culture treated with the antisense oligonucleotide of the present invention is not detected or reduced.

#### EXAMPLE 42

35 25 A subject suffering from an *E. coli* infection is treated with the antisense oligonucleotide preparation of Example 39. The antisense oligonucleotide is provided in a pharmaceutically acceptable carrier at a concentration effective to inhibit the translation of the target gene. The present subject is treated with a concentration of antisense oligonucleotide sufficient to achieve a blood concentration of about 100 micromolar. The patient receives daily injections of antisense oligonucleotide to maintain this concentration for a period of 1 week. At the end of the week a blood sample is drawn and analyzed for the presence or absence using standard techniques well known in the art. There is no detectable evidence of *E. coli* and the treatment is terminated.

#### EXAMPLE 43

##### Preparation and use of Triple Helix Probes

45 50 The sequences of microorganism genes required for proliferation of the present invention are scanned to identify 10-mer to 20-mer homopyrimidine or homopurine stretches that could be used in triple-helix based strategies for inhibiting gene

expression. Following identification of candidate homopyrimidine or homopurine stretches, their efficiency in inhibiting gene expression is assessed by introducing varying amounts of oligonucleotides containing the candidate sequences into a population of bacterial cells that normally express the target gene. The oligonucleotides may be prepared on an oligonucleotide synthesizer or they may be purchased commercially from a company specializing in custom oligonucleotide synthesis, such as GENSET, Paris, France.

The oligonucleotides can be introduced into the cells using a variety of methods known to those skilled in the art, including but not limited to calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection or native uptake.

Treated cells are monitored for a reduction in proliferation using techniques such as monitoring growth levels as compared to untreated cells using optical density measurements. The oligonucleotides that are effective in inhibiting gene expression in cultured cells can then be introduced *in vivo* using the techniques well known in that art at a dosage level shown to be effective.

In some embodiments, the natural (beta) anomers of the oligonucleotide units can be replaced with alpha anomers to render the oligonucleotide more resistant to nucleases. Further, an intercalating agent such as ethidium bromide, or the like, can be attached to the 3' end of the alpha oligonucleotide to stabilize the triple helix. For information on the generation of oligonucleotides suitable for triple helix formation see Griffin et al. (Science 245:967-971 (1989), which is hereby incorporated by this reference).

#### EXAMPLE 44

##### Identification of Bacterial Strains from Isolated Specimens by PCR

Classical bacteriological methods for the detection of various bacterial species are time consuming and costly. These methods include growing the bacteria isolated from a subject in specialized media, cultivation on selective agar media, followed by a set of confirmation assays that can take from 8 to 10 days or longer to complete. Use of the identified sequences of the present invention provides a method to dramatically reduce the time necessary to detect and identify specific bacterial species present in a sample.

In one exemplary method, bacteria are grown in enriched media and DNA samples are isolated from specimens of, for example, blood, urine, stool, saliva or central nervous system fluid by conventional methods. A panel of PCR primers based on identified sequences unique to various species of microorganisms are then utilized in accordance with Example 12 to amplify DNA of approximately 100-200 bases in length from the specimen. A separate PCR reaction is set up for each pair of PCR primers and after the PCR reaction is complete, the reaction mixtures are assayed for the presence of PCR product. The presence or absence of bacteria from the species to which the PCR primer pairs belong is determined by the presence or absence of a PCR product in the various test PCR reaction tubes.

Although the PCR reaction is used to assay the isolated sample for the presence of various bacterial species, other assays such as the Southern blot hybridization are also contemplated.

**WHAT IS CLAIMED IS:**

1. A purified or isolated nucleic acid sequence consisting essentially of one of SEQ ID NOs: 405-485, wherein said nucleic acid inhibits microorganism proliferation.

2. The nucleic acid sequence of Claim 1, wherein said nucleic acid sequence is complementary to at least a portion of a coding sequence of a gene whose expression is required for microorganism proliferation.

3. The nucleic acid sequence of Claims 1 or 2, wherein said nucleic acid comprises a fragment of one of SEQ ID NOs. 405-485, said fragment selected from the group consisting of fragments comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 405-485.

4. The nucleic acid sequence of Claim 3, wherein said nucleic acid sequence is complementary to a coding sequence of a gene whose expression is required for microorganism proliferation.

5. A vector comprising a promoter operably linked to a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 405-485.

6. The vector of Claim 5, wherein said promoter is active in an organism selected from the group consisting of *Escherichia coli*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klasiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species.

7. A host cell containing the vector of Claim 5 or Claim 6.

8. A purified or isolated nucleic acid consisting essentially of the coding sequence of one of SEQ ID NOs: 82-88, 90-242.

9. A fragment of the nucleic acid of Claim 8, said fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 82-88, 90-242.

10. A vector comprising a promoter operably linked to the nucleic acid of Claim 8 or Claim 9.

11. A purified or isolated nucleic acid comprising a nucleic acid sequence complementary to at least a portion of an intragenic sequence, intergenic sequence, sequences spanning at least a portion of two or more genes, 5' noncoding region, or 3' noncoding region within an operon encoding a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs: 243-357, 359-398.

12. A purified or isolated nucleic acid comprising a nucleic acid having at least 70% homology to a sequence selected from the group consisting of SEQ ID NOs 405-485, 82-88, 90-242 or the sequences complementary thereto as determined using BLASTN version 2.0 with the default parameters.

13. The nucleic acid of Claim 12, wherein said nucleic acid is from an organism selected from the group consisting of *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, and *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species.

14. A purified or isolated nucleic acid consisting essentially of a nucleic acid encoding a polypeptide having a sequence selected from the group consisting of SEQ ID NOs: 243-357, 359-398.

15. A vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide having a sequence selected from the group consisting of SEQ ID NOs: 243-357, 359-398.

16. A host cell containing the vector of Claim 15.

17. A purified or isolated polypeptide comprising the sequence of one of SEQ ID NOs: 243-357, 359-398.

18. A purified or isolated polypeptide comprising a fragment of one of the polypeptides of SEQ ID NOs: 243-357, 359-398, said fragment selected from the group consisting of fragments comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of one of the polypeptides of SEQ ID NOs: 243-357, 359-398.

19. An antibody capable of specifically binding the polypeptide of Claim 17 or Claim 18.

20. A method of producing a polypeptide, comprising introducing a vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide having a sequence selected from the group consisting of SEQ ID NOs: 243-357, 359-398 into a cell.

21. The method of Claim 20, further comprising the step of isolating said protein.

22. A method of inhibiting proliferation comprising inhibiting the activity or reducing the amount of a polypeptide having a sequence selected from the group consisting of SEQ ID NOs: 243-357, 359-398 or inhibiting the activity or reducing the amount of a nucleic acid encoding said polypeptide.

23. A method for identifying compounds which influence the activity of a polypeptide required for proliferation comprising:

contacting a polypeptide having a sequence selected from the group consisting of 243-357, 359-398 with a candidate compound; and

determining whether said compound influences the activity of said polypeptide.

24. The method of Claim 23, wherein said activity is an enzymatic activity.

25. The method of Claim 23, wherein said activity is a carbon compound catabolism activity.

- 5                   26.     The method of Claim 23, wherein said activity is a biosynthetic activity.
27.     The method of Claim 23, wherein said activity is a transporter activity.
28.     The method of Claim 23, wherein said activity is a transcriptional activity.
29.     The method of Claim 23, wherein said activity is a DNA replication activity.
- 10               5       30.     The method of Claim 23, wherein said activity is a cell division activity.
31.     A method for assaying compounds for the ability to reduce the activity or level of a polypeptide  
required for proliferation, comprising:
- providing a target, wherein said target comprises the coding sequence of a sequence selected from the  
15                           group consisting of SEQ ID NOs. 82-88, 90-242;
- 10               contacting said target with a candidate compound; and
- measuring an activity of said target.
- 20               32.     The method of Claim 31, wherein said target is a messenger RNA molecule transcribed from a coding  
region of one of SEQ ID. NOs.: 82-88, 90-242 and said activity is translation of said messenger RNA.
33.     The method of Claim 32, wherein said target is a coding region of one of SEQ ID. NOs. 82-88, 90-242  
15                   and said activity is transcription of said messenger RNA.
- 25               34.     A compound identified using the method of Claim 31.
35.     A method for identifying compounds which reduce the activity or level of a gene product required for  
cell proliferation comprising the steps of:
- expressing an antisense nucleic acid against a nucleic acid encoding said gene product in a cell to  
30                           reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell;
- contacting said sensitized cell with a compound; and
- determining whether said compound inhibits the growth of said sensitized cell to a greater extent than  
35                           said compound inhibits the growth of a nonsensitized cell.
36.     The method of Claim 35, wherein said cell is selected from the group consisting of bacterial cells,  
25                   fungal cells, plant cells, and animal cells.
37.     The method of Claim 36, wherein said cell is an *E. coli* cell.
- 40               38.     The method of Claim 36, wherein said cell is from an organism selected from the group consisting of  
*Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*,  
*Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces*  
30                   *cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*,  
45                   *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium*  
*leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *campylobacter jejuni*, and *Chlamydia*  
*trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species.

- 5           39.    The method of Claim 35, wherein said antisense nucleic acid is transcribed from an inducible promoter.
40.    The method of Claim 39, further comprising the step of contacting said cell with a concentration of inducer which induces said antisense nucleic acid to a sublethal level.
- 10           41.    The method of Claim 40, wherein said sub-lethal concentration of said inducer is such that growth inhibition is 8% or more.
42.    The method of Claim 40, wherein said inducer is isopropyl-1-thio- $\beta$ -D-galactoside.
43.    The method of Claim 35, wherein growth inhibition is measured by monitoring optical density of a culture growth solution.
- 15           44.    The method of Claim 35, wherein said gene product is a polypeptide.
45.    The method of Claim 35, wherein said gene product is an RNA.
46.    The method of Claim 44, wherein said gene product comprises a polypeptide having a sequence selected from the group consisting of SEQ ID NOs.: 243-357, 359-398.
- 20           47.    A compound identified using the method of Claim 35.
48.    A method for inhibiting cellular proliferation comprising introducing a compound with activity against a gene corresponding to one of SEQ ID NOs.: 82-88, 90-242 or with activity against the product of said gene into a population of cells expressing a gene.
- 25           49.    The method of Claim 48, wherein said compound is an antisense oligonucleotide comprising a sequence selected from the group consisting of SEQ ID NOs.: 405-485, or a proliferation-inhibiting portion thereof.
50.    The method of Claim 49, wherein said proliferation inhibiting portion of one of SEQ ID NOs. 405-485 is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 405-485.
- 30           51.    The method of Claim 48, wherein said compound is a triple helix oligonucleotide.
52.    A preparation comprising an effective concentration of an antisense oligonucleotide comprising a sequence selected from the group consisting of SEQ ID NOs.: 405-485, or a proliferation-inhibiting portion thereof in a pharmaceutically acceptable carrier.
- 35           53.    The preparation of Claim 52, wherein said proliferation-inhibiting portion of one of SEQ ID NOs. 405-485 comprises at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 405-485.
- 40           54.    A method for inhibiting the expression of a gene in an operon required for proliferation comprising contacting a cell in a cell population with an antisense nucleic acid, said cell expressing a gene corresponding to one of SEQ ID NOs.: 82-88, 90-242, wherein said antisense nucleic acid comprises at least a proliferation-inhibiting portion of said operon in an antisense orientation that is effective in inhibiting expression of said gene.
- 45
- 50
- 55

5 55. The method of Claim 54, wherein said antisense nucleic acid is complementary to a sequence of a gene comprising one or more of SEQ ID NOs.: 82-88, 90-242.

56. The method of Claim 54, wherein said antisense nucleic acid is a sequence of one of SEQ ID NOs.: 405-485, or a portion thereof.

10 5 57. The method of Claim 54, wherein said cell is contacted with said antisense nucleic acid by introducing a plasmid which expresses said antisense nucleic acid into said cell population.

58. The method of Claim 54, wherein said cell is contacted with said antisense nucleic acid by introducing a phage which expresses said antisense nucleic acid into said cell population.

15 59. The method of Claim 54, wherein said cell is contacted with said antisense nucleic acid by introducing a sequence encoding said antisense nucleic acid into the chromosome of said cell into said cell population.

20 60. The method of Claim 54, wherein said cell is contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population.

61. The method of Claim 54, wherein said cell is contacted with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme is complementary to said antisense oligonucleotide.

25 62. The method of Claim 54, wherein said cell is contacted with said antisense nucleic acid by introducing a liposome comprising said antisense oligonucleotide into said cell.

63. The method of Claim 54, wherein said cell is contacted with said antisense nucleic acid by electroporation.

30 20 64. The method of Claim 54, wherein said antisense nucleic acid is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 82-88, 90-242.

65. The method of Claim 54 wherein said antisense nucleic acid is an oligonucleotide.

35 66. A method for identifying bacterial strains comprising the steps of:

providing a sample containing a bacterial species; and

25 identifying a bacterial species using a species specific probe having a sequence selected from the group consisting of SEQ ID NOs. 405-485, 82-88, 90-242.

40 67. A method for identifying a gene in a microorganism required for proliferation comprising:

(a) identifying an inhibitory nucleic acid which inhibits the activity of a gene or gene product required for proliferation in a first microorganism;

30 (b) contacting a second microorganism with said inhibitory nucleic acid;

45 (c) determining whether said inhibitory nucleic acid from said first microorganism inhibits proliferation of said second microorganism; and



(d) identifying the gene in said second microorganism which is inhibited by said inhibitory nucleic acid.

68. A method for assaying a compound for the ability to inhibit proliferation of a microorganism comprising:

(a) identifying a gene or gene product required for proliferation in a first microorganism;

(b) identifying a homolog of said gene or gene product in a second microorganism;

(c) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said second microorganism;

(d) contacting said second microorganism with a proliferation-inhibiting amount of said inhibitory nucleic acid, thus sensitizing said second microorganism;

(e) contacting the sensitized microorganism of step (d) with a compound; and

(f) determining whether said compound inhibits proliferation of said sensitized microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized microorganism.

69. The method of Claim 68, wherein said step of identifying a gene involved in proliferation in a first microorganism comprises:

introducing a nucleic acid comprising a random genomic fragment from said first microorganism operably linked to a promoter wherein said random genomic fragment is in the antisense orientation; and

comparing the proliferation of said first microorganism transcribing a first level of said random genomic fragment to the proliferation of said first microorganism transcribing a lower level of said random genomic fragment, wherein a difference in proliferation indicates that said random genomic fragment comprises a gene involved in proliferation.

70. The method of Claim 69, wherein said step of identifying a homolog of said gene in a second microorganism comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a database using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the default parameters.

71. The method of Claim 69, wherein said step of identifying a homolog of said gene in a second microorganism comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide by identifying nucleic acids which hybridize to said first gene.

72. The method of Claim 69, wherein the step of identifying a homolog of said gene in a second microorganism comprises expressing a nucleic acid which inhibits the proliferation of said first microorganism in said second microorganism.

73. The method of Claim 69, wherein said inhibitory nucleic acid is an antisense nucleic acid.

74. The method of Claim 69, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of said homolog.

5 75. The method of Claim 69, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of the operon encoding said homolog.

10 76. The method of Claim 69, wherein the step of contacting the second microorganism with a proliferation-inhibiting amount of said nucleic acid sequence comprises directly contacting said second microorganism with said nucleic acid.

15 77. The method of Claim 69, wherein the step of contacting the second microorganism with a proliferation-inhibiting amount of said nucleic acid sequence comprises expressing an antisense nucleic acid to said homolog in said second microorganism.

10 78. A compound identified using the method of Claim 68.

15 79. A method of assaying a compound for the ability to inhibit proliferation comprising:

20 (a) identifying an inhibitory nucleic acid sequence which inhibits the activity of a gene or gene product required for proliferation in a first microorganism;

(b) contacting a second microorganism with a proliferation-inhibiting amount of said inhibitory nucleic acid, thus sensitizing said second microorganism;

15 (c) contacting the proliferation-inhibited microorganism of step (b) with a compound; and

25 (d) determining whether said compound inhibits proliferation of said sensitized second microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized second microorganism.

80. The method of Claim 79, wherein said inhibitory nucleic acid is an antisense nucleic acid which inhibits the proliferation of said first microorganism.

30 81. The method of Claim 79, wherein said inhibitory nucleic acid comprises a portion of an antisense nucleic acid which inhibits the proliferation of said first microorganism.

82. The method of Claim 79, wherein said inhibitory nucleic acid comprises an antisense molecule against the entire coding region of the gene involved in proliferation of the first microorganism.

35 83. The method of Claim 79, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of the operon encoding the gene involved in proliferation of the first microorganism.

40 84. A compound identified using the method of Claim 79.

85. A method for assaying compounds for activity against a biological pathway required for proliferation comprising:

30 sensitizing a cell by expressing an antisense nucleic acid against a nucleic acid encoding a gene product required for proliferation in a cell to reduce the activity or amount of said gene product;

45 contacting the sensitized cell with a compound; and

determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

5           86.     The method of Claim 85, wherein said cell is selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

          87.     The method of Claim 86, wherein said cell is an *E. coli* cell.

10         88.     The method of Claim 85, wherein said cell is from an organism selected from the group consisting of  
5         *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*,  
*Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces*  
*cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*,  
15         *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium*  
*leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, and *Chlamydia*  
10         *trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species.

          89.     The method of Claim 85, wherein said antisense nucleic acid is transcribed from an inducible promoter.

20         90.     The method of Claim 89, further comprising contacting the cell with an agent which induces expression  
of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is expressed at a sublethal  
level.

15         91.     The method of Claim 90, wherein said sublethal level of said antisense nucleic acid inhibits proliferation  
25         by 8% or more.

          92.     The method of Claim 90, wherein said agent is isopropyl-1-thio- $\beta$ -D-galactoside (IPTG).

          93.     The method of Claim 91, wherein inhibition of proliferation is measured by monitoring the optical  
density of a liquid culture.

30         94.     The method of Claim 85, wherein said gene product comprises a polypeptide having a sequence  
20         selected from the group consisting of SEQ ID NOs: 243-357, 359-398.

          95.     A compound identified using the method of Claim 85.

35         96.     A method for assaying a compound for the ability to inhibit cellular proliferation comprising:

25         contacting a cell with an agent which reduces the activity or level of a gene product required for  
proliferation of said cell;

          contacting said cell with said compound; and

40         determining whether said compound reduces proliferation to a greater extent than said compound  
reduces proliferation of cells which have not been contacted with said agent.

30         97.     The method of Claim 96, wherein said agent which reduces the activity or level of a gene product  
required for proliferation of said cell comprises an antisense nucleic acid to a gene or operon required for proliferation.

45         98.     The method of Claim 96, wherein said agent which reduces the activity or level of a gene product  
required for proliferation of said cell comprises an antibiotic.

5 99. The method of Claim 96, wherein said cell contains a temperature sensitive mutation which reduces the activity or level of said gene product required for proliferation of said cell.

10 100. The method of Claim 99, wherein said antisense nucleic acid is directed against the nucleic acid encoding the same functional domain of said gene product required for proliferation of said cell to which said antisense nucleic acid is directed.

15 101. The method of Claim 99, wherein said antisense nucleic acid is directed against the nucleic acid a different functional domain of said gene product required for proliferation of said cell than the functional domain to which said antisense nucleic acid is directed.

102. A compound identified using the method of Claim 96.

10 103. A method for identifying the pathway in which a proliferation-required nucleic acid or its gene product lies comprising:

20 expressing a sublethal level of an antisense nucleic acid directed against said proliferation-required nucleic acid in a cell;

15 contacting said cell with an antibiotic, wherein the biological pathway on which said antibiotic acts is known; and

25 determining whether said cell has a substantially greater sensitivity to said antibiotic than a cell which does not express said sublethal level of said antisense nucleic acid.

104. A method for determining the pathway on which a test compound acts comprising:

30 20 (a) expressing a sublethal level of an antisense nucleic acid directed against a proliferation-required nucleic acid in a cell, wherein the biological pathway in which said proliferation-required nucleic acid lies is known,

(b) contacting said cell with said test compound; and

35 (c) determining whether said cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said antisense nucleic acid.

105. The method of Claim 104, further comprising:

25 (d) expressing a sublethal level of a second antisense nucleic acid directed against a second proliferation-required nucleic acid in said cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

40 (e) determining whether said cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said second antisense nucleic acid.

30 106. A purified or isolated nucleic acid consisting essentially of one of SEQ ID NOs: 358, 399-402.

45 107. A compound identified using the method of Claim 23.

108. A compound which interacts with the gene or gene product of a nucleic acid comprising a sequence of one of SEQ ID NOs: 82-88, 90-242 to inhibit proliferation.

5           109.    A compound which interacts with a polypeptide comprising one of SEQ ID NOs. 243-357, 359-398 to inhibit proliferation.

          110.    A compound which interacts with a nucleic acid comprising one of SEQ ID NOs: 358, 399-402 to inhibit proliferation.

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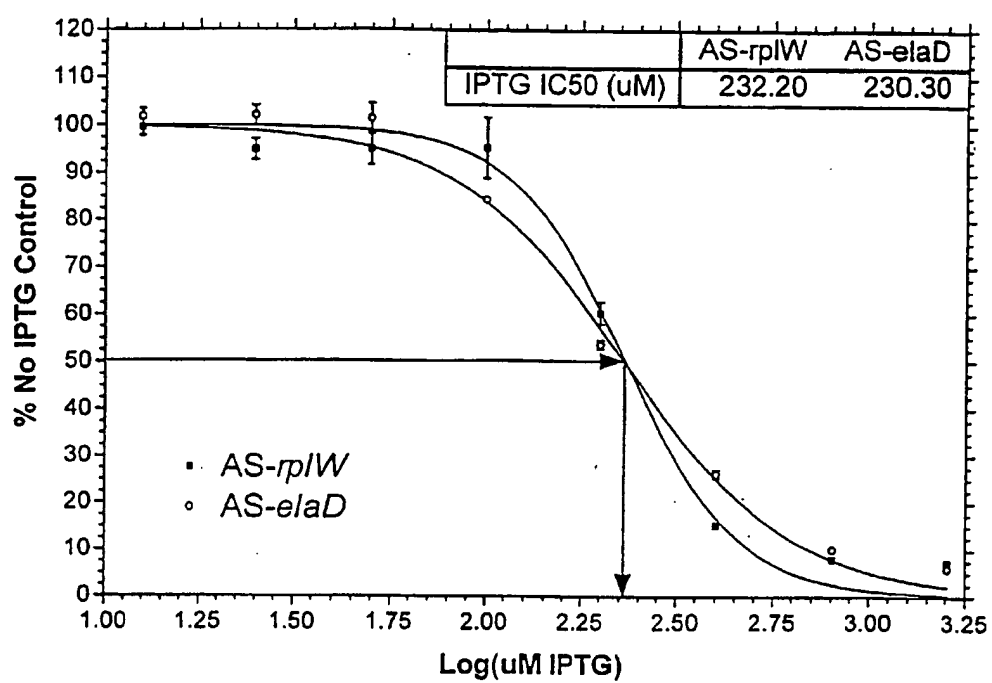
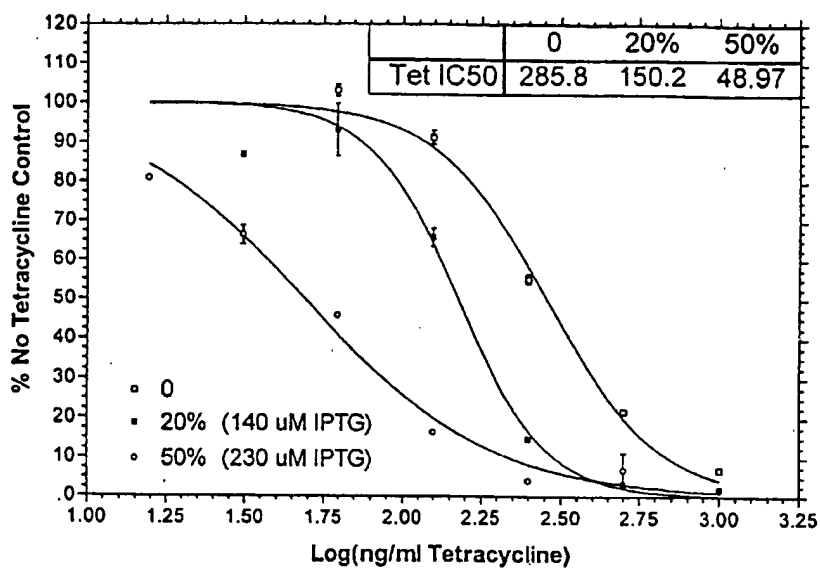
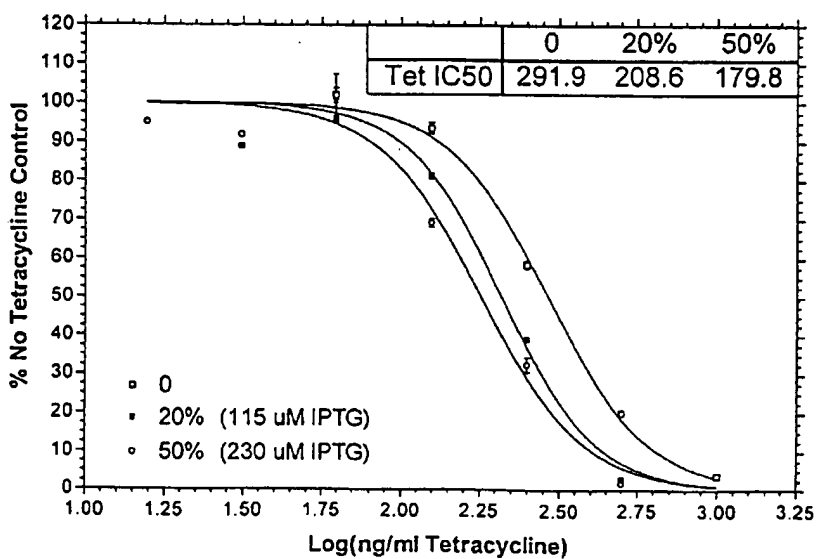


Fig. 1

**AS-rplW****Fig. 2a****AS-elaD****Fig. 2b**

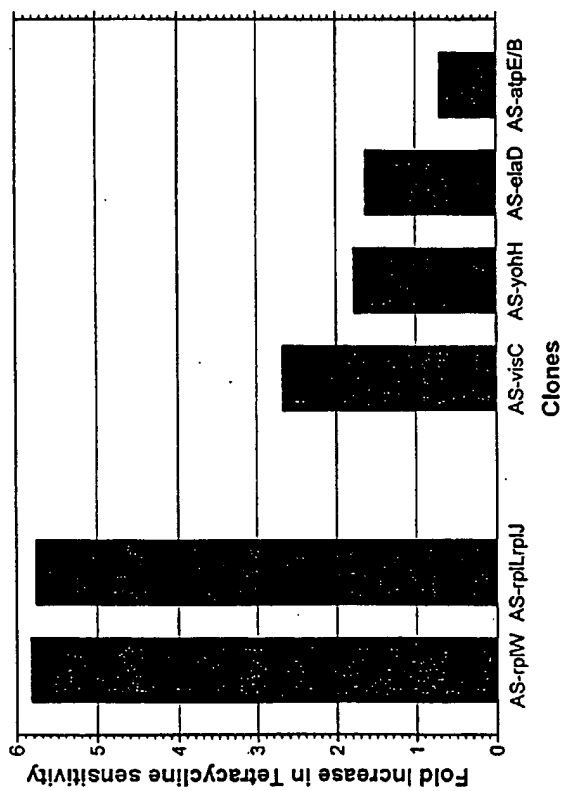


Fig. 3



## SEQUENCE LISTING

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Zyskind, Judith  
 Ohlsen, Kari L.  
 Trawick, John  
 Forsyth, R. Allyn  
 Froelich, Jamie M.  
 Carr, Grant J.  
 Yamamoto, Robert T.  
 Xu, H. Howard

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| cttcaacttc | agcgccagct | tcttccagag  | cttttttcag | tgcttctgcg | tcgtctttgc | 180 |
| tcacgccttc | tttcagagca | gccgggtgcag | attctaccag | gtctttagct | tctttcagac | 240 |
| ccaggccagt | tgcgccacgt | actgctttga  | taacagcaac | tttgtagcgc | ccagcagctt | 300 |
| tcagaattac | gtcgaattca | gttttttctt  | cagcagcttc | aaccgggcca | gcagctacag | 360 |
| ctacagcagc | agcagcgga  | acaccgaatt  | tttcttccat | tgcaagatc  | agttctacaa | 420 |
| c          |            |             |            |            |            | 421 |

<210> 10  
 <211> 126  
 <212> DNA  
 <213> E. Coli

<400> 10

```
agagcctttt tcagtgttc tgcgtcgtct ttgtcacgc cttctttcag agcagccggt    60
gcaga:tccta ccaggtcttt agcttctttc agaccagggc cagttgcgcc acgtactgct    120
ttgata                                     126
```

<210> 11  
 <211> 262  
 <212> DNA  
 <213> E. Coli

<220>  
 <221> misc\_feature  
 <222> (1)...(262)  
 <223> n = A,T,C or G

<400> 11

```
ctgcaacogg aaggggtggc ttatttaact tcaacttcag cgccagcttc ttccagagct    60
tttttcagtg cttctgcgtc gtctttgctc acgccttctt tcagagcagc cgntgcagat    120
tctaccaggt ctttagcttc ttccagaccc aggccagttg cgccacgtac tgctttgata    180
acagcaactt tgttagcgcc agcagctttc agaattacgt cgaattcagt tttttcttca    240
gcagcttcaa ccggggccagc ag                                     262
```

<210> 12  
 <211> 202  
 <212> DNA  
 <213> E. Coli

<220>  
 <221> misc\_feature  
 <222> (1)...(202)  
 <223> n = A,T,C or G

<400> 12

```
gogcataccc tgcagcatcg gcccgatgga gatcaggtcg gcagaacgct gtaccgcttt    60
gtagg:gggtg ttaccgggtg tcagatccgg gaagatgaac acggtagcgc gacctgcaac    120
cggagagttc ggcgctttgg attncgcaac gtcagccatt accgcagcgt cgtactgcag    180
cggaccggcg atcatcaggt ca                                     202
```

<210> 13  
 <211> 261  
 <212> DNA  
 <213> E. Coli

<400> 13

```
tctaggagta agaatagctt caaattcagc agttgacagt ggcataaacg taactggtga    60
cttttgcccg gcatgacgcc gggctttttt tattattccg tgacttccag cgtagtgaag    120
gcaaacttct cgccatcaaa tagccctga ctgggttagtt ttagcgcggg gatcactggc    180
agagaaagaa acgcatctg aataaacggc tcatcgggta acggaccgca ttcacgggag    240
gcggc:ttca aggcgtcaat t                                     261
```

<210> 14  
 <211> 224  
 <212> DNA  
 <213> E. Coli

<400> 14

|            |            |             |             |             |            |     |
|------------|------------|-------------|-------------|-------------|------------|-----|
| ttcttttttt | cgtaacggt  | gtccagaatc  | atttttattta | cctcggggta  | cttatgctga | 60  |
| tttttattat | tatggggaag | gtgtttattta | tgagtttcat  | ttatgccgta  | acgacaatga | 120 |
| actcgggaat | tagtataagc | agcgcgagaa  | taataatcat  | tgtagcaaatg | ctaatttaat | 180 |
| taatactatt | taaatattat | tttgagcata  | tgacataaag  | gttg        |            | 224 |

<210> 15  
 <211> 232  
 <212> DNA  
 <213> E. Coli

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aattcccttc | tttttttcgt | caacgggtgc | cagaatcatt | ttatttacct | cgggtactta | 60  |
| tgctgatttt | tattattatg | gggaagggtg | tatttatgag | tttcatttat | gccgtaacga | 120 |
| caatgaactc | gggaattagt | ataagcagcg | cgagaataat | aatcattgtg | caaagtctaa | 180 |
| tttaattaat | actattttaa | tattattttg | agcatatgca | cataagggtg | gg         | 232 |

<210> 16  
 <211> 212  
 <212> DNA  
 <213> E. Coli

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| aatagcgggt | atgcacgcct | ttcttttttt | cgtaacggt  | gtccagaatc | atttttattta | 60  |
| cctcgggtac | ttatgctgat | ttttattatt | atggggaagg | tgattttat  | gagtttcatt  | 120 |
| tatgccgtaa | cgacaatgaa | ctcgggaatt | agtataagca | gcgcgagaat | aataatcatt  | 180 |
| gtgcaaatgc | taatttaatt | aatactattt | aa         |            |             | 212 |

<210> 17  
 <211> 433  
 <212> DNA  
 <213> E. Coli

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cctttgtaat | tatgccccgt | ggcataaaaa | ctgcgtccaa | acgccgtctt | tgccagcagc | 60  |
| caggccataa | atgccaccag | aattatcgtc | aaccaaccaa | ttgctgaaac | gccaagcagc | 120 |
| agcggggcgg | agagctgttt | cagttcggcg | ggtaaccott | caatccattt | gccgccagtc | 180 |
| cacagcaaca | tgatgcctct | gtacaaccct | aacgtgccaa | gggtggcaac | aatggcaggg | 240 |
| atcttttagc | acgcgaccag | gacaccgttg | aaaaatcccc | cgagcaaaac | aagcagtaaa | 300 |
| gtcgcgacac | aagcaacag  | tagtgaatat | cctgcgttca | gtaacatccc | caacagcacc | 360 |
| gcgcacattc | cggtaatcga | acccactgaa | acatcaatat | tgcgcgtaag | cattaccagc | 420 |
| gtcgcgcca  | ttg        |            |            |            |            | 433 |

<210> 18  
 <211> 658  
 <212> DNA  
 <213> E. Coli

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| cgtagcgttc  | cggttggtgc | aaccgcgaa  | atggcgcggc | ggtaagtatg | gcgggggttat | 60  |
| tccttccccg  | ttgaggacac | cggttggtca | ggttgaccat | acgcttaagt | gacaaccccc  | 120 |
| ctgcaacgcc  | ctctgttatc | aattttcttg | tgacgttttg | cggtatcagt | tttactccgt  | 180 |
| gactgctctg  | cgcgcccttt | taaagtgaat | tttgatgatg | ggtgaatgcg | gctgagcgca  | 240 |
| cgcggaacag  | ttaaaaccaa | aaacagtgtt | atgggtggat | tctctgtatc | cggcgttaat  | 300 |
| tggttaactgg | ttaacgtcac | ctggaggcac | caggcactgc | atcacaaaat | tcattgttga  | 360 |
| ggacgcgata  | atgaaaacgt | tattaccaa  | cgtaataacg | tctgaagggt | gttttgaat   | 420 |
| tggtgtcact  | atcagtaacc | cagtatttac | tgaagatgcc | attaacaaga | gaaaacaaga  | 480 |
| acgggagcta  | ttaataaaaa | tatgcattgt | ttcaatgctg | gctcgtttac | gtctgatgcc  | 540 |
| aaaaggatgt  | gcacaatgaa | ttcagcattt | gtgcttgctc | tgacagtttt | tcttggttcc  | 600 |
| ggagagccag  | ttgatattgc | agtcaagtgg | tcacaggaca | atgcaggagt | gtatgact    | 658 |

<210> 19

<211> 588  
 <212> DNA  
 <213> E. Coli

<220>  
 <221> misc\_feature  
 <222> (1)...(588)  
 <223> n = A,T,C or G

<400> 19  
 gtgactgctc tgcgcgccctt tttaaagtga attttgtgat gtggtgaatg cggctgagcg 60  
 cacgcggaac agttaaaacc aaaaacagtg ttatgggtgg attctctgta tccggcggtta 120  
 attgttaact ggtaaacgtc acctggaggg accaggcact gcatcacaaa attcattgtt 180  
 gaggacgcga taatgaaaac gttattacca aacgttaata cgtctgaagg ttgttttgaa 240  
 attggtgtca ctatcagtaa ccagtgattt actgaagatg ccattaacaa gagaaaacaa 300  
 gaacgggagc tattaaataa aatatgcatt gtttcaatgc tggctcgttt acgtctgatg 360  
 ccaaaggat gtgcacaatg aattcagcat ttgtgcttgt tctgacagtt tttcttgttt 420  
 coggagagcc agttgatatt gcagtcagtg ttcacaggac aatgcangag tgtatgactg 480  
 cagcaaccgg aacagaaaat tcccggtaac tgttaccgg tcgataaagt tattcaccag 540  
 gataatatcg aaatcccgcc aggtctttaa aacagttccg taataaat 588

<210> 20  
 <211> 101  
 <212> DNA  
 <213> E. Coli

<400> 20  
 gatccagcaa gaagatgcgg ttgtaccgtc atcacgcaga tgcgcaaagc tactcagcaa 60  
 ctgacctttc ttcgcaataa gcacgccatt agcgtcatag a 101

<210> 21  
 <211> 465  
 <212> DNA  
 <213> E. Coli

<400> 21  
 tcgcgtgttt accttcaaca tcggtaactt tctggcggat agtttcacgg taagcaacct 60  
 gcgggtttacc tacgttcgct tcaacgttga attcacgctt catacgggtca acgatgatgt 120  
 cgagggtcag ttcgcccata ccgcgatga tggctcgttt agattcttcg tcagtcacata 180  
 cacggaaaaga cgggtcttct ttagccagac ggcccagagc cagaccatt tttctctggt 240  
 cagcttttgt tttcggttca actgcgatgg agattaccgg ctacgggaat tccatacgtt 300  
 ccagaatgat cggcgcatcc ggggtcacaca ggggtgcacc agtgggttacg tctttcagac 360  
 cgatagcagc agcgatgtcg cccgcgcgaa cttctttgat ctcttcacgt ttgttagcgt 420  
 gcatctgaac gatacgaccg aaacgctcac gtgcagcttt cacgg 465

<210> 22  
 <211> 859  
 <212> DNA  
 <213> E. Coli

<220>  
 <221> misc\_feature  
 <222> (1)...(859)  
 <223> n = A,T,C or G

<400> 22  
 tgatcggctc aagcagaact ggtttcgctt tcttaaagcc ttctttaag gcgatagaag 60  
 cagccagttt aaacgccagt tcagaggagt caacgtcatg gtaagaaccg aagtgcagac 120  
 gaatacccat gtctactacc gggtagcctg ccagcggacc tgccttcagc tgttcctgga 180  
 tacctttatc aacggccggg atgtattcgc cagggattac accaccttta atgtcgttga 240  
 tgaactcgta gcctttcggg ttgaaccgg gctccagcgg gtacatgtcg ataacaacat 300

```

gaccatactg accacgacca ccagactggt tcgcgtgttt accctcaaca tcggtaactt 360
tctggcggat agtttcacgg taagcaacct gcggtttacc tacgttcgct tcaacgttga 420
attcacgctt catacgggtca acgatgatgt cgagggtgcag ttcgcccata cccgcgatga 480
tggtctgggt agattcttcg tcagtcacata cacggaaaga cgggtcttct ttagccagac 540
gggccanagc cagaccatt ttttcctggt cagctttggt tttcgggtcaa ctgcgatgga 600
gattaccggc tcanggaatt tccatacctt ccaggaatga tcggcgcatt ccggtcaaac 660
angngntacc aggggggtac ntntttttaa nancgattgc cagcancgga tntnncccg 720
gcnaaacttc ttggaaacnn ttaccgggtt ggtaaccngc cttttnaacn atccaaccga 780
aaaagngtta anngccantt ttccngngtc tnanntncgg ntcccngaa ntaaccnc 840
cggggtnaac ccngnaaaa 859

```

<210> 23  
 <211> 269  
 <212> DNA  
 <213> E. Coli

```

<400> 23
ctttcttaaa gccttcttta aaggcgatag aagcagccag tttaaacgcc agttcagagg 60
agtcaacgtc atggtaagaa ccgaagtga gacgaatacc catgtctact accgggtagc 120
ctgccagcgg acctgtcttc agctgttctt ggataccttt atcaacggcc gggatgtatt 180
cgccagggat tacaccacct ttaatgtcgt tgatgaactc gtacgcttcc gggtttgaac 240
cgggtccag cgggtacatg tcgataaca 269

```

<210> 24  
 <211> 330  
 <212> DNA  
 <213> E. Coli

```

<400> 24
gttttgggga gatgtaagg ctaatctgaa tggtgcatt ccttggttaa ggaaaaacga 60
atgactgatt gccgatacct gattaaacgg gtcatacaaaa tcatcattgc tgttttacag 120
ctgatccttc tgttcttata acacaaggaa acgtacttaa ggtgcgtccg gtgaaccagt 180
cggacgcacc ttttaataact ataaataagt gtctgggcag atactatata aattaactta 240
gtgaatgatt atgctaattg catcaattaa ataaatataa tggcggttaag gcttcccagt 300
aatataatta atactctact tccagagtag 330

```

<210> 25  
 <211> 471  
 <212> DNA  
 <213> E. Coli

<220>  
 <221> misc\_feature  
 <222> (1)...(471)  
 <223> n = A,T,C or G

```

<400> 25
gttttgggga gatgtaagg ctaatctgaa tggtgcatt ccttggttaa ggaaaaacga 60
atgactgatt gccgatacct gattaaacgg gtcatacaaaa tcatcattgc tgttttacag 120
ctgatccttc tgttcttata acacaaggaa acgtacttaa ggtgcgtccg gtgaaccagt 180
tcggacgcac ctttaataac tataaataag tgtctgggca gatactatat aaattaactt 240
agtgaatgat tatgctaatt tcatcaatta aataaatata atggcggtta ggttcccagt 300
taataataatt aatactctac ttccagagta gaataataaa ttttatccgc gtggtgcac 360
agcaaaaatt tatcccacaa ctgttcttct gtctcgacat gcccccgat ctttnacaaa 420
tantattggg ggattnggcc cncctttttg ncagggtggg gtctctctnat g 471

```

<210> 26  
 <211> 379  
 <212> DNA  
 <213> E. Coli

<220>  
 <221> misc\_feature  
 <222> (1)...(379)  
 <223> n = A,T,C or G

<400> 26

|  |     |
|--|-----|
| natctgantg gctgcattcc ttgtttaagg aaacccgaat gactgattgc cgatacctga  | 60  |
| ttaaacgggt catcaaaatc atcattgctg ttttacagct gatccttctg ttcttataac  | 120 |
| acaaggaac gtacttaagg tgcgtccggt gaaccagtcg gacgcacctt taataactat   | 180 |
| aaataagtgt ctgggcagat actatataaa ttaacttagt gaatgattat gctaagtgtca | 240 |
| tcaat:aaat aaatataatg gcgttaaggc ttcccaqtaa tataattaat actctacttc  | 300 |
| cagagt:agaa tattaattt tatccgcgtg gtgcatcagc acaaatttat cccacaactg  | 360 |
| ttcttctgtc tcgacatgc   | 379 |

<210> 27  
 <211> 799  
 <212> DNA  
 <213> E. Coli

<400> 27

|   |     |
|---|-----|
| aaagatgatg tgatgagaaa gtcaatttga ataagacaat attaagagct aaaaaaatgt   | 60  |
| caaaaaacac taaatcaaaa aataatggca tttagaaaata taatgcgaaa acggagggtga | 120 |
| aattagttta ttccaatga ggaaatctc ccggcgaaaa aaccgggaga tgaaagtgtg     | 180 |
| atggggratca aataaacaac agaggagaaa tttttaacgc agccattcag gcaaatcggt  | 240 |
| taatcccatt gcctggcgga taagtgtcgg cttaacgcca ggaagcgtgt cggccagttt   | 300 |
| caaaccaata tcacgcagca gttttttcgc cggattggta ccggaataca gatcgcggaa   | 360 |
| tccctgcata ccagccagca tcaacgccgc actgtgcttg cggctacgct catagcgacg   | 420 |
| cagataaatg tactgcccga tgtctgggat ccgtcgacct gcagccaaagc ttgggctttt  | 480 |
| cagcctgata cagattaaat cagaacgcag aagcggctctg ataaacaga atttgcttg    | 540 |
| cggcagtagc gcggtgggtcc cactgaccc catgccgaac tcagaagtga aacgccgta    | 600 |
| gcgcccgatg gtagtgtggg gtctcccat gcgagagtag ggaactgccg ggcatacaat    | 660 |
| aaaacgaaag gctcagtcga aagactgggc ctttcggttt atctgggtgt tgcggtgaa    | 720 |
| cgctctctga gtaggacaaa tccgccggga gcggattttg aacgttgcca aacaaccggc   | 780 |
| ccggaagggg gtggggggt  | 799 |

<210> 28  
 <211> 636  
 <212> DNA  
 <213> E. Coli

<220>  
 <221> misc\_feature  
 <222> (1)...(636)  
 <223> n = A,T,C or G

<400> 28

|  |     |
|--|-----|
| aggggggtttg ttgtgggcaa tgatgcattt aagttatcgt ctgcagatag aggagatatt | 60  |
| acaataaaca acgaatcagg gcatttgata gtcaataccg caattctatc aggagatata  | 120 |
| gtcactctaa gaggaggaga aattagggtg gtattatagc ttgtgcgcgc catgattggc  | 180 |
| gcgcaattta aacttagtgc ttacatcgc tattgtcttg atttctttga attattttat   | 240 |
| aaattaaaaa aacgactggt atgtataagc aaagggtcgaa cgaaaaatac attccaaata | 300 |
| aatgcttgct taaatctcta tatccttccc cgaaaaatga cacataaaat tgagatattc  | 360 |
| caaaaagaga tactacaaat aaagatgcct ttattttatt atttctaata aaaaatagaag | 420 |
| caataaaaaa taataacaat gatataaatc taatgttttt aaatatattg tcttttatgt  | 480 |
| tagtaatagt cgttagtatg ttgattctc catatattac gtgtagtttt ttatatacat   | 540 |
| ggaaataatt ntctttatac tgagacatca caccatcatc aaatggaagt ttgaagatgg  | 600 |
| tgcttggttt gctaaccaat aaaaagagtg cattcg                            | 636 |

<210> 29  
 <211> 757  
 <212> DNA



&lt;213&gt; E. Coli

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(757)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 29

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| cagcggtcgt | atttttagca | tggtttttta | ttggcggcta  | tgctgccccg | ggagcataaa | 60  |
| gatgaaaaaa | acaacgatta | ttatgatggg | tggtggcgatt | attgtcgtac | tcggcactga | 120 |
| gctgggatgg | tggtaacgtc | acctctaaaa | aatagcaaag  | gctgcctgtg | tgacgccttt | 180 |
| gtgcaattta | agcgttaact | tttaattctt | ctgtagataa  | atagcacgac | aatcgcacca | 240 |
| ataacggcaa | ccacgaagct | gccaaaattg | aagccatcga  | ctttaccaa  | gccaaacagc | 300 |
| gtgctgatcc | atccgcccgc | tacggcaccg | actatcccca  | gcaggatagt | cataaagaat | 360 |
| ccacctccat | ctttacctgg | catgatccac | ttcgccagaa  | taccggcaat | aagcccaaaa | 420 |
| ataatccatg | acagaatgcc | cattgtttcc | tcacttatct  | gttttgcat  | agcgggttag | 480 |
| tcgctgataa | aaagcatagc | acaacatcgg | gagggcaaga  | tttgtgacga | gcacacgga  | 540 |
| ggtttttttt | gcgatggcgc | agaaattgcg | ccatcaacga  | tcagtataa  | ttaccaacca | 600 |
| caaacatcat | gttcgttttc | cgtgtcataa | gaaccgtacg  | ggattcacca | gatcttttat | 660 |
| cacttcaagc | cggcactttc | ggcaccagca | aagtcacgga  | cgtctctggt | tcataatcga | 720 |
| ccggaacgc  | cattgctggt | attggtgaen | gtcacgg     |            |            | 757 |

&lt;210&gt; 30

&lt;211&gt; 392

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 30

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| aattacagaa | aaaggaggca | ataticggga  | aaggcattag | cccacgaat  | acgtcgggct | 60  |
| acaaatatta | ttgtgctgca | ggtgttttag  | cgggttggtg | atccacaggt | tctaactgga | 120 |
| agaccacatc | gacctgatca | tcaaaactgaa | tagcggcctg | ctcgtaaagt | tcctgggcgg | 180 |
| acaccggcgc | ggcatcggct | ttcatcatcc  | gcaccattgg | gctgggctga | tagttggaaa | 240 |
| catggtagcg | cacgttatat | accggcccca  | gtttacgatg | aaagccgttc | gccagttcct | 300 |
| gcgcctgatg | aatcgcggtt | tcaatcgctg  | ccttacgcgc | tttgtcttta | taggcatccg | 360 |
| gctgcgccac | gcccagcgac | acagaacgaa  | tt         |            |            | 392 |

&lt;210&gt; 31

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 31

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| ctatccttga | tgaaccgcgc | agcaaagata  | ggtgattacg | tcattggttt | acagaaaatt | 60  |
| acagaaaaag | gaggcaatat | cgggttaaagg | cattagcccc | acgaatacgt | cgggctacaa | 120 |
| atattattgt | gctgcaggtg | ttttagcggg  | ttgttgatcc | acaggttcta | actggaagac | 180 |
| cacatcgacc | tgatcatcaa | actgaatagc  | ggcctgctcg | taagtttcct | ggcgggacac | 240 |
| cggcgcggca | tcggctttca | tcacccgcac  | cattgggctg | ggctgatagt | tggaacatg  | 300 |
| gtagcgcacg | ctatataccg | gccccagttt  | acgatgaaag | ccgttcgcca | g          | 351 |

&lt;210&gt; 32

&lt;211&gt; 762

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(762)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 32

|            |            |            |            |            |            |    |
|------------|------------|------------|------------|------------|------------|----|
| aattatgaaa | cactgtcttg | aatcgtctga | atgacgggca | catttgcgag | cacgcatcca | 60 |
|------------|------------|------------|------------|------------|------------|----|

```

gtaataaacac aggaaactat tttatctacg cgttagcgat agactgcttg catggcgaaa 120
ggaggtaagc cgacgatttc agcgggacgc tgaaacggga aagcccctcc cgagggaagg 180
gccataaata aggaaagggt catgatgaag ctactcatca tcgtgggtgct cttagtcata 240
agcttccccg cttactaaga ctaccagggc gggggaaaacc ccgctctacc ctactcctg 300
aaagtatgcc ttcacgataa gattgtcaat ccgcaggctt tgtagtctgc gatcctgcca 360
gcaaatattc tttgcgagtc gttacgcaat aatcacagag gaaactattt tattcacgcg 420
ttagcgatag actgcattca gggcgaaaagg aggtaaagccg atgatttcag cgggacgctg 480
aaacgggaaa gcctctcccg gagaagaggg cttttaataa ggaaagggtt atgatgaagc 540
acgtcatcat actgggtgata ctcttagtga ttactctcca ggcttactaa gaacaccagg 600
gggaggggga aacctcttcc taacctcac ttctgaaatt ggggtgctatg acgctggcgt 660
tactgcttan cgctaccagt ttgtctgccc tggcggttgt aacgccagat cggtagccgt 720
ttggatattt taatgaaagc cgacaaatca atcancgtga cg 762

```

<210> 33  
 <211> 293  
 <212> DNA  
 <213> E. Coli

```

<400> 33
gcacatttgc gagcacgcat ccagtaataa cacaggaaac tattttatct acgcgttagc 60
gatagactgc ttgcattggc aaaggaggta agccgacgat ttcagcggga cgctgaaacg 120
ggaaaagcccc tcccagaggaa ggggccataa ataaggaag ggtcatgatg aagctactca 180
tcatcggtgt gctcttagtc ataagcttcc ccgcttacta agactaccag ggcgggggaa 240
accccgctct acctcactc ctgaaagtat gccttcacga taagattgtc aat 293

```

<210> 34  
 <211> 633  
 <212> DNA  
 <213> E. Coli

<220>  
 <221> misc\_feature  
 <222> (1)...(633)  
 <223> n = A,T,C or G

```

<400> 34
atttacactt tttacgaaat catgggatca ctaacaaaa atcgcttgtc agttatattg 60
tatggcagga aagatatgag actgatatta cagatcccca aagtggagag tttatgacca 120
ttaaaaaata gatgttgctg ggtgcgcttt tgctgggtac cagtgcgcgc tgggccgcac 180
cagccaccgc gggttcgacc aatacctcgg gaattttctaa gtatgagtta agtagtttca 240
ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 300
agtacaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcact 360
ggacctatat ggggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag 420
cctacgacgg tgagattttt tatcatcgct aaaaaaagcc ccctcatcat gagggggaaa 480
tgcagacacc ttgntatttt ttattattag ccacttgctc gtcttgcttg gtattaaagc 540
gtatttcacg ttgattaatg cnggtggctc cagtgcgcca gattaacttt gtttgatcg 600
aagacgtagt aactggctgg ttatcggaat tgg 633

```

<210> 35  
 <211> 569  
 <212> DNA  
 <213> E. Coli

```

<400> 35
tatggcagga aagatatgag actgatatta cagatcccca aagtggagag tttatgacca 60
ttaaaaaata gatgttgctg ggtgcgcttt tgctgggtac cagtgcgcgc tgggccgcac 120
cagccaccgc gggttcgacc aatacctcgg gaattttctaa gtatgagtta agtagtttca 180
ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 240
agtacaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcact 300
ggacctatat ggggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag 360
cctacgacgg tgagattttt tatcatcgct aaaaaaagcc ccctcatcat gagggggaaa 420

```

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tgcagacacc | ttgttatttt | ttattattag | ccacttgctc | gtcttgcttg | ttattagtgc | 480 |
| tatttcacgt | tgattaatgc | ggttgcctcc | agtgcgccag | atttaacttt | gtttgtatcg | 540 |
| tagacgtagt | aactggctgg | tatcggaat  |            |            |            | 569 |

<210> 36  
 <211> 338  
 <212> DNA  
 <213> E. Coli

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| <400> 36   |            |            |            |             |            |     |
| cgtattcaca | tccttttgat | tggtgataac | atgcgaatcg | gtattatttt  | tcgggttgta | 60  |
| atcttcatta | cagcggtcgt | atttttagca | tggtttttta | ttggcggcta  | tgctgccccg | 120 |
| ggagcataaa | gatgaaaaaa | acaacgatta | ttatgatggg | tggtggcgatt | attgtcgtac | 180 |
| tcggcactgc | ctgggatggg | ggtaacgtca | cctctaaaaa | atagcaaagg  | ctgcctgtgt | 240 |
| gcagcctttg | tgcaatttaa | gcgttaactt | ttaatcttcc | tgtagataaa  | tagcacgaca | 300 |
| atgcgaccaa | taacggcaac | cacgaagctg | ccaaaaatt  |             |            | 338 |

<210> 37  
 <211> 375  
 <212> DNA  
 <213> E. Coli

|             |             |             |            |            |             |            |     |
|-------------|-------------|-------------|------------|------------|-------------|------------|-----|
| <400> 37    |             |             |            |            |             |            |     |
| ctgaatat    | ttt         | aaaaaggaaa  | acgacatgaa | accgaagcac | agaatcaaca  | ttctccaatc | 60  |
| ataaaaat    | tatt        | tcogtggagc  | attttattat | tgaatataga | ggtttaactc  | cggtaaaaaa | 120 |
| caaagaagca  | ttgaatycag  | ggaaaaataa  | tatggccata | aaaaacatcg | aaagaaactc  |            | 180 |
| ttttaattta  | acatgtaaac  | gcatgggttaa | tcctcatatc | acgggtggag | tggttaagaac |            | 240 |
| atacataaat  | ggagtcaggt  | tttccctttt  | ccatttatca | agttcctgtt | gccgttttag  |            | 300 |
| tcctatctcta | attgcataatt | ttaatttttc  | tgataaatgg | cattgagcat | cgatttcatt  |            | 360 |
| taaaacaact  | gtaca       |             |            |            |             |            | 375 |

<210> 38  
 <211> 446  
 <212> DNA  
 <213> E. Coli

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| <400> 38   |            |            |            |             |            |     |
| ttacgatagc | tattagtaaa | aataaagag  | ttagctgtat | tggtatgtct  | gtggcgaaa  | 60  |
| tgactacctt | cgtttttttg | attaagaatg | attttattat | cgtaagtaaa  | attacatgaa | 120 |
| tatttaaaaa | ggaaaacgac | atgaaaaccg | agcacagaat | caacattctc  | caatcataaa | 180 |
| atatttcctg | ggagcatttt | attattgaat | atagaggttt | aactccggta  | aaaaacaaa  | 240 |
| aagcattgaa | tgacgggaaa | aataaatatg | ccataaaaaa | catcgaaaag  | aactctttta | 300 |
| atttaacatg | taaacgcatg | gttaatcctc | atatcacggg | tgagagtgtta | agaacataca | 360 |
| taaatggagt | catgttttcc | ctttccatt  | tatcaagttc | ctgttgccgt  | tttagtccat | 420 |
| ctctaattgc | atattttaat | ttttct     |            |             |            | 446 |

<210> 39  
 <211> 392  
 <212> DNA  
 <213> E. Coli

<220>  
 <221> misc\_feature  
 <222> (1) ... (392)  
 <223> n = A,T,C or G

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| <400> 39    |            |             |            |            |            |     |
| tcaccccggt  | gccgattttc | aggcatcctg  | atttaactta | gcacccgcaa | cttaactaca | 60  |
| ggaaaaacaaa | gagataaatg | tctaactcctg | atgcaaatcg | agccgatttt | ttaatcttta | 120 |
| cggactttta  | ccgcctgggt | ttattaattg  | cactgtnatc | cgggcgttcg | cccgttttaa | 180 |
| tcacaatagg  | ctgtgtagcc | tgggcctggt  | tctctttcac | ccgcgccaga | gcggcagcaa | 240 |

tcgcacrttt atctttggct gcaggttgaa cggttcgct cttatgtcgt tcaaggcgag 300  
 ccgctttttc gcgctccaga cgagcctggc gcgcttcgaa acgcgctttg gcttctgcgg 360  
 cncgcttttc ttcctgacga atagccgcaa tt 392

<210> 40  
 <211> 208  
 <212> DNA  
 <213> E. Coli

<400> 40  
 taataacgct atctgcggat aaagcagaat aggtgggttaa cccagacat aaaccgagga 60  
 aaataatggt attgtatttc ataacttatt gtcccttagc gacagattgc tgtctgctgg 120  
 ttcagtaagg taccaggaga aacttcagga agcttggtact cgacaatata gtttgagttt 180  
 ttatctttgc cccatgaaac ctgtaatt 208

<210> 41  
 <211> 342  
 <212> DNA  
 <213> E. Coli

<400> 41  
 catcttcaat accgttaaat gcaaccgaa ccccggtgt ccttttgcgt cattcactta 60  
 acgtaactcg aaaaggagcg gctggacttg tgctaccggt cgttggaat tgtctggcac 120  
 tggttttttg gagatctacg gtaaaattaa gcgaatccga tgagactgtg cagccataat 180  
 cgaggacgcg cccgctaatt ttaataacgc tatctgcgga taaagcagaa taggtggtta 240  
 accccagaca taaaccgagg aaaataatgt tattgtattt cataatctat tgttccttag 300  
 cgacagattg ctgtctgctg gtacagtaag gtaccaggag aa 342

<210> 42  
 <211> 841  
 <212> DNA  
 <213> E. Coli

<220>  
 <221> misc\_feature  
 <222> (1)...(841)  
 <223> n = A,T,C or G

<400> 42  
 agatttactg ccaatttccg gcagatcgga aagggttaaa ccatattgat ccataagggt 60  
 acgaatcacg gctataccgc caggcatggc ttgagccatg gcattaaatt ccgcaaattc 120  
 gggcgctgat tcttccacg cggttatttt ggcacacacc agatccagca aggggttntc 180  
 aggatcggtg agcagcagat gatctaccag ttncagcgcc tgggtgtatt gntcctgttt 240  
 ctgaataccc gnnagaaaaa gtgccacagc anttagcttn tctcctgctt gcaagatgtc 300  
 tggcaatngc aatcattttt tgcacttant acgatgnaca ncngtaaaaga aatcgnattt 360  
 ttntatgccg tcataacttt acgtatgtan cactttttgc nattenaaaa aagaccattn 420  
 gctncaacac gtaaattna ttgncccnna catttanaac ataaatgntt aaaattttcc 480  
 ccccnncnnan ttttaagntn ttanagaat ngggaattac ctgcttttna atgnactcan 540  
 anttttttng naatpattcc tntatcnaa ctnntttttn cccaanagnc nnccaaattn 600  
 cggtttntn nttnncnng onttttttta cccnanaann tttattcaan nccttttttg 660  
 tagnttattt naagngnct tntttnnatt aactttccnn ttggncaaat tttggcnnat 720  
 ttttatatan aattntctta tntcntaatt tnggnanccc cngatgnaa tttatggngg 780  
 gantcccnnt ccctntttta tnnatgntct gggntatttt taaancctnn attaanann 840  
 c 841

<210> 43  
 <211> 215  
 <212> DNA  
 <213> E. Coli

<400> 43

```

aataactttt cgtaggcag ttttgggtgt gagggtgcaag aggggagact actgaataac    60
tcaagtttta taatcgaggg gaaaatggtg atggcggttca tagcaaaacg ccctcaacca    120
taaagggtcga gggcgcttaa gatgttaaaa acccgctatc cggttaaaaaa caatgttcaa    180
ctaagggtcag tgacattgctg ctaaaaaaagc gaatt                                215

```

```

<210> 44
<211> 395
<212> DNA
<213> E. Coli

```

```

<220>
<221> misc_feature
<222> (1)...(395)
<223> n = A,T,C or G

```

```

<400> 44
gcattattca tgagaaatgt gtatcgtaaa tcaactgaaa ttaacgcaac catttggtat    60
ttaagggtta attatctgtg tgtgatattt tattgaatgt tttaaatatt gtttttattg    120
gcattgctat aatattggtt atcatttgct gaatggattc agtcttaatg agtgggtttt    180
taagggacag gcatagagta atgatacgtg tgcataacca acatctttac tcattatgtc    240
attgaatgtt gaccctatgt gtttatgaag gagaggtatt ttcagttgat ctggattgnt    300
aaattcatat aatgcgcctt tgctcatgaa tggatgccag tatgtagtgg gaaattataa    360
atattgaaat agtccaacta cttctttatt accaa                                395

```

```

<210> 45
<211> 883
<212> DNA
<213> E. Coli

```

```

<220>
<221> misc_feature
<222> (1)...(883)
<223> n = A,T,C or G

```

```

<400> 45
ataatcaggt aagaaaaaggt gcgcggagat taccgtgtgt tgcgatatat ttttagttt    60
cgcgtggcaa tacatcagtg gcaataaaac gacatatcca gaaaaatata cactaagtga    120
atgatatctt ccgattttatc ttaatcgttt atggataacg gcaaaaggct tcgttttttc    180
ctatacttat tcagcactca caaataaagg aacgccaatg aaaattatac tctgggctgt    240
attgattatt ttcctgattg ggctactggt ggtgactggc gtatttaaga tgatatttta    300
aaattaatta atgcatcag gtccgaaaaa aacgagaata tttcagtctc tcacctgtt    360
gcgctcctgt catgtgcatt gcttcataata atcactggcg caaggagcgc gcgaggcgna    420
gnntgcncgn cgncccacct naccccatgc cgaacttcag aantgaaaac nccntaacnc    480
cgatngtcgg cggnggcctc cccatgcnan agtangggaa ntgccangcg ncnntataaa    540
cgaaaggctn attncaaaga ctgggccttn cntttatctg atgtttgtcg gagaacgctc    600
tcctgagnan gacaaatncc gccgggagcg gatttgaacn ttgcgaagca accgncctcna    660
aggngnngt cntgaenccc nncctctant nnngccttc ttttgcctna angncctcct    720
ancngatggc ctttttngcc ntctacccaa cnntttggtt aatgcttnta aaancctttc    780
canntncaaa tccngtntnn cccatccnnn tnntgaaagn ntncctnccn tgnctantnt    840
anntnngggg gnnngngngc ggcggncccc cccccccccc ccc                                883

```

```

<210> 46
<211> 1024
<212> DNA
<213> E. Coli

```

```

<220>
<221> misc_feature
<222> (1)...(1024)
<223> n = A,T,C or G

```

<400> 46  
 gtttatggat aacggcaaaag ggcttcggtt tttcctatac ttattcagca ctcacaaata 60  
 aaggaacgcc aatgaaaatt atactctggg ctgtattgat tattttcctg attgggctac 120  
 tgggtggtgac tggcgtattt aagatgatat tttaaaatta attaatgtca tcagggtccga 180  
 aaataacgag aatatttcag tctctcatcc tgttgcgctc ctgtcatgtg cattgcttca 240  
 tataatcact ggcgcaagga gcgcgcagag tntcccnant nnnntnnnt nntnnctnn 300  
 nccttcacna tncnnccn nantnnatag nncaccnntn tnnntcnnnn gncncctcc 360  
 nnnnnnnnn ncatnnnatc ccactnnnt tntccannn nnnnnnnntn canccnacia 420  
 antncnaccn annnacctt atacnnannc nancnnnnnn nncactctn nctcgnnctc 480  
 cccnttcnac nncannnnnn cancnntcnn ctnnnnccct nncntaattn tctnnctan 540  
 ntccatncnn cnnacnnncc cancnatcnn nnnatacant cnattnnntn cnnctnctn 600  
 cncnnttcc nntnnnnnc tncncatnc ccnnnnann canntncccc nctnccctna 660  
 ccncncncnc cncncatccc nnnccnnt ccnnantnga caannnnaat cncnnnnncn 720  
 nnnnnnnnn tnnncnccn gcncnnccnt nccntcacnc tnnnnnncta nannnnntac 780  
 nntnacnnt cctnnacnc tncctnnng antccnacha ntannnnanc nanaacnctn 840  
 tnnnnccata atccacacc acnccentnc ancntntnt ncntntccc ttcntatcnc 900  
 agctnnnnnt nctntnnnn tncnccnncn cnnactnncn nncaccnncn cccantcagt 960  
 ccacntccn cnnnnnnnt nnnnnancn ctnncacnc cnantaacct nntnnacct 1020  
 tccc 1024

<210> 47

<211> 236

<212> DNA

<213> E. Coli

<400> 47  
 atatacacta agtgaatgat atcttccgat ttatcttaat cgtttatgga taacggcaaa 60  
 gggcttcggt ttttctata cttattcagc actcacaat aaaggaacgc caatgaaaat 120  
 tatactctgg gctgtattga ttattttcct gattgggcta ctgggtggtga ctggcgtatt 180  
 taagatgata ttttaaaatt aattaatgtc atcagggtccg aaaataacga gaatat 236

<210> 48

<211> 418

<212> DNA

<213> E. Coli

<220>

<221> misc\_feature

<222> (1)...(418)

<223> n = A, T, C or G

<400> 48  
 cggagattac cgtgtgtgc gatataat ttagtttcgc gtggcaatac atcagtggca 60  
 ataaaaacgac atatccagaa aaatatacac taagtgaatg atatcttccg attnatctta 120  
 ntogtttatg gataacggca aagggttcg ttttttcta tacttattca gcaactcacia 180  
 ataaaggaac gcaatgaaa attatactct gggctgtatt gattatttcc ctgattgggc 240  
 tactgtgtgt gactggcgta ttttaagatga ttttttaaaa ttaattaatg tcatcaggtc 300  
 cgaaaataac gagaatattt cagtctctca tctgtgtgcg ctctgtcat gtgcattgct 360  
 tcatataatc actggcgcaa ggagcgcgca ngggcgggcc aatcgccgcc ggcccctg 418

<210> 49

<211> 550

<212> DNA

<213> E. Coli

<400> 49  
 ctgctagtta caggggaacac taatgacaga cagctaaaag ccctgtttta ttacgtatta 60  
 caaacagggg atgccagcg ttttcgtgca tttattggtg agatagcggg acgcgcacca 120  
 caagaaaagg agaaactgat gaccattgct gacagattac gtgaagaagg cgcaatgcag 180  
 ggcaaacacg aagaagccct gcgtattgct caggagatgc tggatagagg ttagacaga 240  
 gaggtagtta tgatggtgac ccgacttica ccagacgac ttatcgcgca aagccactaa 300

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| tcctgtaaca | ccgggagtta | actggcggat | gtttgctgta | aaccacatca  | gcgaacgaca | 360 |
| tccgccagcg | cctcttctaa | atcgtaccag | cgaaacgcaa | aaccgccttc  | ttccagccgt | 420 |
| ttaggcagcg | cgcggtgtcc | acctaatacc | agtactgaag | attcgcccat  | taacagtcga | 480 |
| atggcggtcg | cggggacgcg | caaaatggcc | gggcgatgca | gcgcgatgacc | gagcgcatgg | 540 |
| gcaaattgtt |            |            |            |             |            | 550 |

<210> 50  
 <211> 99  
 <212> DNA  
 <213> E. Coli

|            |            |            |            |            |            |    |
|------------|------------|------------|------------|------------|------------|----|
| ttggcatctc | ggtgttgccg | atcttcata  | tatccagccc | gccggaaact | tcttcccaaa | 60 |
| cggttttgct | gttatccatt | gagtcacgga | actgccct   |            |            | 99 |

<210> 51  
 <211> 259  
 <212> DNA  
 <213> E. Coli

<220>  
 <221> misc\_feature  
 <222> (1)...(259)  
 <223> n = A,T,C or G

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ccgtgcccag | atgatctctg | naccatcatc | cggtgtgaag | tagtgattca | cgacttcaag | 60  |
| gcgcttttca | aaagggtatt | ttggctttga | catattaggg | gctattccat | ttcatcgnc  | 120 |
| aacaaaaatg | gtgcagtaca | tactcattgg | aaatcaacac | aggaggctgg | gaatgccgca | 180 |
| gaaatataga | ttactttctt | taatagtgat | ntgtttcacg | cttttatttt | tnaaanaagt | 240 |
| tnggcttact | tcgccgggn  |            |            |            |            | 259 |

<210> 52  
 <211> 877  
 <212> DNA  
 <213> E. Coli

<220>  
 <221> misc\_feature  
 <222> (1)...(877)  
 <223> n = A,T,C or G

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| cagcagagcg  | cgcccttctt | cgtcagattt | cgccagtagtg | gtaatggtaa | tatccaaacc | 60  |
| acgaacgcgg  | tcgactttat | cgtagtcgat | ttctgggaag  | atgatctgct | cacggacacc | 120 |
| catgctgtag  | ttaccacgac | cgtcgaaaga | cttagcggac  | aggccacgga | agtcacggat | 180 |
| acgagggtaca | gcaatagtga | tcaggcgctc | aaagaactcc  | cacatgcgtt | cgccacgcag | 240 |
| agttacttta  | cagccgatcg | gatagccctg | acggattttg  | aagcctgcaa | cagatttgcg | 300 |
| tgctttgggt  | atcagcggtt | tttgaccgga | gattgctgcc  | aggtctgctg | ctgcgttatc | 360 |
| cagcagtttt  | ttgtcagcga | tcgcttcacc | aacacccatg  | ttcagggtga | tcttctcgac | 420 |
| ccgagggaact | tgcatgacag | aattgtagtt | aaactcagtc  | atgagttttt | taactaettc | 480 |
| gtctttgtag  | taatcatgca | gtttcgccat | cgtactactc  | catgtcggtg | aacgctctcc | 540 |
| tgagtaggac  | aaatccgccg | ggagcggatt | tgaacgttgc  | gaagcaacgg | cccggagggt | 600 |
| ggcgggcagg  | acgcccgcga | taaactgcca | ggcatcaa    | taagcagaag | gccatcctga | 660 |
| cggtatggcct | ttttgcgttt | ctacaaactc | ttttggttat  | ttttctaaat | cattcaata  | 720 |
| tgtatccgnt  | catcccatcc | tatcgatgat | aagctgtcaa  | acatgagaat | ttaatcaatc | 780 |
| taaaagtttta | tggnngttaa | cttgggctgg | cagnttncca  | atggctta   | cagtngaggg | 840 |
| ccctatntta  | acgaactnng | ctantttngg | tcaatcn     |            |            | 877 |

<210> 53  
 <211> 291

<212> DNA  
<213> E. Coli

<400> 53

|   |     |
|---|-----|
| tgaacagcag agatacggcc agtgcggcca atgttttttg tcctttaaac ataacagagt   | 60  |
| cctttaaggga tatagaatag gggatatagct acgccagaat atcgtatttg attattgcta | 120 |
| gttttttagtt ttgcttaaaa atattgttag ttttattaaa tgcaaaacta aattattggt  | 180 |
| atcatgaatt tgttgtaga tgaataaaat atagggggggt atagatagac gtcattttca   | 240 |
| tagggctata aatgcgacta ccatgaagtt ttttaattgaa agtattgggt t           | 291 |

<210> 54  
<211> 282  
<212> DNA  
<213> E. Coli

<400> 54

|  |     |
|--|-----|
| ttattaaatg caaaactaaa ttattggat catgaatttg ttgtatgatg aataaaatat   | 60  |
| agggggggtat agatagacgt cattttcata ggggtataaa tgcgactacc atgaagtttt | 120 |
| taattgaaag tattgggttg ctgataattt gagctgttct attcttttta aatatctata  | 180 |
| taggtctgtt aatggatttt atttttacaa ttttttgtgt ttaggcataa aaaaatcaac  | 240 |
| ccgccatatg aacggcggggt taaaatattt acaacttagc aa                    | 282 |

<210> 55  
<211> 293  
<212> DNA  
<213> E. Coli

<220>

<221> misc\_feature

<222> (1)...(293)

<223> n = A,T,C or G

<400> 55

|  |     |
|--|-----|
| cggggtccgg cgctcatcaa caatcggggg gcagcaaggg gctgaaacgg gaaagcccct  | 60  |
| cccgaagaay gggccttgta taaggaaagg gttatgatga agctcgctcat catactgggt | 120 |
| gtgtngttac tgttaagttt cccgacttac taacaactca tcagaggggg gagaaatcct  | 180 |
| cccttaccct tgttccttta ctctaggttg aaaaaacaac agcgtcaata ggctgccat   | 240 |
| gtacgaagcg agatctgtga accgctttcc ggtagcctt ttttatcctg ttg          | 293 |

<210> 56  
<211> 300  
<212> DNA  
<213> E. Coli

<400> 56

|  |     |
|--|-----|
| tctgcgttcc gctaaaagggt gcaaatgctc aggacgttgc agcgttttgc gtgaccgctc | 60  |
| ggggaaggca aaattgcctc tgggaaaagca ttgcgcgggg tccggcgctc atcaacaatc | 120 |
| ggggggcagc aaggggctga aacgggaaag cccctcccga agaaggggcc ttgtataagg  | 180 |
| aaagggttat gatgaagctc gtcatacatc tggttgtgtt gttactgtta agtttcccga  | 240 |
| cttactaaca actcatcaga ggggggagaa atcctccctt acccttgctc ctttactcta  | 300 |

<210> 57  
<211> 359  
<212> DNA  
<213> E. Coli

<400> 57

|  |     |
|--|-----|
| caacacagga ggctgggaat gccgcagaaa tatagattac tttctttaat agtgatttgt  | 60  |
| ttcacgcttt tattttttcac ctggatgata agagattcac tgtgtgaatt gcatattaaa | 120 |
| caggagagtt atgagctggc ggcgttttta gcctgcaaat tgaaagagta agagtcttcg  | 180 |
| gcgggaaatt attcccgcct tacttacggc gttgcgcatt ctcatcgac ccaaaatttat  | 240 |



tcttcacaaa aataataata gattttatta cgcgatcgat tatttatttc ctgaaaacaa 300  
ataaaaaaat ccccgcaaaa tggcagggat cttagattct gtgcttttaa gcagagatt 359

<210> 58  
<211> 700  
<212> DNA  
<213> E. Coli

<220>  
<221> misc\_feature  
<222> (1)...(700)  
<223> n = A,T,C or G

<400> 58  
aaaccttttt ctctgtttt tcatagaggg caacccatgt cctgacctgg gtccggggga 60  
caccaaaaacg tgcgagatg atcctgtaac catcatcagt tgtgaagtag tgattcacga 120  
cttcaaggcg cttttcaaaa ggggtattttg gctttgacat attaggggct attccatttc 180  
atcgtccaac aaaatgggtg cagtacatac tcgttggaat tcaacacagg aggctgggaa 240  
tgcgcagaaa atatagatta ctttctttaa tagtgatttg ttccacgctt ttatttttca 300  
cctggatgat aagagattca ctgtgtgaat tgcatattaa acaggagagt tatgagctgg 360  
cgcggttttt agcctgcaaa ttgaaagagt aagagtcttc ggccgggaaaat tattcccgcc 420  
ttacttaacg cggttgcgat tctcattgca cccaaattta ttcttcacaa aaataataat 480  
agattttatt acgcgatcga ttattttatt cctgaaaaca aataanaaaa tccccgccaa 540  
atggcagggg tcttagattc tgtgtcttta agcagagatt acaggctggt tacgttacca 600  
gctgcccggc ctttaacgcc gctttcgatg gtgaaggaca ctttctgacc ttcgtccaga 660  
gattgtaacc atcgggtcgg atagccnaga aatgtccaac 700

<210> 59  
<211> 631  
<212> DNA  
<213> E. Coli

<220>  
<221> misc\_feature  
<222> (1)...(631)  
<223> n = A,T,C or G

<400> 59  
tggtggcatt ggttgctgga gagagaaaac ccccgcacgt tgcaggatg cacctgacaa 60  
caccacgggg gctaattctg actctagacc actcaagaat agccgcgaaa cggtgtcatt 120  
acaacacagg cggtatatat acgttcgcag agctgggcat ggccttctgg catgatttag 180  
cggtccgggt cattgtctggc attcttgcca gtatgatcgt gaactggctg aacaagcggg 240  
agtaacgtgt catgcccggc tcaggctgcc gtaatggcaa ttgcccgcg gaccaggccg 300  
caggggggaa actctgcggc ctttttcgtt ctactgcgg gtaaggcacc cagtgcggc 360  
cgttcaggcg aacgtacggt ttatcctggt attgaataac tactgcattt gagttctcgg 420  
agaccggtgc tgtttgtggc aaccactgg tgagtttttt ccagtcaaca ttgtcttcgg 480  
tgaaaatctt gccatcgaga acgcgaacca ccagatcgga gatagccagg aagctgctcg 540  
gttggttcgat gacaatcggg gccccctgat gcggtgcctt catgccgaag aatttcaccc 600  
caacggggac gtcngtgata gaccgggcta g 631

<210> 60  
<211> 648  
<212> DNA  
<213> E. Coli

<220>  
<221> misc\_feature  
<222> (1)...(648)  
<223> n = A,T,C or G

<400> 60

```

ggctcaggcn tgctgattgt ttttttgtgc aatggcccng tattagcgtc gttgctgtcg      60
atggagagaa tcataaacgt ggtgaatgat gattgttagc aaggaaaact gtcaaaaatc      120
ttcaaaaaat ttgagggata aggccggaat ggctccggcc agaggggaagt taaccgcgaa      180
gctgttgctg cttgagggtc gttttaacca gacgccaggc gctccatacg ccaaaaccgc      240
gtctggccca gcgaccagc atattaggat ggcgaatcgt ccagatcgcc atcacgctac      300
tgccaaccag cgcccaggag cgcagactta gcagcatatt ccancgacga tcgtaagcgc      360
ctgttgtctc cagccattca cgcagactgg cgaaggggnc cgcgnetgac caacttgnet      420
tttagtctga tncanattan atnataaac gcagnanncn ggtntgatta atcntatttn      480
gctctngtct ggtagttagc nncggnnngt ctcnttntna cccnnttcnn tttannttac      540
natnngtaan ttatntttnt nngtctnant tntanttgng tactntaagt ntatncgnnn      600
atnntnnnan nnnncagunc ntntttttta aatntttnt nanncnnc      648

```

```

<210> 61
<211> 737
<212> DNA
<213> E. Coli

```

```

<220>
<221> misc_feature
<222> (1)...(737)
<223> n = A,T,C or G

```

```

<400> 61
tgctaataatc tttctcattg agatgaaaat taaggtaagc gaggaacac accacaccat      60
aaacggaggc aaataatgct ggtgaatgat aatgttttta tggccgtact gggaataatt      120
ttattttctg gttttctggc cgcgtatttc agccacaaat gggatgacta atgaacggag      180
ataatccctc acctaacggc ccccttggtta cagtttgtga caaggggcct gatttttatg      240
acggcgaaaa aaaaccgcca gtaaaccggc ggtgaatgct tgcattggata gatttgtgtt      300
ttgtttttac gctaaccaggc attttcctgc actgataacg aatcggtgac acagtagcat      360
cagttttctc aatgaatggt aaacggagct taaactcggg taatcacatt ttgttcgtca      420
ataaacatgc agcgatttct tccggtttgc ttaccctcat acattgcccg gtccgctctt      480
ccaatgacca catccaggag ctcttcagga aatgcgcgac tcacacctgc tgtcacggta      540
atgttgatat gcccttcaga atgtgtgatg gcatgggtat cgactaactg gcaaattctg      600
acacctgcac gacatgcttc ttcattcatc gccgctttga caataatgat aaattcttcg      660
cccccgtagc gataaacctt ttcgtaatna cgcgtccaac tgggntaagt aaagtgcga      720
gggtgccgta atctttac      737

```

```

<210> 62
<211> 648
<212> DNA
<213> E. Coli

```

```

<220>
<221> misc_feature
<222> (1)...(648)
<223> n = A,T,C or G

```

```

<400> 62
tgcttttgaa tatgtgctcg caatcttgag aaggaaatgg cgaccacgaa agaaaaggca      60
aaaaccgata atctgaaaga acccaagtat ttcagtataa gcattgaatg ccgaccagta      120
aactctttcg gattcaccca gaaagtgaan ccaaaatgat aatcgatac ataagtcttt      180
cgagtggctc gttagcaaaa agtttcaaca atggagtaaa tacatccaac atatcaataa      240
ctctcaactg taaggggatt gaaatggtaa cccagctctc tcgcttgagg ggtatagccg      300
agaccaccga agccccggag gtggtgaaat aaaaccgggc acaacacgaa agggcgcat      360
tccgatatcc ataaaagaag tcgggtcttt gtctggtaaa attaaatttg tgggaagtgc      420
gcctccgggt tgtaaatacc gactttgctg ggtgtagcct ggcggcatca agtttttttc      480
tggaagtctg ctgatgtccg ccctttttta agggaatttt ggtgatgccg gtgaatgccg      540
cttaaccccc cgtgggcca gttaaaagtc atggttaagc ctaatnggtt tggggtggga      600
aaagccnact gnaaattggt tacctggttt gcaagtancc ctggaagg      648

```

```

<210> 63

```

<211> 237  
 <212> DNA  
 <213> E. Coli

<220>  
 <221> misc\_feature  
 <222> (1)...(237)  
 <223> n = A,T,C or G

<400> 63  
 ggtgtttant tacaagagat tcactctttgt ntaaaancccn gataagtaat tacgcataaa 60  
 acaacaatga ttataatagc aaaaataaat attatcatct ttgatagatt acttgagata 120  
 gccagcatct tgtaaaqcct ttatcggttt tttatgctct ggattaatat aatcactaca 180  
 tctatctgag caatctgttg ttgatggaca tgtcaaccca tggtcattta cagccaa 237

<210> 64  
 <211> 427  
 <212> DNA  
 <213> E. Coli

<400> 64  
 gataattaga gtttgtcgtc agaaaattga cgttacccat aacaaatgaa aggccaggta 60  
 aatcatgccca ttagtcattg ttgctatcgg tgtaatcttg ttgttgctcc tgatgatccg 120  
 cttcaaaatg aacggcttca tcgctctcgt cctcgtggcg cttgctgttg gattaatgca 180  
 aggaatgccg ctggataaag ttattggctc catcaaagcc ggtgtcggcg ggacgctcgg 240  
 tagccttgcc ctgatcatgg gttttggcgc aatgctggcg aaaatgctgg cagactgcgg 300  
 tggcgacaaa cgatcgcga ccacgctgat tgccaaattt ggtaaaaaac acatccagtg 360  
 ggcggtggta ctgacgggtt ttaccggttg ttttgccctg ttctatgaag tgggctttgt 420  
 gctgatg 427

<210> 65  
 <211> 261  
 <212> DNA  
 <213> E. Coli

<220>  
 <221> misc\_feature  
 <222> (1)...(261)  
 <223> n = A,T,C or G

<400> 65  
 caaagaacct tcaacatgaa aaatatccat ttgtttgcaa aaaaagatta ttaggaagga 60  
 aattaatgca attatcgaaa attcaaaaaa tatccaaaaa tngtatactt tattccagaa 120  
 gagttcaata taatgtttgt cttcaatttt tcttacttca gggtaataata gattgctcat 180  
 tacattgtga gcttcatctt tatttaattt tctgttgact ccagctctcc gtgataacgg 240  
 tttataatt agatgcttat c 261

<210> 66  
 <211> 98  
 <212> DNA  
 <213> E. Coli

<400> 66  
 agatgattgc cgggaacttg ttacgggcac gcaggcggcg gctcgcaccc ttaccctgct 60  
 ctttacgtac ttctgcgttg atagtaaaca tttctttc 98

<210> 67  
 <211> 260  
 <212> DNA  
 <213> E. Coli

<400> 67  
 aagcgcgaac gaagtcgatg tgctgcagct tcggtttgta cgggtgacgc tgtacgtcct 60  
 gagctttaac ttgtatttct ttaccgtcaa caacgatggt cagaacttcg ctgtagaatt 120  
 cagcttttagc ttgcatgttc atgactttgt cgtgatccag ctcgatagcc agcggcgctt 180  
 ctttgcacc gtagatgatt gccgggaact tgtagcggc acgcaggcgg cggctcgcac 240  
 cttaccctg ctctttacgt 260

<210> 68  
 <211> 95  
 <212> DNA  
 <213> E. Coli

<400> 68  
 aaaaacggcg taaagaaagg ttgcaaacat gttaataaaa actcaaattg atccccagta 60  
 tatattacgc cgcaaatcc ttacaataaa caggg 95

<210> 69  
 <211> 174  
 <212> DNA  
 <213> E. Coli

<400> 69  
 ttaattatta aaatagtgtg acgcgattat gtggttatgg gggtaaacad taaataaacc 60  
 agcggggagg ggaggtaaag tgaaaaata aaaagcggat aatcttaata agcaggccgg 120  
 acagcatcgc catccggcac tgatacaggg tttatttcag ctcatcaacc atcg 174

<210> 70  
 <211> 138  
 <212> DNA  
 <213> E. Coli

<400> 70  
 agtctgtaaa aacgtcaaaa agagtgtttt atcaacagaa gaatggaggt ctgacagata 60  
 gtatgaatgc aaaaaaatgg agacttaagt tgaatgaacg ggagttaaagc gaaaagacta 120  
 tagagtgaag gagaaatt 138

<210> 71  
 <211> 191  
 <212> DNA  
 <213> E. Coli

<400> 71  
 tttgttggtc taatattcta ttgttatctt tatttataga tgtttatatt gcatgaggtg 60  
 gtttttgagg agaagaatga ggaagatgag tcgagccaca gaaacgtag cttracatat 120  
 agcggaggtg atgtgaattt aatttacaat agaaataatt tacatatcaa acagtttagat 180  
 gctttttgtc g 191

<210> 72  
 <211> 244  
 <212> DNA  
 <213> E. Coli

<400> 72  
 ggccatttat acaggaaaag cctatgtcag aacgtaaaaa ctcaaaatca cgccgtaatt 60  
 atctcgttaa atgttcctgc ccaaaactgca cccaagagtc agaacacagt ttttcaagag 120  
 tacaataaag tgcccttttg atctgccctc attgcaacaa agtatccag acaaatctta 180  
 aagctgtagc ctgattgatt ttattagtaa caagtatttt ttatatctta ataatatatt 240  
 taaa 244

<210> 73  
 <211> 327

<212> DNA  
<213> E. Coli

<220>  
<221> misc\_feature  
<222> (1)...(327)  
<223> n = A,T,C or G

<400> 73

|   |     |
|---|-----|
| aaattttcag gtacctgtgc accatacttt tttttctgag cattaatgat attttgagct | 60  |
| tcttgaggat ctttaactcc ccacatttgg tggaaagtat tcatattaaa aggaaggntg | 120 |
| aataatttgn ctttataaat cgccagtggg gaattagtaa aacgattaaa ttctactaaa | 180 |
| tnattaaccg naaaaaaatt cccatatata tttatcattg gtatgaaaaa tatgtgcacc | 240 |
| atatttatga atntggatgc cctnacagtc ctctgtgtac gcatttccac cgatatgatt | 300 |
| tcttttctna atcactaaaa cttttttt                                    | 327 |

<210> 74  
<211> 150  
<212> DNA  
<213> E. Coli

<400> 74

|  |     |
|--|-----|
| gcagtgatcg aagcgatgac gaagtgtatg gaaaaatcag aaaaactcag caaatcctga  | 60  |
| tgactttcgc cggacgtcag gccgccactt cgggtgcggtt acgtccggct ttctttgctt | 120 |
| tgtaaacgac caaatctgcc gatttcaacc                                   | 150 |

<210> 75  
<211> 330  
<212> DNA  
<213> E. Coli

<400> 75

|   |     |
|---|-----|
| gaaagtatct tcgttattga catcactgga aaatataact tgcttttcat tattaaactc | 60  |
| gaagcgcgta cgtatctgg acaaacattt atcgagctta ccaaattcct gaagagggtt  | 120 |
| aactacagat aacatttgcg cgtcctttgc agtaatgccc gtcaaatcct tgacgggcat | 180 |
| tatttagatt aaattaccag tttttcttcg gagtgaagaa tattaccagg tatatttaac | 240 |
| acccacgttc gcggaccagt cttgatctac gtcaccacca ccgaggtagt tagcatcggt | 300 |
| ataggcgctg aagttcctgg tgaagctaaa                                  | 330 |

<210> 76  
<211> 194  
<212> DNA  
<213> E. Coli

<400> 76

|   |     |
|---|-----|
| tgtttttttc cagcaacgga gcaaaagggt tgcccttggt cagctcaggg ttaaccactt | 60  |
| taactacgtg gcgacgaccc ggagatgtcg gtttacattt aacaactgcc attgtattac | 120 |
| tcctccgact tactcagcgc cgccaacgaa gtccagattc tggccttctt tcagggtgac | 180 |
| gtaagctttt ttcc   | 194 |

<210> 77  
<211> 188  
<212> DNA  
<213> E. Coli

<400> 77

|  |     |
|--|-----|
| tcccttttaac taccagggtg ttaacgactt cgacttcgac ttcaaacagt ttctgcacag | 60  |
| cagctttgat ttctgctttg gtcgcgtctt tagcaacttt gagtactatg gtgttggtt   | 120 |
| tttccatcgc agtagacgct ttttcagaaa cgtgcggtgc acgcagcacc ttcagcagac  | 180 |
| gtttcttca  | 188 |

<210> 78  
 <211> 173  
 <212> DNA  
 <213> E. Coli

<400> 78  
 acaaaggcga acaaagcctg tgaagcccga aggcctccaca gacagtgccta cttgaaggcc 60  
 ttactgtttc ttcttaggag cgagcaccat gatcatctgg cggccttcga tcttggttg 120  
 gaaggattcg accactgccca gttcttgcaa atcgtctttc acgcgattaa gca 173

<210> 79  
 <211> 272  
 <212> DNA  
 <213> E. Coli

<220>  
 <221> misc\_feature  
 <222> (1)...(272)  
 <223> n = A,T,C or G

<400> 79  
 tggagaaaac ggggtgattga taaagcaatc atcgttctag gggcgtaaat tgcgctgctg 60  
 gaactgatcc cgctttctgc ttcaagcttc tgaactggat acggaacgt aatnagggtc 120  
 aaagaagaca ctactcttag ccctttaaca tttaacgcat tgtcacgaac tcttctgccg 180  
 ccgttggtg aatggcgacg ggtattggtc gaaatctttt ttgggtggcc ccatctttaa 240  
 cgcccaccgc cgaaacctcg caacatttcg tc 272

<210> 80  
 <211> 259  
 <212> DNA  
 <213> E. Coli

<400> 80  
 cgcaggcagc tgatggtcaa caggatgaga gaaaccaga gacaggttaa tcacattgcc 60  
 ttttaaccgt gcacggtaac ctacaccaac cagctgcagc ttcttagtga agccttcggt 120  
 aacaccgata accattgagt tcagcagggc acgcgcggtg ccagcctgtg cccaaccgtc 180  
 tgcgtaacca tcacgcggac cgaaggctcag ggtattatct gcatgtttta cttcaacagc 240  
 atcgttgaga gtacgagtc 259

<210> 81  
 <211> 73  
 <212> DNA  
 <213> E. Coli

<400> 81  
 caggtcggaa cttacccgac aaggaatttc gctaccttag gaccgttata gttacggccg 60  
 ccgtttaccg ggg 73

<210> 82  
 <211> 666  
 <212> DNA  
 <213> E. Coli

<400> 82  
 atgaacgttt tctcgcaaac tcaacgctat aaggcgttgt tctggttatc gttatttcac 60  
 ctgctggtga tcacctccag taactatctg gttcagcttc ccgtctccat tttgggttc 120  
 cataccacct ggggcgcgtt tagctttccg tttatttttc ttgctaccga cctgaccgtg 180  
 cgtatttttg gcgcaccgtt ggcccgcgc attatcttcg cggtaatgat ccctgcgtta 240  
 ttaatctcct acgtcatctc gtcgctattc tatatgggtt cctggcaggg attcggcgca 300  
 ttcgccaact tcaacctgtt tgcgcgccgt atcgccaccg ccagtttcat ggcctacgcg 360  
 ctggggcaaa tctcgcagct gcacgttttt aaccgcctgc gtcagagtcg ccgctggtgg 420

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| ctggcaccga | cagcgteccac | actgttcggt | aacgtcagcg | acacgctggc | ctttttcttc | 480 |
| attgccttct | ggcgtagccc  | ggatgccttt | atggctgaac | actggatgga | aatcgcgctg | 540 |
| gtcgattact | gtttcaaat   | gttaatcagt | atcgtttct  | tccctgcaat | gtatggcgta | 600 |
| ttactcaata | tgctgttgaa  | aagactggca | gataaatccg | aaatcaacgc | tttgacggcg | 660 |
| agtttaa    |             |            |            |            |            | 666 |

<210> 83  
 <211> 612  
 <212> DNA  
 <213> E. Coli

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| <400> 83   |            |            |            |            |             |     |
| gtgataagat | ggatgaatga | gccgttatgg | ccgtttatcg | aaaggaagaa | gtcaatgctc  | 60  |
| aatctggtta | aatatgtcgg | aattggcctg | ctggttatgg | ggcttgccgc | ctgtgatgat  | 120 |
| aaagacacta | acgctacggc | gcagggttcg | gtcgcggaaa | gtaacgctac | cgggaatccc  | 180 |
| gtcaacctgc | ttgatggcaa | gttaagtctc | tcgctgccag | cggatatgac | cgaccagagc  | 240 |
| ggtaagctgg | gaacgcaggc | caataacatg | catgtctggt | ccgacgccac | cgggcagaaa  | 300 |
| gcagtcacgc | tcatcatggg | cgatgatccg | aaagaagatc | tgccggtgct | ggcgaagcgt  | 360 |
| ctggaagatc | agcaacgtag | ccgcgatccg | cagctgcaag | tggttaacaa | ttaaagccatt | 420 |
| gagctgaaag | gtcacaaaat | gcagcagtta | gacagtatta | tctccgcgaa | agccagacag  | 480 |
| gcgtactctt | ccgttattct | gggtaacgtg | ggtaatcaac | tgctgaccat | gcaaattacg  | 540 |
| ctgcccgctg | acgatcagca | aaaagcgccg | accaccgcag | aaaacatcat | taatacgcgtg | 600 |
| gttattcagt | aa         |            |            |            |             | 612 |

<210> 84  
 <211> 975  
 <212> DNA  
 <213> E. Coli

|             |            |             |            |             |             |     |
|-------------|------------|-------------|------------|-------------|-------------|-----|
| <400> 84    |            |             |            |             |             |     |
| atggcggaata | tggttgccct | gattctgggt  | attgccacac | tggtgacggg  | cattttatgg  | 60  |
| tgctgagata  | aattcttttt | cgcacctaaa  | cggcggaac  | gtcaggcagc  | ggcgaggcg   | 120 |
| gctgcggggg  | actcactgga | ttaaagcaacg | ttgaaaaag  | ttgcgccgaa  | gcctggctgg  | 180 |
| ctggaaacgc  | gtgcttctgt | ttttccggta  | ctggctatcg | tattgattgt  | gcgttcgttt  | 240 |
| atttatgaac  | cggtccagat | cccgtcaggt  | tcgatgatgc | cgactctgtt  | aattgggtgat | 300 |
| tttattctcg  | tagagaagt  | tgcttatggc  | attaaagatc | ctatctacca  | gaaaacgcgtg | 360 |
| atcgaaacgc  | gtcatccgaa | acgcggcgat  | atcggtggtc | ttaaatatcc  | ggaagatcca  | 420 |
| aagcttgatt  | acatcaagcg | cgcgggtggg  | ttaccggggc | ataaagtcac  | ttacgatccg  | 480 |
| gtctcaaaag  | agctgacgat | tcaaccggga  | tgcaattccg | gccaggcggtg | tgaaaacgcg  | 540 |
| ctgccgggtc  | cctactcaaa | cgtggaacgc  | agcgatttcg | ttcagacctt  | ctcacgcggt  | 600 |
| aatggtgggg  | aagcgaccag | cggattcttt  | gaagtgcgga | aaaacgaaac  | caaagaaaat  | 660 |
| ggaattcgtc  | tttccgagcg | taaagagaca  | ctgggtgatg | tgacgcaccg  | cattctgaca  | 720 |
| gtgcggattg  | cgcaggatca | ggtgggggatg | tattaccagc | agccagggca  | acaactggca  | 780 |
| acctggattg  | ttcctccggg | acaatacttc  | atgatggggc | acaaccgcga  | caacagcgcg  | 840 |
| gacagccgtt  | actggggctt | tggtccggaa  | gcgaatctgg | tcgggtcgggc | aacggctatc  | 900 |
| tggtatgagct | tcgataagca | agaaggcgaa  | tgcccgactg | gtctgcgctt  | aagtcgcatt  | 960 |
| ggcgcatcc   | attaa      |             |            |             |             | 975 |

<210> 85  
 <211> 1761  
 <212> DNA  
 <213> E. Coli

|            |             |             |             |            |             |     |
|------------|-------------|-------------|-------------|------------|-------------|-----|
| <400> 85   |             |             |             |            |             |     |
| ttgaccatta | cgaaacttgc  | atggcgtgac  | ctggttcctg  | ataccgatag | ctatcaggaa  | 60  |
| atatttgctc | agccacattt  | gattgacgaa  | aacgatccct  | tattcagtga | tactcaaccg  | 120 |
| cggtgcaat  | ttgcgctgga  | gcagtgtgctg | catacgcgag  | catactctct | ttttatgctg  | 180 |
| gcgaaggccc | cggaagagtc  | tgagtatctg  | aattcttattg | ccaatgccgc | gcgtacgcta  | 240 |
| caaagcgatg | caggccaact  | ggtggggcgt  | cactatgagg  | tttccggcca | ctccatccgc  | 300 |
| ttacgtcacg | cagtgaagtgc | agatgataat  | tttgcgactt  | taacgcaagt | tgctcgctgcc | 360 |
| gactgggtag | aagcgagca   | actcctttgc  | tgccctgcgc  | agtttaattg | cgacattacc  | 420 |

|            |             |             |             |            |            |      |
|------------|-------------|-------------|-------------|------------|------------|------|
| ctgcagcctg | gtctggtgca  | tcaggcaaat  | ggcgggtattc | tcattatctc | tttgcgtaca | 480  |
| ctgctggcgc | aacctctgct  | gtggatgcgg  | ctgaaaaata  | tcgttaaccg | cgagcgtttt | 540  |
| gactgggttg | cgtttgatga  | gtcgcgccct  | ctccccgtct  | ctgtgccttc | gatgccattg | 600  |
| aagctgaaag | tcattctggt  | aggcgaacgc  | gaatcattgg  | ctgatttcca | ggagatggag | 660  |
| ccagagcttt | cagagcaggc  | tatttatagc  | gaatttgaag  | atactctgca | gattgtcgat | 720  |
| gcggagtcag | taaccacgtg  | gtgtcgtctg  | gtgacattta  | ccgccagaca | taatcactta | 780  |
| cctgcaccgg | gagcggatgc  | ctggccgata  | cttatccgcg  | aagcagcacg | ctacaccggt | 840  |
| gaacaagaaa | cacttccgct  | tagcccgca   | tggatccctc  | gccagtgtaa | agaggtcgcc | 900  |
| tccctgtgtg | atggcgacac  | cttctccggc  | gagcagctaa  | acttaatgct | gcagcagcgt | 960  |
| gaatggcgcg | aaggtttcc   | cgctgaacgt  | atgcaggatg  | agatccttca | ggagcaaatc | 1020 |
| ctgattgaaa | ccgaaggcga  | acgcacgtgg  | caaattaacg  | ccctttcggg | cattgaattt | 1080 |
| ccgggtcctc | cacgcgcttt  | tggcgaacct  | tctcgatta   | gctgcgttgt | gcatattggc | 1140 |
| gatggtgaat | tcaccgacat  | cgaacgcaaa  | gcggagcttg  | gcggcaatat | ccatgcgaaa | 1200 |
| gggatgatga | tcattcgaagc | gttccctgatg | tcggaactac  | agcttgagca | acagatcccc | 1260 |
| ttctcagcat | cgctgacatt  | tgagcagtca  | tacagtgaag  | ttgatggaga | tagtgcctcg | 1320 |
| atggctgaac | tctgcgctct  | gataacgcgc  | ctcgccgatg  | tgccggtgaa | tcagagtatc | 1380 |
| gctatcacag | gttcagtcga  | tcagttcggg  | cgccgccagc  | cggtcgggtg | tttaaatgag | 1440 |
| aaaatcgaag | gcttctttgc  | tatttgccag  | caacgtgagt  | taaccgggaa | acaaggtgtc | 1500 |
| attatcccca | cagctaacgt  | tcgccattta  | agtcttcaca  | gtgaactggt | gaaagcggtc | 1560 |
| gaagaaggca | aattcaccat  | ctgggcagta  | gacgatgtga  | ctgacgcact | gccgttatta | 1620 |
| ttaaatctgg | tgtgggatgg  | cgaaggccaa  | acgacgtctg  | tgcaaaccat | ccaggaacgt | 1680 |
| atcgcgcaag | catcgcaaca  | ggaaggacgt  | caccgttttc  | catggccatt | acgttggtcg | 1740 |
| aactggttta | ttccgaactg  | a           |             |            |            | 1761 |

&lt;210&gt; 86

&lt;211&gt; 1185

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 86

|            |            |            |            |             |             |      |
|------------|------------|------------|------------|-------------|-------------|------|
| gtgtctaaag | aaaaatttga | acgtacaaaa | ccgcacgtta | acgttggtac  | tatcggccac  | 60   |
| gttgaccacg | gtaaaactac | tctgaccgct | gcaatcacca | ccgtactggc  | taaaacctac  | 120  |
| ggcgggtgtg | ctcgtgcatt | cgaccagatc | gataacgcgc | cggaagaaaa  | agctcgtggt  | 180  |
| atcaccatca | acacttctca | cgttgaatac | gacaccccca | cccgctacta  | cgcacacgta  | 240  |
| gactgcccg  | ggcacgccga | ctatgttaaa | aacatgatca | ccggtgctgc  | tcagatggac  | 300  |
| ggcgcgatcc | tggtagtgtc | tgcgactgac | ggcccgatgc | cgcgactcgc  | tgagcacatc  | 360  |
| ctgctgggtc | gtcaggtagg | cgttccgtac | atcatcgtgt | tcctgaacaa  | atgcgacatg  | 420  |
| gttgatgacg | aagagctgct | ggaactgggt | gaaatggaag | ttcgtgaact  | tctgtctcag  | 480  |
| tacgacttcc | cgggcgacga | cactccgac  | gttcgtgggt | ctgctctgaa  | agcgctggaa  | 540  |
| ggcgacgcag | agtgggaagc | gaaaaatcct | gaactggctg | gcttccctgga | ttcttatatt  | 600  |
| ccggaaccag | agcgtgcgat | tgacaagccg | ttcctgctgc | cgatcgaaga  | cgtattctcc  | 660  |
| atctccggtc | gtggtaccgt | tgttaccggt | cgtgtagaac | gcggatcat   | caaagtgggt  | 720  |
| gaagaagtgt | aaatcgttgg | tatcaaaag  | actcagaagt | ctacctgtac  | tggcgtgaa   | 780  |
| atgttccgca | aactgctgga | cgaaggccgt | gctggtgaga | acgtaggtgt  | tctgctgcgt  | 840  |
| ggatcaaac  | gtgaagaaat | cgaacgtggt | caggtagctg | ctaagccggg  | caccatcaag  | 900  |
| ccgcacacca | agttcgaatc | tgaagtgtac | attctgtcca | aagatgaagg  | cgcccgctcat | 960  |
| actccgttct | tcaaaggcta | ccgtccgcag | ttctacttcc | gtactactga  | cgtgactggt  | 1020 |
| accatcgaac | tgcgggaagg | cgtagagatg | gtaatgccgg | gcgacaacat  | caaaatgggt  | 1080 |
| gttaccctga | tccacccgat | cgcgatggac | gacggtctgc | gtttcgcaat  | ccgtgaaggc  | 1140 |
| ggccgtaccg | ttggcgcggg | cggtgtgtgt | aaagtctctg | gctaa       |             | 1185 |

&lt;210&gt; 87 ~

&lt;211&gt; 2115

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 87

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atggctcgta | caacacccat | cgcacgctac | cgtaacatcg | gtatcagtgc | gcacatcgac | 60  |
| gccggtaaaa | ccactactac | cgaacgtatt | ctgttctaca | ccggtgtaaa | ccataaaatc | 120 |
| ggtgaagtgc | atgacggcgc | tgcaaacatg | gactggatgg | agcaggagca | ggaacgtggt | 180 |
| attaccatca | cttcgcgtgc | gactactgca | ttctggtctg | gtatggctaa | gcagtatgag | 240 |



|              |             |            |             |             |             |      |
|--------------|-------------|------------|-------------|-------------|-------------|------|
| ccgcacatcgca | tcaacatcat  | cgacaccccg | gggcacggtg  | acttcacaaat | cgaagtagaa  | 300  |
| cgttccatgc   | gtgttctcga  | tgggtcggta | atgggtttact | gcgcaggttg  | tgggtgttcag | 360  |
| ccgcagctcg   | aaaccgtatg  | gcgtcaggca | aacaaatata  | aagttccgcg  | cattgctgttc | 420  |
| gttaacaaaa   | tggaccgcat  | gggtgcgaac | ttcctgaaag  | ttgttaacca  | gatcaaaacc  | 480  |
| cgctcggcg    | cgaacccggt  | tccgctgcag | ctggcgattg  | gtgctgaaga  | acatttcacc  | 540  |
| gggtgtgttg   | acctggtgaa  | aatgaaagct | atcaactgga  | acgacgctga  | ccagggcgta  | 600  |
| accttcgaat   | acgaagatat  | cccggcagac | atggttgaa   | tggctaaccga | atggcaccag  | 660  |
| aaactgatcg   | aatccgcagc  | tgaagcttct | gaagagctga  | tggaaaaata  | cctgggtggt  | 720  |
| gaagaactga   | ctgaagcaga  | aatcaaaagt | gctctgcgtc  | agcgcgttct  | gaacaacgaa  | 780  |
| atcatcctgg   | taacctgtgg  | ttctgcgttc | aagaacaaag  | gtgttcaggc  | gatgctggat  | 840  |
| gcggtaattg   | attacctgcc  | atccccggtt | gacgtacctg  | cgatcaacgg  | tatcctggac  | 900  |
| gacggtaaa    | acactccggc  | tgaacgtcac | gcaagtgatg  | acgagccgtt  | ctctgcactg  | 960  |
| gcgttcaaaa   | tcgtaccga   | cccgtttggt | ggtaacctga  | ccttcttccg  | tgtttactcc  | 1020 |
| gggtgtgtta   | actctggtga  | taccgtactg | aactccgtga  | aagctgcacg  | tgagcgtttc  | 1080 |
| ggtcgtatcg   | ttcagatgca  | cgctaacaaa | cgtgaagaga  | tcaaagaagt  | tcgcgcgggc  | 1140 |
| gacatcgtcg   | ctgctatcgg  | tctgaaagac | gtaaccactg  | gtgacaccct  | gtgtgacccg  | 1200 |
| gatgcgcgca   | tcattctgga  | acgtatggaa | ttccctgagc  | cggtaatctc  | catcgcagtt  | 1260 |
| gaaccgaaaa   | ccaaagctga  | ccaggaaaaa | atgggtctgg  | ctctggggccg | tctggctaaa  | 1320 |
| gaagaccctg   | ctttccgtgt  | atggactgac | gaagaatcta  | accagaccat  | catcgcgggt  | 1380 |
| atgggcgaac   | tgacactcga  | catcatcggt | gaccgtatga  | agcgtgaatt  | caacgttgaa  | 1440 |
| gcgaacgtag   | gtaaacgcga  | ggttgcttac | cgtgaaacta  | tccgccagaa  | agttaccgat  | 1500 |
| gttgaaagga   | aacacgcgaa  | acagtctggt | ggtcgtggtc  | agtatggtca  | tggtgttatc  | 1560 |
| gacatgtacc   | cgctggagcc  | gggttcaaac | ccgaaaggtc  | acgagttcat  | caacgacatt  | 1620 |
| aaaggtgggt   | taatccctgg  | cgaatacatc | ccggccggtg  | ataaaggtat  | ccaggaaacag | 1680 |
| ctgaaaagcag  | gtccgctggc  | aggctaccgg | gtagtagaca  | tgggtattcg  | tctgcacttc  | 1740 |
| ggttcttacc   | atgacgttga  | ctcctctgaa | ctggcgttta  | aactggctgc  | ttctatcgcc  | 1800 |
| tttaaaagag   | gctttaagaa  | agcgaaacca | gttctgcttg  | agccgatcat  | gaaggttgaa  | 1860 |
| gtagaaaactc  | cggaagagaa  | caccggtgac | gttatcgggtg | acttgagccg  | tcgtcgtggt  | 1920 |
| atgctcaaa    | gtcaggaaac  | tgaagttact | ggcgttaaga  | tccacgctga  | agtaccgctg  | 1980 |
| tctgaaatgt   | tcggatacgc  | aactcagctg | cggttctctga | ccaaaggtcg  | tgcatcatac  | 2040 |
| actatgggaat  | tcctgaaagta | tgatgaaagc | ccgagtaacg  | ttgctcaggc  | cgtaattgaa  | 2100 |
| gccccgtgga   | ataaa       |            |             |             |             | 2115 |

<210> 88  
 <211> 540  
 <212> DNA  
 <213> E. Coli

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| atgccacgtc  | gtcgcgtcat | tggtcagcgt | aaaattctgc | cggatccgaa  | gttcggatca | 60  |
| gaactgctgg  | ctaaatttgt | aaatatcctg | atggtagatg | gtaaaaaatc  | tactgctgaa | 120 |
| tctatcgtat  | acagcgcgct | ggagaccctg | gctcagcgtc | ctggtaaatac | tgaactggaa | 180 |
| gcattcgaag  | tagctctcga | aaacgtgcgc | ccgactgtag | aagttaagtc  | tcgccgcgtt | 240 |
| gggtggttcta | cttatcaggt | accagttgaa | gtccgtccgg | ttcgtcgtaa  | tgctctggca | 300 |
| atgctgttga  | tcgttgaagc | tgctcgtaaa | cgcggtgata | aatccatggc  | tctgcgcctg | 360 |
| gcgaacgaac  | tttctgatgc | tgcaaaaaac | aaaggtactg | cagttaagaa  | acgtgaagac | 420 |
| gttcaccgta  | tggccgaagc | caacaaggcg | ttcgcacact | accgttggtt  | atcccttcgg | 480 |
| agttttatgc  | accaggcggt | cgcttccagt | aagcagcccg | ctttgggcta  | cttaaatgaa | 540 |

<210> 89  
 <211> 1549  
 <212> DNA  
 <213> E. Coli

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| aaattgaaga | gtttgatcat | ggctcagatt | gaacgctggc  | ggcaggccta  | acacatgcaa | 60  |
| gtcgaacggt | aacaggaagc | agcttgctgc | ttcgtctgacg | agtggcggac  | gggtgagtaa | 120 |
| tgtctgggaa | gctgcctgat | ggagggggat | aactactgga  | aacggtagct  | aataccgcat | 180 |
| aatgtcgcaa | gaccaaagag | ggggaccttc | gggcctcttg  | ccatcggtatg | tgcccatagc | 240 |
| ggattagctt | gttgggtggg | taacggctca | ccaaggcgac  | gatccctagc  | tggtctgaga | 300 |
| ggatgaccag | ccacactgga | actgagacac | gggccagact  | cctacgggag  | gcagcagtgg | 360 |

|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| ggaatattgc  | acaatgggag | caagcctgat  | gcagccatgc  | cgcgtgtatg  | aagaaggcct  | 420  |
| tcgggttgta  | aagtactttc | agcggggagg  | aagggagtaa  | agttaatacc  | tttgctcatt  | 480  |
| gacgttacc   | gcagaagaag | caccggctaa  | ctcgtgcca   | gcagccgag   | taatacggag  | 540  |
| ggtgcaagcg  | ttaatcgga  | ttactgggag  | ttaagcgac   | gcagggggt   | tggttaagtc  | 600  |
| agatgtgaaa  | tccccgggt  | caacctggga  | actgcacatg  | atactggcaa  | gcttgagtct  | 660  |
| cgtagagggg  | ggtagaattc | cagggtgtagc | ggtgaaatgc  | gtagagatct  | ggaggaatac  | 720  |
| cgggtggcga  | ggcggcccc  | tgagcgaaga  | ctgacgctca  | ggtgcgaaag  | cgtggggagc  | 780  |
| aaacaggatt  | agataccctg | gtagtccacg  | ccgtaaaacga | tgtcgacttg  | gaggttgtgc  | 840  |
| ccttgaggcg  | tggettcccg | agctaaccgc  | ttaagtcgac  | cgcctgggga  | gtacggccgc  | 900  |
| aagggttaaaa | ctcaaatgaa | ttgacggggg  | cccgacacaag | cgggtggagca | tgtggtttaa  | 960  |
| ttcgtatgcaa | cgcgaagaac | cttacctggt  | cttgacatcc  | acggaagttt  | tcagagatga  | 1020 |
| gaatgtgcct  | tcgggaaccg | tgagacaggt  | gctgcacggc  | tgtcgctcagc | tcgtgttgtg  | 1080 |
| aaatgttggg  | ttaatcccc  | caacgagcgc  | aacctttatc  | ctttgttgcc  | agcgggtccgg | 1140 |
| cgggaactc   | aaaggagact | gccagtata   | aactggagga  | aggtggggat  | gacgtcaagt  | 1200 |
| catcatggcc  | cttacgacca | gggctacaca  | cgtgctacaa  | tgccgcatac  | aaagagaagc  | 1260 |
| gacctcgca   | gagcaagcgg | acctcataaa  | gtgcgtcgta  | gtcgggattg  | gagtcgtcaa  | 1320 |
| ctcgactcca  | tgaagtcgga | atcgctagta  | atcggtgac   | agaatgccac  | ggtgaatacg  | 1380 |
| ttcccgggcc  | ttgtacacac | cgcccgtcac  | accatgggag  | tggtgttgcaa | aagaagtagg  | 1440 |
| tagcttaacc  | ttcgggaggg | cgttaccac   | tttgtgatc   | atgactgggg  | tgaagtcgta  | 1500 |
| acaaggtaac  | cgtaggggaa | cctgcggtt   | gatcacctcc  | ttaccttaa   |             | 1549 |

&lt;210&gt; 90

&lt;211&gt; 375

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 90

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| atggcaacag | ttaaccagct  | ggtacgcaaa  | ccacgtgctc | gcaaagtgc  | gaaaagcaac | 60  |
| gtgcctgcgc | tggaagcatg  | cccgcaaaaa  | cgtggcgat  | gtactcgtgt | ataactacc  | 120 |
| actcctaaaa | aaaccgaactc | cgcgtgctg   | aaagtatgcc | gtgttcgtct | gactaacggt | 180 |
| ttcgaagtga | cttccctacat | cgggtgtgaa  | ggtcacaacc | tgccagagca | ctccgtgac  | 240 |
| ctgatccgtg | gcggtcgtgt  | ttaaagacctc | ccgggtgttc | gttaccacac | cgtacgtggt | 300 |
| gcgcttgact | gctccggcgt  | ttaaagacctg | aagcaggctc | gttccaagta | tgccgtgaa  | 360 |
| cgtcctaagg | cttaa       |             |            |            |            | 375 |

&lt;210&gt; 91

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 91

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| atgtctatca | ctaaagatca  | aatcattgaa | gcagttgcag  | ctatgtctgt | aatggacgtt | 60  |
| gtagaactga | tctctgcaat  | ggaagaaaaa | ttcgggtgtt  | ccgctgctgc | tgctgtagct | 120 |
| gtagctgctg | gcccgggtga  | agctgctgaa | gaaaaaaactg | aattcgacgt | aattctgaaa | 180 |
| gctgctggcg | ctaacaaggt  | tgctgttata | aaagcagtag  | gtggcgcaac | tgccctgggt | 240 |
| ctgaaagaag | ctaagagacct | ggtagaatct | gcaccggctg  | ctctgaaaga | aggcgtgagc | 300 |
| aaagacgacg | cagaagcact  | gaaaaaagct | ctggaagaag  | ctggcgctga | agttgaagtt | 360 |
| aaataa     |             |            |             |            |            | 366 |

&lt;210&gt; 92

&lt;211&gt; 498

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 92

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| atggctttta | atcttcaaga | caaacagcgc | attgttgctg  | aagtcagcga | agtagccaaa | 60  |
| ggcgcgctgt | ctgcagtagt | tgccgattcc | cgtggcgtaa  | ctgtagataa | aatgactgaa | 120 |
| ctgcgtaaa  | caggtcgca  | agctggcgta | tacatgcgtg  | ttgttcgtaa | caccctgctg | 180 |
| cgcgctgctg | ttgaaggtac | tccgttcgag | tgccgtgaaag | acgcgtttgt | tggtccgacc | 240 |
| ctgattgcat | actctatgga | acaccgggc  | gctgctgctc  | gtctgttcaa | agagttcgcg | 300 |
| aaagcgaatg | caaaatttga | ggtcaaagcc | gctgcctttg  | aaggtgagct | gatcccgccg | 360 |

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| tctcagatcg  | accgcctggc | aactctgccg | acctacgaag  | aagcaattgc | acgcctgatg | 420 |
| gcaacctatga | aagaagcttc | ggctggcaaa | ctgggttcgta | ctctggctgc | tgtacgcgat | 480 |
| gcgaaagaag  | ctgcttaa   |            |             |            |            | 498 |

<210> 93  
 <211> 2145  
 <212> DNA  
 <213> E. Coli

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| <400> 93    |             |             |             |             |             |      |
| gtgtcccgtga | ttattatgct  | gatccctacc  | ggaaccagcg  | tcgggtctgac | cagcgtcagc  | 60   |
| cttggcgtga  | tccgtgcaat  | ggaacgcaaa  | ggcgttcgtc  | tgagcgtttt  | caaacctatc  | 120  |
| gctcagccgc  | gtaccggtgg  | cgatgcgccc  | gatcagacta  | cgactatcgt  | gcgtgcgaac  | 180  |
| tcttccacca  | cgacggccgc  | tgaaccgctg  | aaaatgagct  | acgttgaagg  | tctgctttcc  | 240  |
| agcaatcaga  | aagatgtgct  | gatggaagag  | atcgtcgcga  | actaccacgc  | taacaccaaa  | 300  |
| gacgctgaag  | tcgttctggt  | tgaagggtctg | gtcccgcacac | gtaagcacca  | gtttgccag   | 360  |
| tctctgaact  | acgaaatcgc  | taaaacgctg  | aatgcggaaa  | tcgtcttcgt  | tatgtctcag  | 420  |
| ggcactgaca  | ccccggaaca  | gctgaaagag  | cgatcgaac   | tgacccgcaa  | cagcttcggc  | 480  |
| ggtgccaaaa  | acaccaacat  | caccggcgctt | atcgtaaaca  | aactgaacgc  | accggttgat  | 540  |
| gaacagggtc  | gtactcgccc  | ggatctgtcc  | gagattttcg  | acgactcttc  | caaagctaaa  | 600  |
| gtaaacaatg  | ttgatccggc  | gaagctgcaa  | gaatccagcc  | cgctgcgggt  | tctcggcgct  | 660  |
| gtgccgtgga  | gctttgacct  | gatcgcgact  | cggtcgatcg  | atatggctcg  | ccacctgaat  | 720  |
| gcgacctca   | tcaacgaagg  | cgacatcaat  | actcgcgcgc  | ttaaatccgt  | cactttctgc  | 780  |
| gcacgcagca  | ttccgcacat  | gctggagcac  | ttccgtgccg  | gttctctgct  | ggtgacttcc  | 840  |
| gcagaccgtc  | ctgacgtgct  | gggtggccgct | tgcttggcag  | ccatgaacgg  | cgtagaaatc  | 900  |
| gggtgccctgc | tgctgactgg  | cggttacgaa  | atggacgcgc  | gcattttctaa | actgtgcgaa  | 960  |
| cggtgctttgc | ctaccggcct  | gccgggtattt | atggtgaaca  | ccaacacctg  | gcagacctct  | 1020 |
| ctgagcctgc  | agagcttcaa  | cctggaagtt  | ccggttgacg  | atcacgaacg  | tatcgagaaa  | 1080 |
| gttcaggaat  | acgttgctaa  | ctacatcaac  | gctgactgga  | tcgaatctct  | gaactgccact | 1140 |
| tctgagcgca  | gccgtcgtct  | gtctccgcct  | gcgttccggt  | atcagctgac  | tgaacttgccg | 1200 |
| ccagaagctg  | ttcgcgaaag  | ctatgttgggt | cgctctggctg | aactgcgtaa  | gaacaaaggc  | 1260 |
| gccgctatct  | gtgctgaacg  | tggatcgcga  | acttgcgtac  | tgctgggtaa  | tccggcagag  | 1320 |
| atcaaccgtg  | ttgcagcgct  | tcaggggtga  | gaactgggtg  | cagggattga  | aatcgttgat  | 1380 |
| ccagaagtgg  | ttcgcgaaag  | ctatgttgggt | cgctctggctg | aactgcgtaa  | gaacaaaggc  | 1440 |
| atgaccgaaa  | ccgttgcccgc | cgaacagctg  | gaagacaacg  | tgggtgctcg  | tacgctgatg  | 1500 |
| ctggaacag   | atgaagttga  | tgggtctggtt | tcgggtgctg  | ttcacactac  | cgcaaacacc  | 1560 |
| atccgtccgc  | cgctgcagct  | gatcaaaact  | gcacccggca  | gctccctggt  | atcttccgtg  | 1620 |
| ttcttcatgc  | tgctgcccga  | acaggtttac  | gtttacggtg  | actgtgcgat  | caaccggat   | 1680 |
| ccgacgcgtg  | aacagctggc  | agaaatcgcg  | attcagtcgc  | ctgattccgc  | tgccgccttc  | 1740 |
| ggtatcgaa   | cgcgcgttgc  | tatgctctcc  | tactccaccg  | gtacttctg   | tgcaggtagc  | 1800 |
| gacgtagaaa  | aagttcgcga  | agcaactcgt  | ctggcgcagg  | aaaaacgtcc  | tgacctgatg  | 1860 |
| atcgacggtc  | cgctgcagta  | cgacgctg    | gtaatggctg  | acgttgcgaa  | atccaaagcg  | 1920 |
| ccgaactctc  | cggttgccag  | tcgcgctacc  | gtgttcactc  | tcccggatct  | gaacaccggt  | 1980 |
| aaacaccact  | acaaagcggg  | acagcgttct  | gccgacctga  | tctccatcgg  | gccgatgctg  | 2040 |
| caggggtatgc | gcaagccggg  | taacgacctg  | tcccgtggcg  | cactgggtga  | cgatatcgctc | 2100 |
| tacaccatcg  | cgctgactgc  | gattcagctc  | gcacagcagc  | agtaa       |             | 2145 |

<210> 94  
 <211> 1767  
 <212> DNA  
 <213> E. Coli

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| <400> 94    |             |            |            |             |            |     |
| atgaataatt  | ctattaacca  | taaatttcat | cacattagcc | gggctgaata  | ccaggaattg | 60  |
| ttagccgttt  | cccgtggcga  | cgctggtgcc | gattatatta | ttgataatgt  | ctctattctc | 120 |
| gacctgatca  | atggcggaga  | aatttccggc | ccaattgtga | ttaaaggacg  | ttacattgcc | 180 |
| gggtgttgccg | cagaatacac  | tgatgctccg | gctttgcagc | ggattgatgc  | tcgcggcgca | 240 |
| acggcgggtgc | caggggtttat | tgatgctcac | ctgcatattg | aatccagcat  | gatgacgccg | 300 |
| gtcacttttg  | aaaccgctac  | cctgcgcgcg | ggcctgacga | ccgttatttg  | cgacctcat  | 360 |
| gaaatcgta   | acgtgatggg  | cgaagccgga | ttcgcctggt | ttgcccgcgtg | tgccgaacag | 420 |
| gcaaggcaaa  | accagtactt  | acaggtcagc | tcttgctgac | ccgcctcgga  | aggctgcgat | 480 |

|             |            |             |            |            |             |      |
|-------------|------------|-------------|------------|------------|-------------|------|
| gttaacgggtg | ccagttttac | ccttgaacag  | atgctcgcct | ggcgggacca | tccgcagggt  | 540  |
| accggccttg  | cagaaatgat | ggactaccct  | ggcgtaatta | gcgggcagaa | tgcgctgctc  | 600  |
| gataaactgg  | atgcatttcg | ccacctgacg  | ctggacggtc | actgcccggg | tttgggtggg  | 660  |
| aaagaactta  | acgcctatat | tactgcgggt  | attgaaaact | gccacgaaag | ttatcagctg  | 720  |
| gaagaaggac  | gccggaaatt | acaactcggc  | atgtcggtga | tgatccgcga | aggggtccgct | 780  |
| gcccgcgaatc | tcaacgcgct | ggcaccgttg  | atcaacgaat | ttaacagccc | gcaatgcatg  | 840  |
| ctctgtaccg  | atgaccgtaa | cccgtgggag  | atcgcccatg | aaggacacat | cgatgcctta  | 900  |
| attcgccggc  | tgatcgaaac | acacaatgtg  | ccgctgcacg | tgcatatcg  | cgctgccagc  | 960  |
| tggtcgacgg  | cgcgccactt | tggtctgaat  | cacctcggtc | tactggcacc | cggaagcag   | 1020 |
| gccgatatcg  | tcctgttgag | cgatgcgcgt  | aaggtcacgg | tgacgcagg  | actggtgaaa  | 1080 |
| ggcgagccga  | ttgatgcgca | aaccttacag  | gcggaagagt | cgccgagact | ggcacaatcc  | 1140 |
| gtcccgccat  | atggcaacac | cattgcccgc  | cagccagttt | ccgccagcga | ctttgccctg  | 1200 |
| caatttacgc  | ccggaaaacg | ctatcggttc  | attgacgtca | tccataacga | attgattacg  | 1260 |
| cactcccact  | ccagcgtcta | cagcgaaaaa  | ggttttgatc | gcgatgatgt | gagctttatt  | 1320 |
| cccgtacttg  | agcgttacgg | gcaacgcgctg | gctccggctt | gtggtttgct | tgccggcctt  | 1380 |
| ggactgaatg  | aaggtgcgct | ggctgcgacg  | gtcagccatg | acagccataa | tattgtggtg  | 1440 |
| atcggtcgca  | gtgccgaaga | gatggcgctg  | gcggtcaatc | aggtgattca | ggatggcgcg  | 1500 |
| gggctgtgcg  | tggtacgtaa | cgccaggtga  | caaatgcac  | tgccgttacc | cattgccggg  | 1560 |
| ctgatgagca  | ccgacacggc | gcagtcgctg  | gcggaacaaa | ttgacgcctt | gaaagccgcc  | 1620 |
| gcccgtgaat  | gcggtccggt | acccgatgag  | ccgtttattc | agatggcggt | tctttctctg  | 1680 |
| ccagtgatcc  | ccgcgctaaa | actaaccagt  | caggggctat | ttgatggcga | gaagtttgcc  | 1740 |
| ttcactacgc  | tggaagtac  | ggaataa     |            |            |             | 1767 |

<210> 95  
 <211> 1227  
 <212> DNA  
 <213> E. Coli

<400> 95

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| atggcggtatt | gcaatccggg  | cctggaatcc  | aggccgaata  | agagaaacgc | cctccggcgt  | 60   |
| catgttgtaa  | cagggcatagg | tatgaaaatc  | gtaatcgccc  | cagactctta | taaagaaagt  | 120  |
| ttatctgccca | gcgaggttgc  | gcaggcgata  | gaaaaaggat  | ttcgggaaat | ttttcctgat  | 180  |
| gcacagtacg  | ttctgttcc   | ggttgccgac  | ggtggcgaa   | gaacgggtga | agcgatgatt  | 240  |
| gcagccaccc  | agggggctga  | acgtcacgcc  | tggtttacag  | ggccgctggg | cgagaaagt   | 300  |
| aatgccagtt  | gggggatctc  | cgccgatggc  | aaaaccgcgt  | ttattgaaat | ggcgcgcc    | 360  |
| agtgggtggtg | agctgtgtacc | tgccgaaaaa  | cgcgatccac  | tcgtgaccac | ttcacgcggc  | 420  |
| acaggcgagt  | taactctgca  | ggcgctggag  | agcggtgcga  | caaacattat | tatcggcatt  | 480  |
| ggcgccagcg  | ctacaaatga  | tgccggcgca  | ggcatggtac  | aggcgctggg | ggcgaaatta  | 540  |
| tgccagcgcca | acggcaatga  | aattgggttt  | ggcgcggtga  | gtcttaatac | tctgaatgat  | 600  |
| attgatattt  | ccggcctcga  | tccgcgctta  | aaagattgct  | tcattcgctg | cgcttgtgat  | 660  |
| gtcaccaatc  | cgctgggtgg  | cgataacggc  | gcacgcgcga  | tccttgcccc | acaaaaggga  | 720  |
| gccagtgaa   | cgatgattgt  | tgagctggac  | aataacctct  | ctcactatgc | cgaggtcatt  | 780  |
| aaaaaagcgc  | tgcatgttga  | tgtgaaagat  | gtccccgggtg | caggagctgc | gggtggtatg  | 840  |
| ggcgcgggcg  | taatggcggt  | tcttggtgctg | gaactgaaaa  | gtggtattga | aatcgctcact | 900  |
| acggcgctga  | atctggagga  | acatattcac  | gattgtacgc  | tggtgatcac | cggtgaagg   | 960  |
| cgtattgaca  | gccagagtat  | tcacgggaag  | gtaccgattg  | gtgctgcaaa | cgtggcgaa   | 1020 |
| aagtaccata  | aaccgggtgat | tgccattgctg | ggtagcctga  | ccgatgatgt | tgccgttgta  | 1080 |
| catcagcatg  | gcattgatgc  | ggtcttcagc  | gtattgacca  | gcataggtag | gttgagcga   | 1140 |
| gcattccgcg  | gggtttatga  | caatatctgc  | cgtgcttcac  | gtaatatcgc | cgcgacactg  | 1200 |
| gcgattggaa  | tgccgcaacgc | gggtgtga    |             |            |             | 1227 |

<210> 96  
 <211> 900  
 <212> DNA  
 <213> E. Coli

<400> 96

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| atgattgata | tgactatgaa | agttgggttt  | attggcctgg | ggattatggg | taaaccaatg | 60  |
| agtaaaaaac | ttctgaaagc | aggttactcg  | ctggtggttg | ctgaccgtaa | cccagaagct | 120 |
| attgctgacg | tgattgctgc | aggtgcagaa  | acagcgtcta | cggtctaaag | gatcgctgaa | 180 |
| cagtgcgacg | tcatacatac | catgctgccca | aactccccct | atgtgaaaga | gggtggcgtg | 240 |

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| gggtgagaatg | gcattattga  | aggcgcggaag | ccaggtacgg | tattgatcga | tatgagttct | 300 |
| atcgccaccgc | tggcaagccg  | tgaatcagc   | gaagcgctga | aagcgaaaag | cattgatatg | 360 |
| ctggatgctc  | cggtgagcgg  | cggtgaaccg  | aaagccatcg | acggtagcgt | gtcagtgatg | 420 |
| gtgggcgggc  | acaaggctat  | tttcgacaaa  | tactatgatt | tgatgaaaag | gatggcgggt | 480 |
| tccgtgggtgc | ataccgggga  | aatcggtgca  | ggtaacgtca | ccaaactggc | aaatcaggtc | 540 |
| attgtggcgc  | tgaatattgc  | cgcgatgtca  | gaagcggtta | cgctggcaac | taaagcgggc | 600 |
| gttaaccggg  | acctgggtta  | tcaggcaatt  | cgcggtggac | tggcgggcag | taccgtgctg | 660 |
| gatgccaaaag | cgcgatgggt  | gatggaccgc  | aacttcaagc | cgggcttccg | tattgatctg | 720 |
| catattaagg  | atctggcgaa  | tgcgtggat   | acttctcacg | gcgtcgggcg | acaactgccg | 780 |
| ctcacagctg  | cggttatgga  | gatgatgcag  | gcactgcgag | cagatggttt | aggaacggcg | 840 |
| gatcatagcg  | ccctggcggtg | ctactacgaa  | aaactggcga | aagtcgaagt | tactcgtaa  | 900 |

<210> 97  
 <211> 771  
 <212> DNA  
 <213> E. Coli

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| <400> 97   |             |            |            |             |            |     |
| atgaataacg | atgttttccc  | gaataaatcc | aaagccgcac | tggctgcgaa  | acaggtacaa | 60  |
| attgggttgc | ggtcagcact  | ctctaaccgc | attagcactg | aagttcttgg  | tttggtcggg | 120 |
| tttgactggc | tgggtctgga  | tggcgaacat | gcgccaaacg | atatctccac  | gtttattccg | 180 |
| cagttaatgg | ccttgaaaag  | cagcgccagc | gcgccagtag | tgcgagtgcc  | gaccaacgag | 240 |
| ccggtaatga | tttaagcgtct | tctggatata | ggtttctata | acttctctgat | tccttttcta | 300 |
| gaaacaaaag | aggaagcaga  | gctggcgggt | gcatacaacc | gttaccaccc  | ggaaggcatt | 360 |
| cgcgcgctct | ccgttttctca | ccgcgccaat | atgtttggca | ccgtggcgga  | ttatttcgct | 420 |
| cagtcgaaca | agaacatcac  | tattctgggt | cagatagaaa | gtcagcaggg  | cgtagataac | 480 |
| gtcgtatgca | tggccgctac  | cgaagggcta | gacggcatct | tcgtcggccc  | cagcgatctg | 540 |
| gccgcggcat | tagggcatct  | cgccaatgca | tcacaccggg | atgtacaaaa  | agcaattcag | 600 |
| cacattttta | accgtgccag  | cgcgcacggc | aaacccagcg | gtatcctcgc  | gccggtcgaa | 660 |
| gccgatgcgc | gtcgttatct  | ggaatggggc | gcgacgtttg | tggctgtcgg  | cagcgatctc | 720 |
| ggcgtcttcc | gctctgccac  | tcagaaactg | gctgatacct | ttaaaaata   | a          | 771 |

<210> 98  
 <211> 1335  
 <212> DNA  
 <213> E. Coli

|             |            |            |             |            |            |      |
|-------------|------------|------------|-------------|------------|------------|------|
| <400> 98    |            |            |             |            |            |      |
| atgattctcg  | acaccgttga | cgaaaaaag  | aaaggcggtg  | ataccgcgta | tttaatatga | 60   |
| ctgattattt  | ttattgttac | cgccgttaac | tacgcccagc  | gtgcaacgct | gtctattgct | 120  |
| ggtaaccgaag | tggcaaaaga | gttgacgtta | agtgcggttt  | cgatgggtta | catcttctcc | 180  |
| gcttttggct  | gggcctactt | gctgatgcaa | atccccggcg  | gctggctgct | tgataagttt | 240  |
| ggctcgaaaa  | aagtttacac | ctacagcctc | tttttctggt  | cgctattcac | cttctcgcaa | 300  |
| ggctttgttg  | atatgttccc | gctggcctgg | gcagggatct  | ccatgttctt | tatgcgcttt | 360  |
| atgctcggct  | tctcggaagc | gccatcattc | ccggcgaaac  | cccgaattgt | cgccgcctgg | 420  |
| ttcccagcga  | aagaacgtgg | tactgcctcc | gccatcttta  | actcggcgca | atatctctcg | 480  |
| ctggcgctct  | tttcgcccgt | gcttggctgg | ctgaatttgc  | cctggggctg | ggagcacgtc | 540  |
| tttaccgtta  | tgggggtgat | tggttttgtg | ctgacggcgc  | tgtggatcaa | gttgattcat | 600  |
| aacccgacag  | atcaccacag | tatgtctgcg | gaagagctga  | agtttatctc | tgaaaatggc | 660  |
| gcgggtggtc  | atatggacca | caaaaagccg | ggcagtgccg  | cagcaagcgg | acccaaactg | 720  |
| cattacatca  | agcaattgct | ctctaaccgc | atgatgctgg  | gcgtattttt | cggacaatat | 780  |
| tttatcaaca  | ccatcacctg | gttcttcctc | acctgggttc  | cgatttatct | ggtgcaggaa | 840  |
| aaaggcatgt  | cgattctgaa | agtgggtctg | gtcgcctcga  | ttccagcact | gtgtggtttt | 900  |
| gcgggcccgc  | tgtctgggag | tgtcttctcg | gatttatctga | tcaaacgcgg | tttatccctg | 960  |
| accctggcac  | gtaagctacc | gatttgtctg | ggaatgttgc  | tggcttccac | catcatctta | 1020 |
| tgtaactaca  | ccaacaacac | cacgctgggt | gtcatgctga  | tggcgctggc | tttctttggc | 1080 |
| aaaggatttg  | gtgcgctggg | ctggccgggt | atttctgaca  | ccgcgccgaa | agagattgtt | 1140 |
| ggcctctgcg  | gcggcgctct | taacgtcttt | ggcaatgttg  | cctccattgt | cactccactg | 1200 |
| gtgattggct  | acctggtaag | tgaactgcac | tccttcaatg  | cagcactggg | tttcgtggga | 1260 |
| tgttcagcgc  | tgatggcgat | ggtctgctac | ctcttcgtag  | ttggcgacat | taaacgtatg | 1320 |
| gaattgcaga  | aataaa     |            |             |            |            | 1335 |

<210> 99  
 <211> 1536  
 <212> DNA  
 <213> E. Coli

<400> 99

|             |             |            |            |            |             |      |
|-------------|-------------|------------|------------|------------|-------------|------|
| atgcaaacga  | gtgatacccg  | cgcgttaccg | ctactttgcg | cccgcctcgg | ttataaacag  | 60   |
| tattcagggg  | tcaatgtcct  | gaaaggcatc | gattttacgt | tgcatcaggg | ggaggtccac  | 120  |
| gcctctgctg  | gcggcaatgg  | tgccggtaaa | tcgacgttaa | tgaagattat | tgccggtatt  | 180  |
| acccctgctg  | atagcggtag  | gctggagatt | gagggcaaca | actacgtcag | attaacgcca  | 240  |
| gttcatgctc  | atcagctggg  | tatttatctc | gttccccagg | aaccgctgct | tttcccaagc  | 300  |
| ctgtcgataa  | aagaaaacat  | cctgtttggg | ctggcaaaaa | aacagctctc | catgcagaaa  | 360  |
| atgaagaact  | tgctggcgcc  | gctgggctgc | cagtttgatc | tgcatagtct | ggcaggatcg  | 420  |
| ctggatgtcg  | ccgatcgcca  | aatggtggaa | atcctccgcg | ggctgatgcg | cgactcgccg  | 480  |
| attctgatcc  | tcgatgaacc  | taccgcctcg | cttaccctcg | cggaaccgga | acgcttggtt  | 540  |
| agtcgcttgc  | aagagctgct  | tgctactggc | gtgggtattg | tttttatctc | gcataagctg  | 600  |
| ccggaaattc  | gccagattgc  | cgatcgaatt | agcgtgatgc | gcgacggaa  | catcgcccta  | 660  |
| agcggcaaaa  | ccagcgaaact | gtctaccgac | gacattatct | aggccatcac | cccagcggtg  | 720  |
| cgggaaaaat  | cgctctctgc  | cagccaaaaa | ttatggctgg | agttacctgg | taaccgcccc  | 780  |
| caacatgccg  | ccggaacgcc  | ggtgctgaca | ctggaaaaat | tgaccggcga | aggttttcagg | 840  |
| aatgtcagcc  | tgacgctcaa  | tgccggagaa | attctgggcc | tggtctgggt | gggtggggcc  | 900  |
| ggacgcacag  | aactggccga  | gacgctctat | ggtctgcgta | ctttgcgtgg | cgacgcatt   | 960  |
| atgctgaatg  | gtaaaagagt  | caataaatta | tccactggag | aacgtttact | gcgcggtctg  | 1020 |
| gtttatctgc  | cggaagatcg  | ccagtcattc | ggactgaatc | tcgatgcttc | gctggcctgg  | 1080 |
| aacgtctgcg  | cccttactca  | taaccttcgt | ggattctggg | cgaaaaccgc | gaaagataat  | 1140 |
| gccaccctgg  | aacgtttatc  | tcgggctgct | aatattaaat | tcaaccaacc | ggaacaaagt  | 1200 |
| gcacggacat  | tatccggtgg  | caaccagcaa | aaaatcctca | ttgccaaatg | cttggaaagt  | 1260 |
| tcgccgcaag  | tattgattgt  | cgatgagccg | acgcgcggcg | tggatgtctc | ggcccgtaat  | 1320 |
| gatatctacc  | agctgttgcg  | cagcatcgcc | gcacaaaaat | tggtctgtgt | gcttatctcc  | 1380 |
| tccgacctgg  | aagagatcga  | actgatggca | gatcgtgtgt | atgtgatgca | tcaggggcga  | 1440 |
| attaccctact | ctgcactgac  | cgagcgcgat | attaatgtcg | agactattat | gcgcgttgcc  | 1500 |
| ttcggcgata  | gtcagcgta   | ggaggcgta  | tgctga     |            |             | 1536 |

<210> 100  
 <211> 1029  
 <212> DNA  
 <213> E. Coli

<400> 100

|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| atgctgaagt | ttattcagaa | caaccgtgaa | atcacggcac  | tgctggcggg | ggtgctgctg | 60   |
| tttgtattac | ccggttttct | cgaccgccag | tatttaagt   | tgcaaacgct | gaccatgggt | 120  |
| tatagcagcg | cgcaaatcct | gatcctgctg | gcaatggcgg  | cgacgctggt | aatgcttacg | 180  |
| cgcaatattg | atgtttcagt | gggttcgatt | accggaatgt  | gcgcggtgct | gttggggatg | 240  |
| ttactgaacg | caggatatct | actacctggt | gcttggtgct  | cgactttact | gcttggtttg | 300  |
| ctcgcgggat | ttttcaacgg | tgctcctggt | gcgtggctaa  | agatccctgc | cattgttgcc | 360  |
| acccttggca | cgtaggggtt | gtacagaggg | atcatgttgc  | tgtaggactg | cggaacatgg | 420  |
| attgaagggt | taccgcgcga | actgaaacag | ctctccgccc  | cgctgctgct | tgccgtttca | 480  |
| gcaattgggt | ggttgacgat | aattctgggt | gcatttatgg  | cctggctgct | ggcaagacg  | 540  |
| gcgtttggac | gcagttttta | tgccacgggc | gataatttac  | agggcgctcg | tcaactgggc | 600  |
| gttcgtactg | aagccattcg | cattgtggca | ttttcgttga  | acggctgcat | ggcggcactg | 660  |
| gcgggaattg | tgtttgcttc | gcagattggt | tttatcccca  | accagaccgg | taccgggctg | 720  |
| gagatgaaag | caattgcagc | ctgcgtgctg | ggcggcatta  | gtttgctcgg | tggttccggt | 780  |
| gcgatcattg | gtgcggtact | cgccgcatgg | ttcctgacgc  | agatcgatag | cgtactgggt | 840  |
| ctggtgcgca | ttccggcatg | gtggaatgat | tttatcgccg  | gtctggttct | gctggcggtg | 900  |
| ctgggtgttg | atggacgcct | gcgtttgtcg | ctggaaacgta | atctacggcg | gcaaaaatat | 960  |
| gccccgttta | tgacgccacc | gcatccggtt | aaaccgcgtt  | cgtcaggtaa | aaaacgggag | 1020 |
| gccgcataa  |            |            |             |            |            | 1029 |

<210> 101  
 <211> 993

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 101

|     |     |       |      |     |     |     |     |     |     |     |     |    |     |     |     |     |    |    |     |     |     |     |
|-----|-----|-------|------|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|-----|----|----|-----|-----|-----|-----|
| atg | cg  | tattc | gct  | acg | gtt | g   | gaa | act | ggc | ctt | gcc | gc | ac  | tgc | gtt | at  | tg | ag | att | gtc | 60  |     |
| gc  | att | tg    | gtg  | ca  | att | a   | ccc | gc  | ga  | at  | gt  | ta | gat | ct  | ca  | ata | tg | gt | gc  | gtt | 120 |     |
| ga  | ctt | t     | at   | ct  | gc  | att | gg  | cat | tg  | tc  | gc  | cc | ta  | ac  | ga  | tg  | gt | gc | att | gt  | 180 |     |
| at  | cg  | at    | att  | cg  | tt  | gg  | ttc | ga  | cc  | at  | cg  | gc | ct  | tc  | gc  | gc  | ca | tt | gc  | att | gg  | 240 |
| caa | ag  | tg    | gtg  | tg  | cc  | ga  | tg  | gc  | g   | ct  | gg  | cg | ata | ct  | ct  | gc  | ac | ct | gc  | tc  | gg  | 300 |
| gg  | gc  | t     | gat  | ca  | ac  | gc  | cg  | att | a   | att | at  | ct | at  | ac  | caa | ag  | tt | a  | cc  | cg  | tc  | 360 |
| gg  | ca  | gc    | ct   | gt  | at  | ct  | gt  | tt  | gc  | cg  | ga  | gc | gt  | ct  | gc  | ct  | tt | cc | gc  | gt  | at  | 420 |
| gg  | gt  | ac    | ga   | ag  | gt  | att | gg  | gg  | att | cc  | cg  | at | g   | gc  | gt  | tt  | ac | ag | att | tc  | gt  | 480 |
| ct  | gg  | ga    | ct   | cc  | cg  | tt  | cc  | gc  | t   | gat | at  | ct | tc  | gc  | tt  | tt  | ct | gc | tt  | tt  | ct  | 540 |
| ct  | gc  | ata   | aaaa | cc  | cat | gc  | cc  | g   | ac  | gt  | aa  | tg | t   | tt  | tt  | tg  | at | gg | caa | ag  | ccc | 600 |
| ct  | tt  | at    | ag   | cg  | ga  | tt  | cc  | ag  | t   | aa  | cc  | gt | ac  | t   | at  | gt  | gc | gc | t   | at  | gc  | 660 |
| gc  | gt  | ct    | gc   | gc  | tg  | cc  | gc  | ct  | gt  | gc  | gt  | gt | ta  | tc  | gt  | at  | tt | tg | tt  | gc  | ac  | 720 |
| gg  | tg  | gc    | tc   | gc  | t   | tt  | ct  | ga  | tg  | cc  | gc  | at | cc  | gc  | gc  | tg  | gc | tt | gg  | cg  | gg  | 780 |
| gg  | tg  | gt    | tc   | cc  | g   | gt  | tc  | cc  | at  | ta  | tc  | gc | gc  | gc  | gc  | gc  | gc | gc | gc  | gc  | gc  | 840 |
| ca  | ag  | gt    | tt   | gc  | aa  | at  | gg  | ca  | gc  | ag  | gc  | gc | gc  | gc  | gc  | gc  | gc | gc | gc  | gc  | gc  | 900 |
| ct  | tt  | at    | gc   | tc  | g   | tg  | tc  | gc  | tg  | ag  | gc  | gc | gc  | gc  | gc  | gc  | gc | gc | gc  | gc  | gc  | 960 |
| ct  | gg  | cg    | gc   | gc  | gc  | gc  | gc  | gc  | gc  | gc  | gc  | gc | gc  | gc  | gc  | gc  | gc | gc | gc  | gc  | gc  | 993 |

&lt;210&gt; 102

&lt;211&gt; 1023

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 102

|    |     |    |     |    |    |    |    |    |    |    |    |    |    |    |     |    |    |    |    |    |    |      |
|----|-----|----|-----|----|----|----|----|----|----|----|----|----|----|----|-----|----|----|----|----|----|----|------|
| at | ga  | ca | ct  | tc | at | gc | ct | tt | aa | ga | aa | tc | gc | tt | act | ta | gc | gc | gc | at | tc | 60   |
| t  | ct  | at | ga  | at | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc  | gc | gc | gc | gc | gc | gc | 120  |
| t  | t   | t  | t   | t  | t  | ta | ca | gc | gc | gc | gc | gc | gc | gc | gc  | gc | gc | gc | gc | gc | gc | 180  |
| ac | ct  | ta | gc  | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc  | gc | gc | gc | gc | gc | gc | 240  |
| gt | ca  | at | ca  | ag | gt | ta | ta | ac | gc | ca | tt | at | ct | gc | tt  | ct | gc | gc | gc | gc | gc | 300  |
| gc | act | g  | aaa | ac | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc  | gc | gc | gc | gc | gc | gc | 360  |
| cc | gg  | ag | tg  | gc | gc | ct | ta | ct | ta | ca | ta | ta | ca | gc | gc  | gc | gc | gc | gc | gc | gc | 420  |
| gt | gg  | at | at  | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc  | gc | gc | gc | gc | gc | gc | 480  |
| ag | ccc | ac | cc  | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc  | gc | gc | gc | gc | gc | gc | 540  |
| ga | gc  | at | cc  | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc  | gc | gc | gc | gc | gc | gc | 600  |
| tt | aca | aa | cc  | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc  | gc | gc | gc | gc | gc | gc | 660  |
| ga | gc  | ca | gc  | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc  | gc | gc | gc | gc | gc | gc | 720  |
| gc | gc  | at | tg  | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc  | gc | gc | gc | gc | gc | gc | 780  |
| aa | ga  | at | tt  | gc | ct | gt | gg | gc | gc | gc | gc | gc | gc | gc | gc  | gc | gc | gc | gc | gc | gc | 840  |
| gc | att | at | tg  | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc  | gc | gc | gc | gc | gc | gc | 900  |
| ca | gg  | tt | ga  | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc  | gc | gc | gc | gc | gc | gc | 960  |
| at | gc  | ta | ct  | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc  | gc | gc | gc | gc | gc | gc | 1020 |
| tg | a   |    |     |    |    |    |    |    |    |    |    |    |    |    |     |    |    |    |    |    |    | 1023 |

&lt;210&gt; 103

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 103

|    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|
| at | gg | ca | gc | at | ta | ag | at | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | 60  |
| aa | ta | tc | cc | ct | ta | cc | ct | ga | ag | gt | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | 120 |
| tc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | 180 |
| tt | tc | ag | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | 240 |
| ca | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | 300 |
| aa | ta | gg | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | 360 |
| ga | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | 420 |
| ca | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | gc | 480 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gatgccggaa | tgaagtgagg | aatgccgacc | atggccgtga | ctggcgtggg | caaagatatg | 540 |
| gtgcgcgac  | agcggtattt | ctcgctcgcg | actcgaatcg | ccgctgaaat | gggggcgcaa | 600 |
| attatcaaaa | cctattatgt | cgaaaaaggt | tttgaaacga | ttgttgccgg | atgtccggta | 660 |
| cccattgtta | ttgctggcgg | taaaaaatta | ccggagcgcg | aggcgctgga | aatgtgctgg | 720 |
| caggctatcg | atcagggcgc | ttctgggttg | gatatggggc | gtaatatatt | ccagtctgac | 780 |
| catccgggtg | cgatgatgaa | agccgtacag | gcgggtggtc | accataacga | aacggctgat | 840 |
| cgggcatatg | aactctatct | gagtgaaaaa | cagtaa     |            |            | 876 |

<210> 104  
 <211> 291  
 <212> DNA  
 <213> E. Coli

<400> 104

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| atgcacgtca | cactggttga | aattaacgtt | catgaagaca  | aggttgacga | gtttatcgaa | 60  |
| gtttttcgcc | agaaccacct | gggctctgta | caggaagaag  | gcaatttgcg | cttcgatgtc | 120 |
| ttacaggacc | cggaagtga  | ttcgcgcttt | tatatctacg  | aagcctataa | agatgaagac | 180 |
| gcagtggcgt | tccataaaac | cacgccccac | tacaaaaacct | gtgtcgcgaa | actggaatct | 240 |
| ttaatgaccg | ggccgcgtaa | aaaacgtctg | ttcaatggtt  | tgatgccgtg | a          | 291 |

<210> 105  
 <211> 1152  
 <212> DNA  
 <213> E. Coli

<400> 105

|             |            |            |             |             |             |      |
|-------------|------------|------------|-------------|-------------|-------------|------|
| atgtttgaac  | caatggaact | taccaatgac | gcgggtgatta | aagtcacg    | cgctggcgcc  | 60   |
| ggcgccggta  | atgctgttga | acacatggtg | cgcgagcgca  | ttgaaggtgt  | tgaattcttc  | 120  |
| gcggtaataa  | ccgatgcaca | agcgctgcgt | aaaacagcgg  | ttggacagac  | gattcaaatac | 180  |
| ggtagcggtta | tcaccaaagg | actgggcgct | ggcgctaatc  | cagaagttgg  | ccgcaatgcg  | 240  |
| gctgatgagg  | atcgcgatgc | attgctgctg | gcgctggaag  | gtgcagacat  | ggtctttatt  | 300  |
| gctgcgggta  | tgggtggttg | taccggtaca | ggtgcagcac  | cagtcgtcgc  | tgaagtggca  | 360  |
| aaagattttg  | gtatcctgac | cgttgctgtc | gtcactaagc  | ctttcaactt  | tgaaggcaag  | 420  |
| aagcgtatgg  | cattcgcgga | gcaggggatc | actgaaactgt | ccaagcatgt  | ggactctctg  | 480  |
| atcactatcc  | cgaacgacaa | actgctgaaa | gttctggggc  | gcggatatctc | cctgctggat  | 540  |
| gcgttttgcg  | cagcgaacga | tgtactgaaa | ggcgctgtgc  | aaggtatcgc  | tgaactgatt  | 600  |
| actcgtccgg  | gtttgatgaa | cgtggacttt | gcagacgtac  | gcaccgtaat  | gtctgagatg  | 660  |
| ggctacgcaa  | tgatgggttc | tggcggtggc | agcggtgaa   | accgtgcgga  | agaagctgct  | 720  |
| gaaatggcta  | tctcttctcc | gctgctggaa | gatatcgacc  | tgtctggcgc  | gcgcggcggtg | 780  |
| ctgggttaaca | tcacggcggg | cttcgacctg | cgtctggatg  | agttcgaaac  | ggtaggtaac  | 840  |
| accatccgtg  | catttgcttc | cgacaacgcg | actgtggtta  | tcggtaacttc | tcttgaccgg  | 900  |
| gatatgaatg  | acgagctgcg | cgtaaccgtt | gttgcgacag  | gtatcgccat  | ggacaaaacgt | 960  |
| cctgaaatca  | ctctggtgac | caataagcag | gttcagcagc  | cagtgtatga  | tcgctaccag  | 1020 |
| cagcatggga  | tggctccgct | gacccaggag | cagaagccgg  | ttgctaaagt  | cgtgaatgac  | 1080 |
| aatgcgccgc  | aaactgcgaa | agagccggat | tatctggata  | tcccagcatt  | cctgcgtaaag | 1140 |
| caagctgatt  | aa         |            |             |             |             | 1152 |

<210> 106  
 <211> 3048  
 <212> DNA  
 <213> E. Coli

<400> 106

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| atggacgtca | gtcgcagaca | attttttaaa | atctgcgcgg | gcggatatgc  | tggaacaaca | 60  |
| gtagcggcat | tgggctttgc | cccgaagcaa | gcactggctc | aggcgcgaaa  | ctacaaatta | 120 |
| ttacgcgcta | aagagatccg | taacacctgc | acatactgtt | ccgtagggtg  | cgggctattg | 180 |
| atgtatagcc | tgggtgatgg | cgcaaaaaac | gccagagaag | cgatttatca  | cattgaaggt | 240 |
| gacccggatc | atccggtaa  | ccgtggtgcg | ctgtgcccca | aaggggccgg  | ttgtctggat | 300 |
| tacgtcaaca | gtgaaaaccg | tctgcgctac | ccggaatatc | gtgcgccagg  | ttctgacaaa | 360 |
| tggcagcgca | ttagctggga | agaagcatte | tcccgtattg | cgaagctgat  | gaaagctgac | 420 |
| cgtgacgcta | actttattga | aaagaacgag | cagggcgtaa | cggtaaaaccg | ttggttttct | 480 |



|             |            |             |            |            |              |      |
|-------------|------------|-------------|------------|------------|--------------|------|
| accggtatgc  | tgtgtgcctc | cgggtgccagc | aacgaaaccg | ggatgctgac | ccagaaattt   | 540  |
| gcccgcctccc | tcgggatgct | ggcggtagac  | aaccaggcgc | gcgtctgaca | cggaccaacg   | 600  |
| gtagcaagtc  | ttgctccaac | atttggctgc  | gggtcgatga | ccaaccactg | gggtggatatac | 660  |
| aaaaacgcta  | acgtcctgat | gggtgatgggc | ggtaacgctg | ctgaagcgca | tcccgtcgggt  | 720  |
| ttccgctggg  | cgatggaagc | gaaaaacaac  | aacgacgcaa | ccttgatcgt | tgctgatccc   | 780  |
| cgttttacgc  | gtaccgcttc | tgtggcggat  | atttacgcgc | ctattcgttc | cggtagcgac   | 840  |
| attacgttcc  | tgtctggcgt | tttgcgctac  | ctgatcgaaa | acaacaaaat | caacgccgaa   | 900  |
| tacgttaagc  | attacaccaa | cggcagcctg  | ctggtgcgtg | atgattttgc | tttcgaagac   | 960  |
| ggtctgttca  | gcgggtacga | cgctgaaaaa  | cgtaaatcgc | ataaatcgtc | ctggaactat   | 1020 |
| cagctcgtatg | aaaacggcta | tgcgaaacgc  | gatgaaacac | tgactcatcc | gcgctgtgtg   | 1080 |
| tggaaacctgc | tgaagagca  | cgtttcccg   | tacacgcgg  | acgtcgttga | aaacatctgc   | 1140 |
| ggtagcctcaa | aagccgactt | cctgaaagtg  | tgtgaagtgc | tggcctccac | cagcgaccgc   | 1200 |
| gatcgaccaa  | ccaccttcc  | gtacgcgctg  | ggctggagcg | agcacactgt | gggtgcgcag   | 1260 |
| aaactccgtg  | ctatggcgat | gatccagttg  | ctgctcggtg | acatgggtat | ggcgggtggc   | 1320 |
| ggcgtgaacg  | catctgcgtg | tcactccaac  | attcagggtt | tgactgactt | aggcctgtct   | 1380 |
| tctaccagcc  | tgccaggtta | tctgacgctg  | ccgtcagaaa | aacaggttga | tttgagtcg    | 1440 |
| tatctggaag  | cgaacacgcc | gaaagcgacg  | ctggctgac  | aggtgaacta | ctggagcaac   | 1500 |
| tatccgaagt  | tcttcgttag | cctgatgaaa  | tctttctatg | gcgatgccgc | gcagaaagag   | 1560 |
| aaacaactggg | gctatgactg | gctgccgaag  | tgggaccaga | cctacgacgt | catcaagtat   | 1620 |
| ttcaacatga  | tggatgaagg | caaagtcacc  | ggttatttct | gccagggtt  | taaccgggtt   | 1680 |
| gcgtccttcc  | cggacaaaaa | caaagtgggt  | agctgcctga | gcaagctgaa | gtacatggtg   | 1740 |
| gttatcgatc  | cgctggtgac | tgaacctct   | accttctggc | agaaccacgg | tgagtcgaac   | 1800 |
| gatgtcgatc  | cggcgtctat | tcagactgaa  | gtattccgtc | tgccttcgac | ctgctttgct   | 1860 |
| gaagaagatg  | gttctatcgc | taactccggt  | cgctgggtgc | agtggcactg | gaaaggctcag  | 1920 |
| gaacgcgcgg  | gcgaagcgcg | taacgacgg   | gaaattcttg | cgggtatcta | ccatcatctg   | 1980 |
| cgcgagctgt  | accagtcga  | aggtggtaaa  | ggcgtagaac | cgctgatgaa | gatgagctgg   | 2040 |
| aactacaagc  | agccgcacga | accgcaatct  | gacgaagtgg | ctaaagagaa | caacggctac   | 2100 |
| gcgctggaag  | atctctatga | cgctaattgg  | gtgcttattg | cgaagaaagg | tcagttgctg   | 2160 |
| agtagctttg  | cgcactctgc | tgatgacgg   | acaaccgcat | cttcttgcgt | gatctacacc   | 2220 |
| ggtagctgga  | cagagcagg  | caaccagatg  | gctaaccgcg | ataactccga | cccgctccgg   | 2280 |
| ctgggggaata | cgctgggatg | ggcctggggc  | tggccgctca | accgtcgcgt | gctgtacaac   | 2340 |
| cgctgcttcg  | cggatatcaa | cggtaaaccg  | tgggatccga | aacggatgct | gatccagtg    | 2400 |
| aacgcgcagca | agtggacggg | taacgatatt  | cctgacttcg | gcaatgccgc | accgggtacg   | 2460 |
| ccaaccgggc  | cgtttatcat | gcagccggaa  | gggatgggac | gcctgtttgc | catcaacaaa   | 2520 |
| atggcggaag  | gtccggttcc | ggaacactac  | gagccgattg | aaacgccgct | gggcactaac   | 2580 |
| ccgctgcac   | cgaacgtggt | gtctaaccgc  | gttggtcgtc | tgtatgaaca | agacgcgctg   | 2640 |
| cggatgggta  | aaaaagagca | gttcccgat   | gtgggtacga | cctatcgtct | gaccgagcac   | 2700 |
| ttccacacct  | ggaccaagca | cgcatctgct  | aacgcaattg | ctcagccgga | acagtttgtg   | 2760 |
| gaaatcagcg  | aaacgctggc | ggcggcgaaa  | ggcattaata | atggcgatcg | tgtcactgtc   | 2820 |
| tccagcaagc  | gtggctttat | ccgcgcgggt  | gctgtggtaa | cgcgtcgtct | gaaaccgctg   | 2880 |
| aatgtaaatg  | gtcagcaggt | tgaacgggtg  | ggtattccaa | tccactgggg | ctttgagggg   | 2940 |
| gtcgcgcgta  | aaggttatat | cgctaactac  | ctgacgcgga | atgtcgggtg | tgcaaaactcg  | 3000 |
| caaacgcggg  | aatataaagc | gttcttagtc  | aacatcgaga | aggcgtaa   |              | 3048 |

&lt;210&gt; 107

&lt;211&gt; 885

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 107

|             |            |            |             |            |             |     |
|-------------|------------|------------|-------------|------------|-------------|-----|
| atggctatgg  | aaacgcagga | cattatcaaa | aggtccgcaa  | ctaactccat | cacgccgcct  | 60  |
| tctcaggtgc  | gtgattacaa | agcagaagtc | gcaaaactta  | tcgacgtttc | cacctgtatc  | 120 |
| ggctgtaaag  | cctgtcaggt | ggcgtgttcg | gagtggaaacg | acatccgtga | tgaagtgggg  | 180 |
| caactgcgtgc | gggtttacga | taaccccgcc | gatctgagcg  | ccaagtcctg | gacgggtgatg | 240 |
| cgcttttagcg | aaaccgaaca | gaacggcaag | ctggagtggc  | tgatccgtaa | agacggctgt  | 300 |
| atgcactgtg  | aagatccccg | ctgcctgaag | gcgtgcccgt  | ctgctggtgc | aatcattcag  | 360 |
| tacgctaacg  | ggattgtcga | tttccagtcg | gaaaactgca  | tcggctgtgg | ttactgcatt  | 420 |
| gccgggtgtc  | cgtttaatat | tcgcgccttc | aacaaagagg  | ataaccgggt | atataaatgc  | 480 |
| acgctctgcg  | tcgatcgcg  | cagcgtcggc | caggaaaccg  | cttgtgtgaa | aacctgtccg  | 540 |
| accggggcta  | tccacttcgg | caccaagaag | gagatgctgg  | agctggcgga | acagcgcgtg  | 600 |
| gcgaaactga  | aagcgcgtgg | ttacgaacat | gctggcgctc  | acaaccggga | aggggtcgg   | 660 |

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| ggtagcgcacg | ttatgtacgt | gctgcacac  | gccgatcagc | cggagctgta | tcacggctctg | 720 |
| ccgaagatc   | cgaagatcga | cacctcggtg | agcctgtgga | aaggcgctt  | gaaaccgctg  | 780 |
| gcagcggctg  | gctttattgc | cacttttgcc | gggttgattt | tccactacat | cggtattggc  | 840 |
| ccgaataaag  | aagtggacga | tgacgaggag | gatcatcatg | agtaa      |             | 885 |

<210> 108  
 <211> 654  
 <212> DNA  
 <213> E. Coli

|             |             |            |             |             |             |     |
|-------------|-------------|------------|-------------|-------------|-------------|-----|
| <400> 108   |             |            |             |             |             |     |
| atgagtaagt  | cgaaaaatgat | tgtgcgcacc | aaattttattg | atcgcgcctg  | tcactggacc  | 60  |
| gtgggtgattt | gcttcttcct  | ggtggcgctg | tccgggattt  | cgttcttcct  | cccgcgcctg  | 120 |
| caatggctga  | cgcaaacctt  | cggtacgccg | cagatgggac  | gcattttgca  | cccgttcttc  | 180 |
| ggcattgcga  | ttttcgtcgc  | actgatgttt | atgtttgtgc  | gtttttgtgca | tcacaacatc  | 240 |
| ccggataaga  | aagatattcc  | gtggctgttg | aacattgtcg  | aagtattgaa  | aggcaatgag  | 300 |
| cataaagtgg  | cggtatgtcgg | taagtacaac | gccgggcaaa  | agatgatgtt  | ctggtcgac   | 360 |
| atgagcatga  | ttttcgtgct  | gctggtgacc | gggggtgatta | tctggcgctc  | gtactttgctg | 420 |
| cagtaactcc  | cgatgcaggt  | tgttcgctac | agcctgctga  | tccacgcggc  | tgcgggtatc  | 480 |
| atcctgatcc  | acgccatcct  | gatccatag  | tatatggcat  | tttgggtgaa  | aggatcgatt  | 540 |
| aaagggatga  | tcgaagggaa  | ggtaagtcgt | cgctgggcga  | agaaacacca  | tccgcgctgg  | 600 |
| tatcgtgaaa  | tcgagaaggc  | agaagcga   | aaagagagt   | aagaaggat   | ataa        | 654 |

<210> 109  
 <211> 261  
 <212> DNA  
 <213> E. Coli

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| <400> 109  |            |            |            |            |            |     |
| atggcggtgt | taataactaa | aaaatgcac  | aattgtgata | tgtgtgaacc | cgaatgcccg | 60  |
| aatgaggcga | tttcaatggg | agatcatatc | tacgagatta | acagcgataa | gtgtaccgaa | 120 |
| tgctagggc  | actacgagac | accaaactgc | cagaaggtgt | gcccgatccc | caatactatt | 180 |
| gtgaaagatc | cgccgcctgt | cgagacagaa | gaacagttgt | gggataaatt | tgtgctgatg | 240 |
| caccacgcgg | ataaaattta | a          |            |            |            | 261 |

<210> 110  
 <211> 1203  
 <212> DNA  
 <213> E. Coli

|             |             |            |            |            |            |      |
|-------------|-------------|------------|------------|------------|------------|------|
| <400> 110   |             |            |            |            |            |      |
| atgcaaatg   | ttgatgtagc  | cattgttggc | ggcggcatgg | tggggctggc | ggttgcctgt | 60   |
| ggcttacagg  | ggagcggctt  | acgcgttgcc | gtactggagc | agcgcgtaca | ggaacctctg | 120  |
| gcggcgaatg  | caccaccaca  | actgcgcgtt | tccgctatca | atgccgccag | cgaaaaatta | 180  |
| ctcaccgcgc  | ttggcgtctg  | gcaggacatt | ctctctcgta | gggccagctg | ttatcacggg | 240  |
| atggaaagtgt | gggacaaaaga | cagctttggg | cacatttcgt | ttgacgatca | aagcatgggc | 300  |
| tatagccatc  | ttgggcatat  | cggtgaaaat | tcagtgtatc | actacgcgct | gtggaacaaa | 360  |
| gcgcacatc   | cgatcagata  | cactctgtta | gccccgcgag | aattacagca | ggtcgcctgg | 420  |
| ggagaaaaatg | aaaccttcct  | gacgctgaaa | gatggcagca | tgtaaaccgc | gcgtctggtg | 480  |
| attggcgcg   | acggcgctaa  | ttcctgggtg | cgcaacaaa  | ccgatatcc  | gctgactttc | 540  |
| tgggattatc  | agcatcacgc  | gctggtagcg | accattcgca | cggagaacc  | gcatgatgcg | 600  |
| gtggcgcgcc  | aggttttcca  | tggcggaagg | attctggcct | ttttaccgct | tagcgatccg | 660  |
| catctttgct  | cgattgtctg  | gtcactgtcg | ccagaggaag | cgacgcggat | gcagcaggca | 720  |
| agtgaagacg  | aatttaacgc  | cgcgtaaat  | atcgcttttg | ataatcgctt | gggcttatgc | 780  |
| aaagttgaga  | gcgcgcgtca  | ggtgttccca | ctgacggggc | gttatgcgcg | ccagtttgcc | 840  |
| tcgcaccgct  | tggcgctggg  | gggcgacgcc | gcacatacca | ttcaccgcct | ggcggggcag | 900  |
| ggggtaaatc  | tcggctttat  | ggatgctgca | gagctgattg | ccgaactgaa | acggttgcat | 960  |
| cgctcagggga | aagacatcgg  | gcagtacatt | tatctgcgtc | gctatgagcg | tagccgcaag | 1020 |
| cacagtcggg  | cgttgatgct  | ggctgggtat | cagggattcc | gcgatctgtt | ttccggtacc | 1080 |
| aatccggcga  | aaaaactgct  | gcgtgatatt | ggtttgaaac | tggccgacac | gcttctggc  | 1140 |
| gttaagccgc  | aacttatccg  | ccaggcaatg | ggattaaacg | atttgctga  | atggctgcgt | 1200 |

taa

1203

<210> 111  
 <211> 1179  
 <212> DNA  
 <213> E. Coli

<400> 111

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| atgagcgtaa | tcacgcgcgg | tggcggcgcg | gcggggcgca | cgctggcgct | ggctatttcc | 60   |
| cggttaagtc | acggggcgct | gccggtacat | ttgattgaag | cgactgcgcc | agagtcacat | 120  |
| gtccatccgg | gctttgatgg | acgagcgata | gcgctggcgg | cggttacctg | tcagcaactg | 180  |
| gcgcgcacgc | gcgtctggca | atctctggcg | gattgcgcaa | ctgccatcac | caccgtgcat | 240  |
| gtcagcgatc | gtggtcacgc | tggatttgct | accctcgccg | cagaagatta | ccaactggcg | 300  |
| gcgctgggac | aggttgtcga | attgcacaat | gtcgggcaac | ggctgtttgc | attgctgcgt | 360  |
| aaagcacctg | gcgtaacgct | gcattgccct | gacgcgctgg | ctaacggttc | ccgtactcag | 420  |
| agtcacgttg | aagtgcgcgt | ggagagtggc | gagacgctga | cgggccgcgt | gctggtagca | 480  |
| gctgatggca | cccattcagc | gttagccacc | gcgtgcggcg | ttgactggca | gcaggagcct | 540  |
| tacgaacaac | tggccgtgat | tgccaacgtt | gctacttccg | ttgcgcata  | agggcgcgct | 600  |
| tttgaacgct | ttacgcaaca | tggcccgcgt | gcgatgttgc | cgatgtctga | cggacgctgt | 660  |
| tcgctggctt | ggtgtcatcc | actggaacgg | cgcgaaagag | tggtgtcgct | gagtgacgag | 720  |
| aagttttgcc | gtgaactcca | gtcggccctt | ggctggcgac | ttgggaaaa  | taccacgct  | 780  |
| ggtaaacgca | gtgcttatcc | gctggcgctt | acccacgccg | ccagatctat | taccatcgt  | 840  |
| accgtgctgg | tgggcaatgc | ggcgcaaat  | ctgcaccgca | ttgcggggca | agggtttaac | 900  |
| ctcggatgc  | gagatgtgat | gagtccttgc | gaaaccctga | ctcaggcgca | ggagcgcgga | 960  |
| gaagacatgg | gggattacgg | cgtattgtgc | cgttatcagc | agcgtcgaca | gagcgatcgc | 1020 |
| gaagcaacca | ttggcgctac | ggacagcctt | gtacatcttt | ttgccaaccg | ttgggcaccg | 1080 |
| ctgggtgtcg | ggcgcaacat | cgggctgatg | acgatggaa  | tattcacc   | ggcacgcgat | 1140 |
| gtgctggcgc | agcgacacct | cgggtgggtg | gcgcgttga  |            |            | 1179 |

<210> 112  
 <211> 1326  
 <212> DNA  
 <213> E. Coli

<400> 112

|            |            |             |            |            |            |      |
|------------|------------|-------------|------------|------------|------------|------|
| atgagtgaga | tatcccggca | agagtttcag  | cgctcgccgc | aggccctggt | ggagcaaatg | 60   |
| caaccgcgca | gcgcgcgcgt | gatttttgct  | gcaccagaag | taaacagtag | cgccgacagc | 120  |
| gaataccctt | atcgtcagaa | cagtgaactt  | tggtaactca | ccggctttta | cgaaccggaa | 180  |
| gcggtgctgg | tgctgattaa | aagcgatgac  | actcataacc | acagcgcttc | gtttaaccgc | 240  |
| gttcgcgacc | tgacggcgga | gatctggttt  | ggcgtcgct  | taggccagga | tgccgcgcca | 300  |
| gagaaactgg | gcgttgaccg | cgcaactggca | ttcagcgaaa | tcaatcagca | actttatcaa | 360  |
| ctacttaacg | gcctggatgt | ggtttaccat  | gcccaggcg  | aatatgcata | tgctgatgta | 420  |
| atcgtgaaca | gtgcgctgga | aaaactgcgt  | aaagggttcg | ggcaaaatct | caccgcaccg | 480  |
| gcaacgatga | tcgactggcg | tcctgttggt  | catgaaatgc | gcctgttcaa | atcgccagaa | 540  |
| gagattgccg | tactccgcgc | cgcgggagaa  | atcaccgcga | tggcacatac | acgggcgatg | 600  |
| gaaaaatgcc | gtccgggaat | gttcgagtac  | catctggaag | gcgaaattca | ccacgaattt | 660  |
| aaccggcacg | gtgcgcgcta | tccgtcctat  | aacaccattg | tcggcagcgg | tgaaaacggc | 720  |
| tgcatctctg | actacaccga | aaacgagtgt  | gaaatgcgcg | acggcgacct | ggtgttgatt | 780  |
| gacgcgggtt | gtgaatacaa | aggttacgct  | ggcgatatta | cccgcacctt | cccgttcaac | 840  |
| ggcaaatcca | cccaggccca | gcgtgaaatc  | tacgacattg | tgctggagtc | tctcgaaacc | 900  |
| agcctgcgcc | tgtatcgtcc | gggaacttcc  | attctggaag | tcaactggtg | agtgggtgcg | 960  |
| atcatggtta | gcggcctggt | aaaactcgcc  | atcctgaaag | gtgatgttga | tgaactgatc | 1020 |
| gtcagaacgc | cccatcgctc | tttctttatg  | catggcctta | gccactggtt | aggactggat | 1080 |
| gtccatgacg | tgggtgttta | tggtcaggat  | cgctcgcgca | ttctggaacc | gggcatggta | 1140 |
| ctgaccgtag | agccagggct | gtatattgcg  | ccgatgcag  | aagtgccaga | acaatatcgc | 1200 |
| ggtatcggga | ttcgtattga | agacgacatt  | gtgattaccg | aaaccggtta | cgaaaacctc | 1260 |
| accgccagcg | tgggtgaaaa | gccggaagaa  | atcgaagcgt | tgatggttgc | tgcagaaaa  | 1320 |
| caatga     |            |             |            |            |            | 1326 |

<210> 113  
 <211> 585

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 113

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| atgcttatgt | ctatacagaa | cgaaatgcct | ggttacaacg  | aaatgaacca | gtatctgaac | 60  |
| caacaaggga | cggtctgac  | cccagctgag | atgcatggtt  | taatcagcgg | gatgatatgt | 120 |
| ggcggtaacg | atgacagctc | atggctaccg | ctacttcacg  | acctgacgaa | cgaaggcatg | 180 |
| gctttcggtc | atgagctggc | acaggcactg | cgtaaaatgc  | actctgccac | cagcgatgcc | 240 |
| ctgcaggatg | acggcttctt | ttttcagctt | tatctgcctg  | atggcgatga | tgtcagcggt | 300 |
| ttcgatcggg | ctgatgcatt | ggcagggttg | gtcaatcact  | tcctgcttgg | tcttggcggt | 360 |
| acgcaaccga | agctggataa | agtgaccggc | gaaaccgggtg | aagctatcga | cgatctgcgt | 420 |
| aacattgcgc | aactgggtta | cgacgaagac | gaagatcagg  | aagagcttga | aatgtcgctt | 480 |
| gaagagatca | tcgaatacgt | tcgtgttgcc | gcgctgttat  | gccacgacac | ctttactcat | 540 |
| ccgcaaccga | ccgcgcgaga | agtacaaaaa | ccgactctac  | actaa      |            | 585 |

&lt;210&gt; 114

&lt;211&gt; 363

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 114

|             |             |            |             |            |            |     |
|-------------|-------------|------------|-------------|------------|------------|-----|
| atgtttaaagc | tatttgcaaa  | gtacacctct | attgggtgtgc | tgaacaccct | tatacactgg | 60  |
| gtgggttttg  | gtgtttgtat  | ctatgtcgcg | catacaaaac  | aagctcttgc | aaacttcgca | 120 |
| ggtttcgttg  | tggtctgtgag | ctttagcttc | ttcgcgaaatg | caaaattcac | attcaaggca | 180 |
| tcgactacaa  | cgatgcgcta  | catgctatat | gttgggttca  | tggggacact | gagtgcact  | 240 |
| gttggatggg  | ctgctgatag  | atgcgcactt | cccccgatga  | taactcttgt | caccttctcc | 300 |
| gccatcagcc  | tggtgtgcgg  | tttcgtctat | tcaaagtcca  | ttgtctttag | ggatgcgaaa | 360 |
| tga         |             |            |             |            |            | 363 |

&lt;210&gt; 115

&lt;211&gt; 921

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 115

|             |             |             |             |            |             |     |
|-------------|-------------|-------------|-------------|------------|-------------|-----|
| atgaagatat  | ctcttgtagt  | tcctgtcttc  | aatgaagaag  | aagcgatacc | aattttttat  | 60  |
| aaaacggtag  | gtgaattcga  | agaattgaag  | tcatatgaag  | tggaaatcgt | tttcataaat  | 120 |
| gacggcgagca | aagacgctac  | ggagtcaatc  | attaatgtct  | tggtctgttc | agatcctcta  | 180 |
| gttgttcgcg  | tgatctttac  | acgcaacttt  | ggtaaagaac  | cagcattggt | tgtaggggtta | 240 |
| gaccatgcaa  | ccgggggatgc | gataatccca  | attgatgttg  | acctgcaaga | cccgattgag  | 300 |
| gttattcctc  | atcttattga  | aaaatggcaa  | gcagggtgctg | atatgggtct | tgctaaaaga  | 360 |
| tctgaccgct  | caactgatgg  | acgcctgaag  | cgaaaaacgg  | ctgagtgggt | ctataagctc  | 420 |
| cacaataaaa  | taagcaatcc  | taaaattgaa  | gagaatgttg  | gtgatttcag | gctgatgagc  | 480 |
| cgatgatgtg  | tcgaaaatat  | taaacttatg  | ccagaacgaa  | accttttcat | gaaagggtatt | 540 |
| ctgagctggg  | taggaggaaa  | gacagatatt  | gttgaatacg  | tgcgagcggg | aagaattgct  | 600 |
| ggagatacaa  | aatttaaatgg | atggaaaact  | tggaaatttag | cacttgaggg | tattacaagc  | 660 |
| ttttccacat  | tccctcttcg  | catctggaca  | tacatagggt  | tagtggtagc | cagtgtagca  | 720 |
| tttatttatg  | ggcgtggat   | gatttttagat | actatcatat  | ttggaaatgc | tgtaggggga  | 780 |
| tatccttcac  | tacttggttc  | aatactgttt  | ttaggtggaa  | ttcagatgat | tggaatagga  | 840 |
| gtatttaggtg | aatatattgg  | acgcacatac  | attgaaacca  | aaaaacgccc | gaaatacatc  | 900 |
| atcaagagag  | tcaaaaaatg  | a           |             |            |             | 921 |

&lt;210&gt; 116

&lt;211&gt; 1332

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 116

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| atgaataaag  | caataaaagt  | atcattgtat | atatcttttg | ttttgattat | ttgcgcctta  | 60  |
| tctaataaaca | taatgatgtt  | aaatacatct | gatttcggaa | gagccattaa | gccattaatt  | 120 |
| gaagacatac  | cagcattttac | atatgactta | cctttattgt | ataaattgaa | aggatcatatt | 180 |

|             |             |             |            |             |            |      |
|-------------|-------------|-------------|------------|-------------|------------|------|
| gattcaattg  | atagctatga  | gtatataagt  | tcatatagtt | atattttgta  | tacatacgtc | 240  |
| ctggtttatta | gcattttttac | tgaatatctt  | gatgctaggg | tggtatcgtt  | atttctaaaa | 300  |
| gtaatatata  | tttatttcatt | atatgcgata  | tttacttcat | atataaaaaac | agaaaaggat | 360  |
| gtaacctttt  | ttacattctt  | tatttttagct | tttcttatgt | gttcttcatc  | aacctgtgca | 420  |
| atggttgcat  | cattctatca  | agagcaata   | gttataattt | tccttccatt  | tttggtgat  | 480  |
| tcattaacat  | gcaaaaaaca  | taaatctatg  | cttttgctat | tttttctgtt  | gctaataata | 540  |
| tctactgcta  | aaaatcaatt  | tatattaacc  | ccactaatag | tgtattcata  | ttatatTTTT | 600  |
| tttgatagac  | acaaactaat  | tattaaatct  | gtaatatgcg | tggtgtgctt  | gcttgcgta  | 660  |
| atatttgcaa  | tatcttattc  | aaaagggtgt  | gttgaattaa | ataagtacca  | tgcaacatac | 720  |
| ttcggtagtt  | atctttatat  | gaaaaacaac  | gggtataaaa | tgccatcgta  | tggtgatgat | 780  |
| aagtgtgttg  | ggtagatgc   | ctggggtaat  | aaattcgaca | tatcatttgg  | cgcaacccca | 840  |
| acagaagttg  | gaacggaatg  | tttcgaatct  | cataaagatg | aaacgttttc  | gaatgcactc | 900  |
| tttttattgg  | ttagcaaac   | aagcaccatc  | ttcaaaactc | catttgatga  | tggtgtgatg | 960  |
| tctcagtata  | aagaaaatta  | tttccatgta  | tataaaaaac | tacacgtaat  | atatggagaa | 1020 |
| tcaaacatac  | taacgactat  | tactaacata  | aaagacaata | tatttaaaaa  | cattagattt | 1080 |
| atatcattgt  | tattattttt  | tattgcttct  | atttttatta | gaaataataa  | aataaaggca | 1140 |
| tctttatttg  | tagtatctct  | ttttggaata  | tctcaatttt | atgtgtcatt  | tttcggggaa | 1200 |
| ggatataagag | atttaagcaa  | gcattttatt  | ggaatgtatt | tttcggtcga  | cctttgctta | 1260 |
| tacataacag  | tcgttttttt  | aatttataaa  | ataattcaaa | gaaatcaaga  | caatagcgat | 1320 |
| gtaaagcact  | aa          |             |            |             |            | 1332 |

<210> 117  
 <211> 249  
 <212> DNA  
 <213> E. Coli

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| atgggcattc | tgcatggat  | tatttttggg | cttattgccg | gtattctggc | gaagtggatc  | 60  |
| atgccaggta | aagatggagg | tggtattctt | atgactatcc | tgctggggat | agtcgggtgcc | 120 |
| gtagtcggcg | gatggatcag | cacgctgttt | ggctttggta | aagtcgatgg | cttcaatttt  | 180 |
| ggcagcttcg | tggttgccgt | tattggtgcg | attgtcgtgc | tatttatcta | caggaagatt  | 240 |
| aaaagttaa  |            |            |            |            |             | 249 |

<210> 118  
 <211> 183  
 <212> DNA  
 <213> E. Coli

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| atgggcataag | caacgtatac | cgtgaccgtc | accaataaca | gcaatggcgt | ttctgtcgat | 60  |
| tatgaacag   | agacgccgat | gactttgctg | gtgccagaag | tgccggctga | agtgataaaa | 120 |
| gatctggtga  | ataccgtacg | ttcttatgac | acggaaaacg | aacatgatgt | ttgtggttgg | 180 |
| taa         |            |            |            |            |            | 183 |

<210> 119  
 <211> 360  
 <212> DNA  
 <213> E. Coli

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgcttcaaa | tcccacagaa | ttatattcat | acgcgctcaa | cgcttttctg | gaataaacia | 60  |
| actgcacctg | ccggaatatt | cgaacgtcat | cttgataaag | gaacgcgcc  | gggggtttac | 120 |
| ccacgccttt | ccgttatgca | tggggcggtc | aaatatctcg | gctacgctga | tgaacacagt | 180 |
| gcagagcctg | atcaggtgat | ccttatcgaa | gcggggcagt | ttgcggtgtt | ccctccagaa | 240 |
| aagtggcaca | acattgaagc | catgactgac | gatacttatt | tcaacattga | cttcttcgtg | 300 |
| gctcctgaag | tcctgatgga | aggtgcgcaa | caacggaaa  | tcattcataa | cgggaaatga | 360 |

<210> 120  
 <211> 741  
 <212> DNA  
 <213> E. Coli

&lt;400&gt; 120

|             |            |             |             |            |             |     |
|-------------|------------|-------------|-------------|------------|-------------|-----|
| gtgaagtcca  | aagttatcgc | cctggcgcca  | ttaatgggta  | ttagcgggat | ggcagcgag   | 60  |
| gctaacgaat  | tgccgatgg  | accgcataatt | gtcacctccg  | gtacggcaag | cgtggatgag  | 120 |
| gtgccagaca  | ttgccactct | tgcgattgaa  | gttaacgtgg  | ccgcgaagga | tgccgctact  | 180 |
| gccaaagaaac | aggcagatga | gcgcgtcgca  | caatacatatt | ccttccttga | actcaatcag  | 240 |
| atcgcgaaaa  | aagatatcag | ctcagcgaac  | ttacgcaccc  | agccagatta | tgattatcag  | 300 |
| gatggtaaaa  | gtatccttaa | aggctacgcg  | gctgtgagaa  | cggtggaagt | cacgctccgt  | 360 |
| cagttagaca  | aactgaattc | cttgctggat  | ggcgcgctga  | aggcgggtct | taacgaaatt  | 420 |
| cgttctgtgt  | cgctgggctg | ggcgagccg   | gatgcctata  | aagacaaagc | gcgtaaaggca | 480 |
| gcgattgata  | acgcgattca | tcaggcgag   | gaactggcga  | acggctttca | tcgtaaactg  | 540 |
| ggcccggtat  | atagcgtgcg | ctaccatgtt  | tccaactatc  | agcccagccc | aatggtgcgg  | 600 |
| atgatgaaag  | ccgatgccgc | gccggtgtcc  | gcccaggaaa  | cttacgagca | ggccgctatt  | 660 |
| cagtttgatg  | atcaggtcga | tgtggtcttc  | cagttagaac  | ctgtggatca | acaaccgcgt  | 720 |
| aaaacacctg  | cagcacaata | a           |             |            |             | 741 |

&lt;210&gt; 121

&lt;211&gt; 1395

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 121

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| gtgttattac | tggtgcgtg   | ctcgcaaatg  | tgcccgtcat  | tcagacgatt  | ccagacagtg  | 60   |
| tttcataatt | cctccatttt  | tctcccttat  | tggtggcta   | cactagtatc  | attccgcgaa  | 120  |
| acgtttcagg | aagagaaact  | cttaacgatg  | aaaggtagtt  | ataaatcccg  | ttgggtaatc  | 180  |
| gtaatcgtgg | tggttatcgc  | cgccatcgcc  | gcattctggt  | tctggcaagg  | ccgcaatgac  | 240  |
| tcccggagtg | cagccccagg  | ggcgacgaaa  | caagcgagc   | aatcgccagc  | gggtggtcga  | 300  |
| cgtggtatgc | gttccggccc  | attagccccg  | gttcaggcgg  | cgaccgcccgt | agaacaggca  | 360  |
| gttcgcggtt | acctcacccg  | gcttggcacc  | attaccgccc  | ctaataccgt  | tacggtgcgc  | 420  |
| agccgcgtgg | acggccaaact | gatagcggtta | catttccagg  | aaggccagca  | ggtcaaagca  | 480  |
| ggcgatttac | tggcagaaat  | tgaccccgag  | cagttcaaaag | ttgcattagc  | acaagcccag  | 540  |
| ggccaaactg | caaaaagataa | agccacgctt  | gccaaacgccc | gccgtgacct  | ggcgcggtat  | 600  |
| caacaactgg | caaaaaaccaa | tctcgtttcc  | cgccaggagc  | tggtgcccc   | acaggcgctg  | 660  |
| gtcagtgaag | ccgaaggcac  | cattaaggct  | gatgaagcaa  | gcgttgccag  | cgcgagctg   | 720  |
| caactcgact | ggagccggat  | taccgcacca  | gtcgatggtc  | gcgttggtct  | caagcagggt  | 780  |
| gatgttgta  | accaaactct  | cagtgtgtat  | accaccggga  | tcgtgtgtat  | caccagagc   | 840  |
| catcctatcg | atttagtctt  | taccctgccc  | gaaagcgata  | tcgctaccgt  | agtgcaggcg  | 900  |
| cagaaagccg | gaaaaccgct  | ggtggtagaa  | gcctgggac   | gcaccaactc  | gaagaaatta  | 960  |
| agtgaaggca | cgctgttaag  | tctagataac  | caaatcgatg  | ccactaccgg  | tacgattaaa  | 1020 |
| gtgaaagcac | gctttaataa  | tcaggatgat  | gcgctgtttc  | ccaatcagtt  | tgtaaagcg   | 1080 |
| cgcatgttag | tcgacaccga  | acaaaacgcc  | gtagtgtacc  | caacagccgc  | cctgcaaatg  | 1140 |
| ggcaatgaag | gccattttgt  | ctgggtgctg  | aatagcgaaa  | acaaggtcag  | caaacatctg  | 1200 |
| gtgacgcggg | gcatttcagga | cagtcagaaa  | gtggtgatcc  | gtgcaggat   | ttctgcgggc  | 1260 |
| gatcgcgtgg | tgacagacgg  | cattgatcgc  | ctgaccgaag  | ggcggaaggt  | ggaagtgggtg | 1320 |
| gaagcccaga | gcgccactac  | tccggaagag  | aaagccacca  | gccgcgaata  | cgcgaaaaaa  | 1380 |
| ggagcacgct | cctga       |             |             |             |             | 1395 |

&lt;210&gt; 122

&lt;211&gt; 3123

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 122

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| atgcaggtgt | tacccccgag | cagcacaggc | ggcccgtcgc | gcctgtttat  | tatgcgtect | 60  |
| gtggccacca | cgctgctgat | ggtggcgatc | ttactcgccg | ggattatcgg  | ttatcgcgcc | 120 |
| ctgcccgttt | cgcgctgcc  | ggaagtggac | tatccgacca | ttcagtggtg  | cacgctctac | 180 |
| ccaggtgcc  | gcccggatgt | catgacctct | gccgttaccg | cgccgctaga  | acgccagttc | 240 |
| gggcagatgt | ctggcctgaa | acagatgtcg | tcgcaaaagt | ccggcggtgc  | gtcagttatc | 300 |
| actttgcagt | tccagctaac | attaccgctc | gatgtcgccg | agcagggaagt | gcaggccgag | 360 |
| attaacgctg | cgaccaactt | gttgcgagc  | gatctgccta | acccgcccgt  | ttacagcaaa | 420 |
| gtgaaccggg | cagatccgcc | gatcatgacg | ctcgccgtca | cctcaaccgc  | catgccgatg | 480 |

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| acgcaagtgg  | aagatatggt  | ggaacccgc   | gtcgcgcaga  | aaatctcgca  | gatttccggc  | 540  |
| gtcggcctgg  | tgacgctttc  | cggcggtcag  | cgteccggctg | ttcgcgtcaa  | acttaacgct  | 600  |
| caggcgattg  | ccgcccctcg  | cctgaccagc  | gaaaccgtgc  | gcaccgccat  | taccggcgct  | 660  |
| aacgttaact  | cgcaaaaagg  | tagcctcgac  | ggcccttccc  | gtgcgggtcac | gctttccgcg  | 720  |
| aacgaccaga  | tgcaatccgc  | cgaagagtat  | cgccagctaa  | tcacgccta   | ccagaacggc  | 780  |
| gcgccaattc  | gtctgggcga  | tgctgcgaact | gtagagcaag  | gtgcagaaaa  | cagctggctc  | 840  |
| ggcgcggtgg  | cgaacaaaga  | acaggccatt  | gtgatgaatg  | ttcagcgcca  | gcccgggtgct | 900  |
| aacattatct  | ccaccgcccga | cagcattcgg  | cagatgctgc  | cacagctcac  | tgagagtctg  | 960  |
| ccgaaatcgg  | tgaaggtgac  | agtgtttcc   | gatcgacca   | ccaatatccg  | cgcattccgtc | 1020 |
| gatgatactc  | agtttgaatt  | gatgatggct  | atcgcgctgg  | tagtcatgat  | tatctacctg  | 1080 |
| tttttgcgca  | atattccggc  | gacccatcatt | cccgggtgtg  | ctgtaccgct  | gtcgttaatc  | 1140 |
| ggcactttcg  | cggttatggt  | gtttctcgat  | ttttcaatca  | ataacctgac  | actgatggcg  | 1200 |
| ttactatcgc  | ccaccggatt  | cgtggtcgat  | gacgccatcg  | tggtgatcga  | aaacatttcc  | 1260 |
| cgctatatcg  | aaaaagcgga  | aaaaccgttg  | gcggcgggcg  | tcaagggcg   | agggtgaaatc | 1320 |
| ggctttacca  | ttatctcgct  | gacctttcca  | ctgattgcgg  | tggtgatccc  | actgctgttt  | 1380 |
| atggggcgata | tcgtcggcgg  | actgttccgc  | gaatttgcta  | ttacctggc   | ggtagcgatt  | 1440 |
| ttgatctcag  | cgggtggtgc  | gtgacctgc   | acaccgatga  | tggtcgcgcg  | gatgctcagc  | 1500 |
| caggagtctg  | tgctgaaaca  | gaaccgcttc  | tcocgtgcct  | cgaaaaaat   | gttcgacagg  | 1560 |
| ataatcgccg  | cctatggtcg  | tggaactggc  | aaagtgtctga | atcatccgtg  | gctgacctta  | 1620 |
| agcgtggcac  | tcagcacgct  | gctgcttagc  | gtgctgtgtg  | gggtgttcat  | tccgaaagg   | 1680 |
| ttcttcccg   | tacaggacaa  | tggcattatt  | cagggcactt  | tgcaaggcac  | gcaatccagc  | 1740 |
| tcctttgcc   | atatggccca  | gcgacaacgc  | caggtcgcgg  | acgtgatttt  | gcaggatccg  | 1800 |
| gcagtgcaca  | gcctgacctc  | atgtgttggc  | gttgatggca  | ctaaccgctc  | gctgaacagt  | 1860 |
| gcacgtttac  | aaatcaacct  | caaaccgttg  | gatgaacgtg  | atgatcgggt  | gcaaaaagtc  | 1920 |
| atcgcccgct  | tgcaaacggc  | ggtagataaa  | gtgccggcg   | tcgatctctt  | cctgcaacca  | 1980 |
| acgcaggatc  | tgactattga  | tactcaggtc  | agccgcaccc  | agtaccagtt  | taccttgacg  | 2040 |
| gccacgtcac  | tggtgctgct  | cagtacctgg  | gtgccacagt  | tgatggaaaa  | actccagcaa  | 2100 |
| ctgccacagc  | ttctgatgt   | ctccagcgac  | tgccaggaca  | aagggtggt   | ggcgtatgtc  | 2160 |
| aatgttgatc  | gcgacagcgc  | cagccgtctg  | gggatcagca  | tgccggatgt  | cgataacgcc  | 2220 |
| ctgtacaacg  | cgtttggtca  | gcggctgatt  | tccactattt  | atactcaggg  | caaccagtat  | 2280 |
| cgcgtggtg   | tggaagcaca  | caccgaaaa   | acccagggcc  | tcgcggcgct  | ggataccatt  | 2340 |
| cgccctgacca | gcagcgacgg  | cggcggtggg  | ccgctaagct  | caattgccaa  | aattgagcag  | 2400 |
| cgttttgccg  | cgtcttccat  | caaccatctg  | gatcagttcc  | cggtaacgac  | catctccttt  | 2460 |
| aacggtgccg  | ataactatc   | gctgggcgat  | gcggtgcagg  | cgattatgga  | caccgaaaa   | 2520 |
| acgctgaatc  | tgccggtgga  | tatcaccacg  | cagttccagg  | gcagcaccc   | gccttccag   | 2580 |
| tcggcgctgg  | gcagcactgt  | ctggctgatt  | gtcgcggcgg  | tggtggcgat  | gtatatcgtg  | 2640 |
| ctcgccattc  | tgtacgagag  | ctttattcac  | ccgatcacca  | ttctctcgac  | gctaccaccc  | 2700 |
| gcagggttgg  | gcgcactgct  | ggcggttctg  | attgctggta  | gcgaactgga  | tggtattgct  | 2760 |
| attatcgcca  | ttattttgct  | gatcggtatc  | gtgaagaaga  | acgccatcat  | gatgatcgac  | 2820 |
| ttcgcgctgg  | ctgctgagcg  | cgagcaaggc  | atgtcgccgc  | gcagggcaat  | ctaccaggct  | 2880 |
| tgctctgtgc  | gttttcgtcc  | gacccctgat  | accactctgg  | cgctctgct   | tgccgcgctg  | 2940 |
| ccgctgatgt  | tgagtaccgg  | ggtcggcgcg  | gaactgcgtc  | gtccgttagg  | tatcggcatg  | 3000 |
| gtcggcggtc  | tgattgtcag  | ccagggtgct  | acgctgttta  | ccacgccggt  | gatttatttg  | 3060 |
| ctgttcgacc  | gcctggcatt  | gtgggaccaa  | agccgctttg  | cccgtcatga  | agaggaggcg  | 3120 |
| taa         |             |             |             |             |             | 3123 |

&lt;210&gt; 123

&lt;211&gt; 3078

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 123

|            |             |            |             |             |            |     |
|------------|-------------|------------|-------------|-------------|------------|-----|
| gtgaagtgtt | ttgccctctt  | catttaccgc | ccggtggcga  | cgattttact  | gtcggttgcc | 60  |
| attacctgt  | gcggcatact  | gggttccgt  | atgctgccgg  | tcgccccgct  | gccgcaggtc | 120 |
| gattttccgg | tgattatcgt  | cagcgccctc | ctgcccgggtg | cgtaaccaga  | aacaatggcg | 180 |
| tcttccggtg | ccacgccgct  | ggagcgctca | cttggggcga  | ttgccggagt  | cagtgaatg  | 240 |
| acctccagca | gttcgctcgg  | cagcacgctg | attattttgc  | agtttgattt  | tgaccgggat | 300 |
| atcaacggcg | cagcgcggtga | tgtagcggcg | gcgatcaacg  | ctgcacaaag  | tttgcgtccc | 360 |
| agtgggatgc | ccagccggcc  | gacctatcgc | aaagcgaacc  | cgtcggatgc  | gccaattatg | 420 |
| atcttcacgc | tgacgtccga  | tacttattcg | cagggtgaac  | tgtaacgattt | gcctcgacg  | 480 |
| cagctggctc | cgacgatttc  | gcaaatcgac | ggtgttgggt  | atgtcgatgt  | cggaggcagc | 540 |

|             |            |             |             |             |            |      |
|-------------|------------|-------------|-------------|-------------|------------|------|
| tcaactgcccg | ccgtacgcgt | cgggctgaat  | ccgcaggcgc  | tgtttaatca  | gggcgtgtcg | 600  |
| ctggacgacg  | tacgcaccgc | cgtcagcaat  | gccaacgtgc  | gtaaacgcga  | gggcgcgctg | 660  |
| gaagatggca  | ctcaccgctg | gcagatccag  | accaatgatg  | agctaaaaac  | cggcgtgaa  | 720  |
| tatcagccgt  | tgattattca | ctacaacaac  | ggcggcgcgg  | ttcgtctggg  | cgatgtggcg | 780  |
| acggtgaccg  | actcagtgca | ggatgtgcgc  | aacgccggga  | tgaccaacgc  | caaaccggct | 840  |
| attttactga  | tgatccgcaa | actgccggaa  | gccaatatta  | tccagacggt  | tgacagcatc | 900  |
| cgggcacaaa  | taccggagtt | gcaggaacc   | attccggcgg  | cgattgatct  | gcaaatgtcc | 960  |
| caggatcgct  | ccccaccat  | tcgcgcctcg  | ctggaagaag  | tcgagcaaac  | gctgattatc | 1020 |
| tcgggtggcg  | tggtgattct | ggtggtgttt  | ttattcctgc  | gctcgggtcg  | cgccactatt | 1080 |
| attcccgccg  | tttcggtgcc | ggtttcgtcg  | attggtacgt  | ttgcggcgat  | gtacctgtgc | 1140 |
| ggattcagtc  | tcaataacct | ttcgttaatg  | gcgctcacca  | tcgctactgg  | ttcgtgggtg | 1200 |
| gatgacgcc   | tcgtggtgct | ggaaaacatt  | gcacgtcatc  | tggaagcggg  | aatgaaaccg | 1260 |
| ttgcaagccg  | cactgcaagg | tactcgcgaa  | gtcggtttta  | cgtggtgtgc  | gatgagtcgt | 1320 |
| tcactgggtg  | cgggtttcct | gcgcgtgctg  | ttgatgggcg  | gattgccggg  | ccgactgtta | 1380 |
| cgcgaaattg  | ccgtgacgct | ttctgtcgcc  | attggtatat  | cgttgctggg  | ttctctgaca | 1440 |
| ttaacgcgaa  | tgatgtgtgg | ctggatgctg  | aaagccagca  | agccgcgcga  | gcaaaagcga | 1500 |
| ctgcgtgggt  | ttggtcgcat | gttggtagcc  | ctgcaacaag  | gctacggcaa  | gtcactaaaa | 1560 |
| tggtgtctca  | atcatacccg | ttcgtgtggc  | gtggtgtctg  | ttggcaccat  | tgcgctgaat | 1620 |
| atctcggtgt  | atatctcgat | cccgaaaaac  | ttcttcccgg  | agcaggacac  | tggtgtgttg | 1680 |
| atggggcgga  | ttcaggcgga | tcagagtatt  | tcgtttcagg  | cgatgcgcgg  | taagtgtcag | 1740 |
| gatttcattga | aaattatccg | tgacgatccg  | gcagtgata   | atgtcacccg  | ctttacaggc | 1800 |
| ggttcgcgag  | tgaacagcgg | gatgatgttt  | atcacctcca  | agccacgcga  | cgaacgcagc | 1860 |
| gaaacggcgc  | agcaaatat  | cgaccgtctg  | cgcgtaaaac  | tgcgcaaaaga | accggggcg  | 1920 |
| aatctgttcc  | tgatggcggg | acaggatatt  | cgcgttggtg  | ggcgtcagtc  | gaacgccagc | 1980 |
| taccagtaca  | cgttgttata | cgacgacctg  | gcggcactgc  | gagaatggga  | gccgaaaaac | 2040 |
| cgcaaaaaac  | tggtgacgtt | gccggaaactg | gcggacgtga  | actccgatca  | gcaggataac | 2100 |
| ggcgcggaga  | tgaatctggt | ttacgaccgc  | gacaccatgg  | cacggctggg  | aatcgacgta | 2160 |
| caagccgcga  | acagtctgtt | aaataacgcc  | ttcggtcagc  | ggcaaatctc  | gaccatttac | 2220 |
| cagccgatga  | accagtataa | agtgtgtgat  | gaagtggatc  | cgcgtataac  | ccaggacatc | 2280 |
| agtgcgtcgg  | aaaaaatgtt | cgttatcaat  | aacgaaggca  | aagcgatccc  | gctgtcgtat | 2340 |
| ttcgtcaaat  | ggcaaccggc | gaatgcccc   | ctatcggtga  | atcatcaggg  | attatcggcg | 2400 |
| gcctcgacca  | tttcgtttta | cctgccgacc  | ggaaaaatgc  | tctcggacgc  | cagtgcggcg | 2460 |
| atcgatcgcg  | caatgaccca | gcttggtgtg  | ccttcgacgg  | tgccgcggcag | ttttgccggc | 2520 |
| acggcgcagg  | tggtccagga | gacgatgaac  | tcgcagggtga | tcctgattat  | cgcggccatc | 2580 |
| gccacggtgt  | atatcgtgct | gggtatcctt  | tacgagagtt  | acgtacatcc  | gctgacgatt | 2640 |
| ctctccaccc  | tgccctcggc | gggcgttgga  | gcgctgttgg  | cgtcggagct  | gttcaatgcc | 2700 |
| ccgttcagcc  | taatcgccct | gataggatc   | atgctattaa  | tcggcatcgt  | gaagaaaaac | 2760 |
| gccattatga  | tggtcgattt | tgcgcttgaa  | gccccaacggc | acggtaacct  | gacgccgcag | 2820 |
| gaagctattt  | tccaggcctg | tctgtctgct  | tttcgcccga  | ttatgatgac  | taccctggcg | 2880 |
| gcgctgtttg  | gtgcgctgcc | gctggtattg  | tcgggcggcg  | acggctcgga  | gctgcggcaa | 2940 |
| ccctcgggga  | tcaccattgt | cggcggactg  | gtaatgagcc  | agctccttac  | gctgtatacc | 3000 |
| acgcgggtgg  | tgtatctctt | tttcgaccgt  | ctgcggctgc  | gtttttcgcg  | taaacctaaa | 3060 |
| caaacggtaa  | ccgagtaa   |             |             |             |            | 3078 |

&lt;210&gt; 124

&lt;211&gt; 1416

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 124

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| atgacagatc  | ttcccagacg | caccggttgg | caattgtgga | ttgtggcttt  | cggtctcttt  | 60  |
| atgcagtcgc  | tggaaccac  | catcgtaaac | accgcccttc | cctcaatggc  | gcaaaagcctc | 120 |
| ggggaaagtc  | cgttgcatat | gcacatggtc | attgtctctt | atgtgctgac  | cgtggcgggtg | 180 |
| atgtgccccg  | ccagcggctg | gctggcggac | aaagtcggcg | tgcgcaatat  | tttctttacc  | 240 |
| gccatcgtgc  | tgtttactct | cggttcactg | ttttgcgcgc | tttccggcac  | gctgaaacgaa | 300 |
| ctgttgctgg  | caecgcgctt | acagggcgtt | ggcggcgcga | tgatgggtgcc | ggtcggcgaga | 360 |
| ttgacgggtga | tgaaaatcgt | accgcgcgag | caatatatgg | cggcgatgac  | ctttgtcacg  | 420 |
| ttaccgggtc  | aggtcgggtc | gctgctcggt | ccggcgcctc | gcggctcgtc  | ggtggagtac  | 480 |
| gcatcgtggc  | actggatctt | tttgatcaac | attccgggtg | ggattatcgg  | tgcgatcgcc  | 540 |
| acattgctgt  | taatgccgaa | ctacacatg  | cagacgcggc | gctttgatct  | ctccgatttt  | 600 |
| ttattgtctg  | cggttggcat | ggcgttatta | accctggcgc | tggaacggcag | taaaagtaca  | 660 |



|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| gggttatcgc | cgctgacgat  | tgcaggcctg  | gtcgcagttg  | gcgtgggtggc | actgggtgctt | 720  |
| tatctgctgc | acgccagaaa  | taacaaccgt  | gccctgttca  | gtctgaaact  | gttccgtact  | 780  |
| cgtacctttt | cgctgggcct  | ggcggggagc  | tttgccggac  | gtattggcag  | tggcatgttg  | 840  |
| ccctttatga | caccgggttt  | cctgcaaat   | ggcctcggtt  | tctcgccgtt  | tcatgccgga  | 900  |
| ctgatgatga | tcccgatggg  | gcttggcagc  | atgggaatga  | agcgaattgt  | ggtacaggtg  | 960  |
| gtgaatcgct | ttggttatcg  | tccgggtactg | gtagcgacca  | cgctgggtct  | gtcgtggtc   | 1020 |
| acccgtgtgt | ttatgactac  | cgcctgtctg  | ggctgggtact | acgttttgcc  | gttcgtcctg  | 1080 |
| tttttacaag | ggatgggtcaa | ctcgacgcgt  | ttctcctcca  | tgaacaccct  | gacgtgaaa   | 1140 |
| gatctcccg  | acaatctggc  | gagcagcggc  | aacagcctgc  | tgtcgatgat  | tatgcaattg  | 1200 |
| tcgatagata | tccgggtcac  | tatcgccggg  | ctgttgctgg  | gactttttgg  | ttcacagcat  | 1260 |
| gtcagcgctg | acagcggcac  | cacacaaacc  | gtctttatgt  | acacctggct  | tagcatggcg  | 1320 |
| ttgatcatcg | cccttcgggc  | gttcattctt  | gccagagtgc  | cgaacgatac  | gcatcaaaat  | 1380 |
| gtagctattt | cgcggcgaaa  | aaggagcgcg  | caatga      |             |             | 1416 |

<210> 125  
 <211> 1035  
 <212> DNA  
 <213> E. Coli

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| <400> 125   |             |             |            |             |             |      |
| atggaaattc  | gcataatgct  | atttatatta  | atgatgatgg | ttatgcctgt  | gagctatgcg  | 60   |
| gcatgttata  | gtgagttatc  | tggtcagcac  | aacttggttg | ttcaggggga  | ttttgcaactt | 120  |
| actcaaacac  | aaatggcgac  | atatgagcat  | aattttaatg | attcgatcatg | cgtaagtaca  | 180  |
| aatactatca  | cccctatgag  | cccgtcggat  | attattgttg | gactttataa  | cgataccata  | 240  |
| aaattaaatt  | tacattttga  | atggaccaat  | aaaaacaaca | tcacgttgctc | aaataatcag  | 300  |
| accagtttca  | ccagtgggta  | ttcagttacg  | gtgacacctg | cggccagtaa  | tgcaaaagtg  | 360  |
| aatgtttctg  | cggggggcgg  | cgggttcagtg | atgattaatg | gtgttgcgac  | attatccagt  | 420  |
| gcttcatcat  | cgacacggcg  | gagtgccgca  | gtacaatttc | tactgtgttt  | attaggtggc  | 480  |
| aaagtcatggg | atgcatgtgt  | aaatagctac  | agaaatgcat | tgccacaaaa  | tgcaaggtgtc | 540  |
| tattccttta  | atctgacatt  | gtcatacaac  | ccgataacca | caacctgcaa  | accggacgat  | 600  |
| ttatttaata  | ctttagacag  | tattcccgtt  | tcacaattac | cagccacagg  | taacaaagca  | 660  |
| acaataaata  | gtaaacagg   | ggatattatt  | ctgcgttgta | aaaattttatt | aggtaacaaa  | 720  |
| aatcaaacat  | cacggaaaat  | gcagggtgat  | ttatcaagtt | ctgacttggt  | aaccaacagc  | 780  |
| aacacaatac  | tgaaagggtgc | ggaagataat  | ggcgtaggat | ttattcttga  | aagtaatggt  | 840  |
| tcgccagtea  | cactttttaa  | tatcactaac  | agcagtaaa  | gatatacaaa  | tttaaaaggaa | 900  |
| gttgccggcga | agtcaaaact  | tacagataca  | acggtttcaa | ttccgataac  | agccagttac  | 960  |
| tacgtctacg  | atacaaacaa  | agttaaatct  | ggcgcaactg | aggcaaccgc  | attaatcaac  | 1020 |
| gtgaaatac   | actaa       |             |            |             |             | 1035 |

<210> 126  
 <211> 2481  
 <212> DNA  
 <213> E. Coli

|             |             |            |            |             |             |     |
|-------------|-------------|------------|------------|-------------|-------------|-----|
| <400> 126   |             |            |            |             |             |     |
| atgttgagaa  | tgaccccaact | tgcacagca  | atcgtagcgt | tattgctcgg  | cattgaagct  | 60  |
| tatgcagctg  | aagaaacctt  | tgatacccat | tttatgatag | gtggaatgaa  | agaccagcag  | 120 |
| gttgcaata   | ttcgtcttga  | tgataatcaa | cccttaccgg | ggcagtatga  | catcgatatt  | 180 |
| tatgtcaata  | agcaatggcg  | cgggaaatat | gagattattg | ttaaagacaa  | cccgaagaa   | 240 |
| acatgtttat  | caagagaaagt | tatcaagcgg | ttaggcatta | atagcgataa  | cttcgccagc  | 300 |
| ggtaagcaat  | gtttaacatt  | tgagcaactt | gttcagggtg | ggagctatac  | ctgggatatac | 360 |
| gggggttttc  | gtctcgattt  | cagtgtcccg | caggcctggg | tggaagaact  | ggaaagtggc  | 420 |
| tatgttccac  | cggaaaaactg | ggagcggggg | attaatgcgt | tttatacctc  | ttattatctg  | 480 |
| agtcagtatt  | acagcgacta  | taaaagcgtc | ggtaataaca | agagtacata  | tgtacgtttt  | 540 |
| aacagcgggt  | taaaatttact | gggttgga   | ctgcattctg | atgccagttt  | cagtaaaaca  | 600 |
| aataacaatc  | caggggtgtg  | gaaaagcaat | accctgtatc | tggaacgtgg  | atttgcccaa  | 660 |
| cttctcggca  | cgcttcgcgt  | gggtgatatg | tacacatcaa | gcgatatttt  | tgattctgtt  | 720 |
| cgcttcagag  | gtgtgcggtt  | gtttcgtgat | atgcagatgt | tgccataactc | gaaacaaaat  | 780 |
| tttacgccac  | gggtgcaggg  | gattgctcag | agtaacgcgc | tggttaactat | tgaacagaat  | 840 |
| ggttttgtgg  | tttatcagaa  | agaggttcc  | cctggcccgt | tcgcgattac  | agatttgag   | 900 |
| ttggccgggtg | gtggagcaga  | tcttgatgtc | agcgtgaaa  | aggcggaacg  | ctcggtaacc  | 960 |

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| acctatctgg  | tgccttatgc  | agcgggtgcca | aatatgctgc | aacccggcgt  | gtcgaatat   | 1020 |
| gatttagcgg  | cggttcgtag  | ccatattgaa  | ggggcgagca | aacaaagtga  | ttttgtccag  | 1080 |
| gcggttatc   | agtaggttt   | taataattta  | ttgacgctgt | atggtggctc  | gatggtcgcg  | 1140 |
| aataattatt  | acgcgtttac  | tttgggggct  | ggctggaata | cacgcattgg  | tgccatttcc  | 1200 |
| gtcgatgcca  | ctaagtcgca  | tagtaaaca   | gacaacggcg | atgtgtttga  | cgggcaaat   | 1260 |
| tatcaaattg  | cctacaacaa  | atattgtgagc | caaacgtcga | cgcgttttgg  | tctggcggcc  | 1320 |
| tggcgttatt  | cgctcgctga  | ttaccggaca  | tttaacgac  | acgtttgggc  | aaacaataaa  | 1380 |
| gataattatc  | gccgtgatga  | aaacgatgtc  | tatgacattg | ccgattatta  | ccagaacgat  | 1440 |
| tttggccgca  | aaaatagctt  | ttccgccaat  | atgagccagt | cattgccaga  | aggttggggg  | 1500 |
| tctgtgtcat  | taagtacgtt  | atggcgagat  | tactgggggc | gtagcggcag  | tagtaaggat  | 1560 |
| tatcagttga  | gttattccaa  | caacctgcga  | cgataaagct | ataccctcgc  | ggcaagccag  | 1620 |
| gcttatgacg  | agaatcatca  | tgaagagaaa  | cgttttaata | tttttatatc  | gattcccttt  | 1680 |
| gattgggggtg | atgacgtttc  | gacgcctcgt  | cggaataat  | atatgtctaa  | ctcaacgacg  | 1740 |
| tttgatgatc  | aggggtttgc  | ctcaataat   | acgggattat | caggaacagt  | agggagtcgg  | 1800 |
| gatcagttca  | attatggtgt  | caacctgagt  | catcaacatc | agggaaatga  | aacgacagct  | 1860 |
| ggggcggaatt | tgacctggaa  | cgcccggtt   | gcgacagtga | atggcagttta | tagtcagtcg  | 1920 |
| agtaacttatc | gacaggtctg  | agccagtgtt  | tcagggggca | ttgtcgcttg  | gtcgggtggc  | 1980 |
| gttaactctg  | cgaaaccgtct | ttccgaaacg  | tttgcgtgta | tgaatgcgcc  | aggaattaaa  | 2040 |
| gatgcttatg  | tcaatgggca  | aaaatatcgc  | acaacaaacc | gtaatggagt  | ggtgatatac  | 2100 |
| gacggataga  | caccttatcg  | ggaaaaatcac | ctgatgctgg | atgtgtcgca  | aagcgatagc  | 2160 |
| gaagcagaaat | tacgtggcaa  | ccggaaaatt  | gccgccctt  | atcgccgcgc  | ggttgtagctg | 2220 |
| gttaattttg  | ataccgatca  | gcgcaagcca  | tggtttataa | aagcgttaag  | agcagatggg  | 2280 |
| caatcattaa  | cgtttgggta  | tgaagtcaat  | gatatccatg | gtcataatat  | tggcgttgct  | 2340 |
| ggccagggaa  | gtcagttatt  | tattcgacac  | aatgaagtac | cgccatcggt  | taatgtggca  | 2400 |
| attgataagc  | aacaaggact  | ttcatgcaca  | atcaccttcg | gtaaagagat  | tgatgaaagt  | 2460 |
| agaaattata  | tttgccagta  | a           |            |             |             | 2481 |

&lt;210&gt; 127

&lt;211&gt; 720

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 127

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| atggccgcta | tcccattggcg | gccttttaat | ttaagaggca | ttaaaatgaa | aggattatta  | 60  |
| tctttactca | ttttttctat  | ggtccttct  | gcacatgccg | gaattgttat | ctacgggacg  | 120 |
| cgcattattt | acccggcaga  | aaataaagaa | gtgatgggtg | agttgatgaa | ccagggaaac  | 180 |
| cggttcttcg | tgtcgagcg   | gtggattgat | gatggcgata | cgctattacc | accagaaaaa  | 240 |
| attcaggttc | ctttcatggt  | aacgccacca | gtggcaaaaa | taggggcaaa | ttccgggcag  | 300 |
| caagtataaa | tcaaaattat  | gccgaataaa | ctgcccacta | ataaagaaag | cattttttat  | 360 |
| ctgaatgttc | tggaatttcc  | accaaatagt | ccagagcaag | aaggtaagaa | tgcaactgaag | 420 |
| tttgcgatgc | aaaacagaat  | taagttgttt | taccggccag | cgggtattgc | tccggtaaat  | 480 |
| aaagcgacat | ttaaaaaatt  | gctggtaaat | cgagtgggca | atggtttggt | gataaaaaat  | 540 |
| gactcagcta | attgggtgac  | gatttcggat | gtcaaagcta | ataatgtcaa | agtcaattat  | 600 |
| gaaactatta | tgattgcccc  | cttagaaagt | cagagtgtta | atgtcaaaag | taataatgca  | 660 |
| aataactggc | atctgaccat  | tatcgatgac | catggcaact | atattagtga | caaaatttaa  | 720 |

&lt;210&gt; 128

&lt;211&gt; 543

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 128

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| atgaaacgtt | caattattgc  | tgccgctgtc | ttttcttctt | tttttatgag | cgctggagta | 60  |
| tttgctgcag | acgttgatac  | cggaacatta | actattaagg | ggaatattgc | agaatctccg | 120 |
| tgtaaatctg | aagcgggtgg  | tgattcagta | agtattaata | tgccgactgt | accaaccagt | 180 |
| gtctttgaag | gtaaagctaa  | atattctacc | tatgatgatg | cagtcgggtg | aaccagcagc | 240 |
| atgttaaaaa | ttagctgccc  | gaaagaagtt | gctgggtgta | aactctcggt | gattaccaac | 300 |
| gataaaataa | ccggtaacga  | taaggcgata | gccagtagca | acgataccgt | gggttactat | 360 |
| ctctattttg | gtgataacag  | cgatgtcctg | gatgtttctg | caccttttaa | cattgagagt | 420 |
| tataaaacag | cggaagggtca | atatgctatt | ccgttttaag | caaaatacct | gaaactgaca | 480 |
| gataactcag | tgcaatcagg  | tgatgtgtta | tcttctcttg | ttatgcgtgt | ggcgcaggat | 540 |

taa

543

<210> 129  
 <211> 339  
 <212> DNA  
 <213> E. Coli

<400> 129

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgagttcag | agcgagatct | ggtaatttt  | cttggcgatt | tttcaatgga | tgtggccaaa | 60  |
| gcagttatag | ccggtggtgt | tgcaaccgct | attggaagtc | tggtctcttt | tgctctgtgt | 120 |
| agctttggct | ttccagtaat | tcttgtcggg | ggagcaattt | tactgacagg | gatagtgtgt | 180 |
| acagttgttt | taaatgaaat | cgatgctcaa | tgccatttat | cagaaaaatt | aaaatatgca | 240 |
| attagagatg | gactaaaacg | gcaacaggaa | cttgataaat | ggaaaaggga | aaacatgact | 300 |
| ccatttatgt | atgttcttaa | cactccaccc | gtgatatga  |            |            | 339 |

<210> 130  
 <211> 582  
 <212> DNA  
 <213> E. Coli

<400> 130

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| atgactgact | acctgttact  | gtttgtcggg | actgtactgg | tcaataactt | tgtactggtc  | 60  |
| aagtttctcg | gtctctgtcc  | gtttatgggg | gtttccaaaa | aactggaaac | cgcgatgggc  | 120 |
| atggggctcg | caacaacggt  | tgtgatgacg | ctggcgctta | tttgcgcctg | gcttatcgat  | 180 |
| acgtggattt | tgatcccaact | taatctgatt | tacctgcgca | ccctggcatt | tattctgggtg | 240 |
| attgctgtgg | tcgtgcagtt  | caccgagatg | gtgggtgcga | aaaccagccc | ggtgctttac  | 300 |
| cgctctgctg | ggattttttt  | gccgcttata | accaccaact | gtgcagtgtc | cggcgtggcg  | 360 |
| ttgctgaata | tcaatctcgg  | gcacaatttc | ttgcagtcgg | cgctgtacgg | tttttccgcc  | 420 |
| gctgtcggtt | tctcgctggt  | gatggtgtct | ttcgccgcca | tccgcgaacg | ccttgcgtgtg | 480 |
| gctgatgtcc | cggcaccttt  | tcgcggtaat | gccattgcgt | taattaccgc | aggtcttatg  | 540 |
| tctctggcct | ttatgggctt  | tagtggtttg | gtgaagttgt | aa         |             | 582 |

<210> 131  
 <211> 579  
 <212> DNA  
 <213> E. Coli

<400> 131

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| atgaatgcta | tctggattgc | cggttgcgcg | gtgagcctgc | tgggcctggc  | gtttggcgcc  | 60  |
| attctggggt | atgcctcccg | ccgtttttgc | gtggaagacg | atccggctcg  | tgagaaaaatt | 120 |
| gacgaaatct | taccgcagag | ccagtgtggt | cagtgcggtt | atcccggtcg  | tcgcccctac  | 180 |
| gcggaagcca | tcagctgtaa | cggtgaaaaa | atcaaccggt | gcgccccagg  | tggcgaagct  | 240 |
| gtgatgctaa | aaattgccga | gttgcttaat | gtcgagccgc | agccgctgga  | tggcgaagcg  | 300 |
| caagagataa | cgccctgcgc | gatggtggcg | gttattgatg | aaaaataactg | tattggctgc  | 360 |
| actaaatgta | ttcaggcggt | tccggtagac | gccatcggtg | gcgctacccg  | tgccatgcot  | 420 |
| acggtaatga | gtgatctctg | tacgggctgc | aatttatgtg | ttgatccgtg  | cccgacgcac  | 480 |
| tgcatctcgt | tgcaaccggt | cgcagaaaca | cctgactcct | ggaaatggga  | tctgaacacc  | 540 |
| attcccgctg | gtatcattcc | cgtggaacac | catgcttaa  |             |             | 579 |

<210> 132  
 <211> 2223  
 <212> DNA  
 <213> E. Coli

<400> 132

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgcttaagt | tattctctgc | attcagaaaa | aataaaatct | gggatttcaa | cggcggcatc | 60  |
| catccaccgg | agatgaaaac | ccagtccaac | ggtacaaccc | tcgcccaggt | acccttgccg | 120 |
| cagcgttttg | ttattccact | gaaacagcat | attggcgctg | aaggtgagtt | gtgcgttagc | 180 |
| gtcggcgata | aagtattgcg | cggcacggcg | cttaccgctg | gtcggggcaa | aatgctgcct | 240 |
| gttcacgcgc | ccacctcggt | taccgttacg | gctattgcgc | cccactctac | ggctcatcct | 300 |
| tcagctttag | ctgaattaag | cgtgattatt | gatgccgatg | gtgaagactg | ctggatcccg | 360 |

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| cgcgacggct  | gggcccatta  | tcgcactcgc  | agtcgcgaag  | agttaatcga  | gcgcatacat  | 420  |
| cagtttgggt  | ttgccgggct  | gggcggtgca  | ggattcccga  | caggcggttaa | attgcagggt  | 480  |
| ggcggagata  | agattgaaac  | gttgattatc  | aacgcgggctg | agtgcgagcc  | gtacattacc  | 540  |
| gccgatgacc  | gtttgatgca  | ggattgcgcg  | gctcaggctcg | tagaggggat  | tcgcattctt  | 600  |
| gcgcataatc  | tcgagccacg  | cgaattctt   | atcggcattg  | aagataacaa  | accgcaggcg  | 660  |
| atttccatgc  | tcgcgcgggt  | gctggcgac   | tctaacgata  | tttctctgcg  | ggtgattcca  | 720  |
| accaaaatc   | cttctggcgg  | tgctaaacaa  | ttaacctaca  | ttctgaccgg  | gaagcagggt  | 780  |
| ccacatggcg  | ggcggttcac  | cgatatcggc  | gtattaatgc  | aaaacgtcgg  | cactgcttat  | 840  |
| gcagtgaac   | gtgccgttat  | tgatggcgag  | ccgattaccg  | agcgtgttgt  | aaccttgact  | 900  |
| ggcgaagcaa  | tcgctcgccc  | gggcaacgtc  | tgggcacggc  | tggggacggc  | agtgcgtcat  | 960  |
| ttattgaatg  | atgccggatt  | ctgcccctct  | gccgatcaaa  | tggtgattat  | gggtggcccg  | 1020 |
| ctaattgggt  | ttaccttgcc  | atggctggat  | gtcccggctg  | taaagattac  | caactgtctg  | 1080 |
| ttggctccct  | ctgccaatga  | acttggcgaa  | ccacaggaag  | aacaaagctg  | catccgggtg  | 1140 |
| agcgccctgtg | ctgacgcctg  | ccctgcggat  | cttttgccgc  | aacagttgta  | ctgggttcagc | 1200 |
| aaaggtcagc  | aacacgataa  | agctaccacg  | cataacattg  | ctgattgcat  | tgaatgtggg  | 1260 |
| gcttgcgcgt  | gggtttgccc  | gagcaatatt  | cccctggctg  | aattatttccg | tcaggaaaaa  | 1320 |
| gctgaaattg  | cggtctattcg | tcaggaagaa  | aagcgcgcgc  | cagaagccaa  | agcgcgtttc  | 1380 |
| gaagcgcgc   | aggctcgtct  | ggagcgcgaa  | aaagcggctc  | gccttgaacg  | acataagagc  | 1440 |
| gcagccgttc  | aacctgcagc  | caaaagataa  | gatgcgattg  | ctgccgctct  | ggcgcgggtg  | 1500 |
| aaagagaaac  | aggcccaagg  | tacacagcct  | attgtgatta  | aagcgggcga  | acgcccggat  | 1560 |
| aacagtgcga  | ttattgcagc  | acgggaagcc  | cgtaaagcgc  | aagccagagc  | gaaacaggca  | 1620 |
| gaactgcagc  | aaactaacga  | cgcagcaacc  | gttgctgac   | cacgtaaaaa  | tgccgttgaa  | 1680 |
| gcagctatcg  | cccgcgcaaa  | agcgcgcaag  | ctggaacagc  | aacaggtctaa | tgccgaacca  | 1740 |
| gaacaacagc  | tcgatccgcg  | caaaagccgc  | gtcgaagccg  | ctattgccc   | tgccaaagcg  | 1800 |
| cgcaagctgg  | aacagcaaca  | ggctaattgcg | gaaccagaag  | aacaggtcga  | tcgcgcgcaa  | 1860 |
| gcccgcgtcg  | aagccgctat  | tgcccgtgcc  | aaagcacgca  | agctggaaca  | gcaacagggt  | 1920 |
| aatgccgagc  | cagaacaaca  | ggtcgatccg  | cgcaaaagcc  | ccgtcgaaagc | cgctattgcc  | 1980 |
| cgagccaaag  | cgcgcaaacg  | ggaacagcaa  | ccggctaattg | cggagccaga  | agaacagggt  | 2040 |
| gatccgcgca  | aagctgcccgt | cgaagcggtc  | attgcacgcg  | ccaaagcagc  | caagctggaa  | 2100 |
| caagcaacagc | ctaattgcgtg | accagaagaa  | caggttgatc  | cgcgcgcaagc | ggcagttgcc  | 2160 |
| gcccgtattg  | cccgcgctca  | ggccaaaaaa  | gcccgcacgc  | agaaggttgt  | aaacgaggac  | 2220 |
| taa         |             |             |             |             |             | 2223 |

<210> 133  
 <211> 1059  
 <212> DNA  
 <213> E. Coli

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| <400> 133   |             |             |            |             |             |      |
| atgggtattca | gaatagctag  | ctcccccttat | accataaacc | agcgcagac   | atcgcgcatt  | 60   |
| atgctgttg   | tggtgctcgc  | agccgtgccca | ggaatcgag  | cgcaactgtg  | gttttttgg   | 120  |
| tggtgtactc  | tcgttcagat  | ccgtgttgcca | tcggttagtg | ctctgttagc  | cgaagctctc  | 180  |
| gtactcaaac  | tacgcaagca  | gtcggtagcc  | gcaacgttga | aagataaactc | agcatttgctg | 240  |
| acaggcttat  | tgctggcgggt | aagtattccc  | cccctcgcgc | catgggtggat | ggtcgtgctg  | 300  |
| ggtacgggtg  | ttcgggtgat  | catcgctaaa  | cagttgtatg | gcggtctggg  | acaaaaccgc  | 360  |
| tttaatcccg  | caatgattgg  | ttatgtggtc  | ttactgatct | ccttccccgt  | gcagatgacc  | 420  |
| agctggttac  | cgccacatga  | aattgcggtc  | aacatccctg | gttttatcga  | cgccatccag  | 480  |
| gttattttta  | gcggtcatac  | cgccagtggt  | ggtgatatga | acacactacg  | cttaggtatt  | 540  |
| gatggcatta  | gtcaggcgac  | accgctggat  | acatttaaaa | cctctgtccg  | tgccgggtcat | 600  |
| tcggttgaac  | agattatgca  | atatccgatc  | tacagcggtg | ttctggcggg  | cgctggttgg  | 660  |
| caatgggttaa | atctcgccgt  | gctggctggc  | ggcgataggt | tgctatggca  | gaaagcgatt  | 720  |
| cgctggcata  | ttccccctcag | cttcttagta  | acgctggcgt | tatgcgcaat  | gttgggctgg  | 780  |
| ttgttctcac  | cagaaacact  | ggcagcaccg  | caaattcatc | tgctgtctgg  | agcgaccatg  | 840  |
| ctcggcgcat  | tctttatatt  | gactgacccg  | gttaccgctt | ctacgaccaa  | tcgtggctgt  | 900  |
| cttatttttcg | gcgcgcttgc  | gggcttatta  | gtctggttga | tcgcaggttt  | cgccggctat  | 960  |
| cctgacggcg  | tggtcttttcg | cgtcctgctg  | gcgaacatca | cgggtccctc  | gatcgattac  | 1020 |
| tacacgcgtc  | cgcgctcta   | cgcccatcgc  | aaagggttaa |             |             | 1059 |

<210> 134  
 <211> 621  
 <212> DNA

&lt;213&gt; E. Coli

&lt;400&gt; 134

|             |            |            |             |             |             |     |
|-------------|------------|------------|-------------|-------------|-------------|-----|
| atgctgaaaa  | ctatccgaaa | acacggcatt | acgttggcgc  | tatttgcagc  | gggttcaaca  | 60  |
| gggttaactg  | cgcccatcaa | ccagatgacc | aaaacgacga  | ttgctgaaca  | ggccagtctg  | 120 |
| caacaaaagg  | cgttatttga | tcaggtgctg | ccagccgaac  | gctataacaa  | tgcgctggca  | 180 |
| cagagttgct  | atctggtaac | tgcgccagag | ttaggtaaag  | gtgagcatcg  | ggtttacatc  | 240 |
| gccaaaacagg | atgacaaacc | ggtagccgcc | gttctggaag  | caaccgcgcc  | agatggctat  | 300 |
| tccggtgcga  | ttcagctgct | ggtgggagcc | gattttaacg  | gcacggctact | tggcacgcgc  | 360 |
| gtgacagagc  | accacgaaac | gccagggctt | ggcgataaaa  | tcgaactgcg  | cctttctgac  | 420 |
| tggatcaccc  | attttgcggg | taaaaaaatc | agtgggtgcag | atgatgcgca  | ctgggcgggtg | 480 |
| aagaaaagatg | gtggtgattt | cgaccagttc | accggcgcga  | cgattactcc  | ccgcgcgggtg | 540 |
| gttaatgcgg  | taaaacgcgc | cggattgtac | gctcagacgt  | taccggcaca  | actttctcaa  | 600 |
| cttcctgcct  | gtggagaata | a          |             |             |             | 621 |

&lt;210&gt; 135

&lt;211&gt; 696

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 135

|             |             |             |            |            |             |     |
|-------------|-------------|-------------|------------|------------|-------------|-----|
| gtgagcgaaa  | ttaaagacgt  | tattgttcag  | gggttggtga | aaaacaactc | tgcgctgggtc | 60  |
| cagtttgctcg | gcctttgtcc  | tctgttggcg  | gtcacgtcca | ctgccactaa | cgctctgggt  | 120 |
| ttaggacttg  | cgactacgct  | ggtactgacg  | ctgaccaacc | tgaccatttc | gacgctgcgt  | 180 |
| cactggacgc  | cagccgagat  | ccgcattccc  | atttacgtga | tgatcatcgc | ctcggtggtc  | 240 |
| agcgcgtgac  | agatgctgat  | caacgcctac  | gcctttggcc | tgtatcaatc | attagggatt  | 300 |
| tttatccgcg  | tgattgtcac  | taactgtatc  | gttgtgggcc | gcgctgaagc | cttcgcccgc  | 360 |
| aaaaaaggtc  | cggcgctttc  | ggcactggac  | ggcttttcaa | ttggtatggg | cgcaacctgc  | 420 |
| gccatgttgc  | tgcctgggtc  | actacgcgaa  | attatcggca | atggcacatt | gtttgacgggt | 480 |
| gcagatgcgc  | tgttaggtag  | ctgggcacaaa | gtattacgcg | tggagatttt | ccacaccgac  | 540 |
| tcccctttcc  | tgctggcgat  | gctgccacca  | ggtgcattta | ttggcctggg | actgatgctg  | 600 |
| gcaggaaaat  | acctgattga  | tgaagaatg   | aaaaagcgcc | gtgctgaagc | agctgcagaa  | 660 |
| cgtgcattgc  | caaacgggtga | aacaggggaat | gtctga     |            |             | 696 |

&lt;210&gt; 136

&lt;211&gt; 636

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 136

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| atgaataaag | caaaacgcct  | ggagatccct | actcgcctgc | gtgagaacaa | tcctcatccc  | 60  |
| accaccgagc | ttaatttcag  | ttcgcccttt | gaattgctga | ttgccgtact | gctttccgct  | 120 |
| caggcgaccg | atgtcagtgt  | taataaggcg | acggcgaaac | tctaccgggt | ggcgaataacg | 180 |
| cctgcagcga | tgcttgaaact | ggcggttgaa | gggtgaaaaa | cctatatcaa | aacgattggg  | 240 |
| ctttataaca | gcaaagcaga  | aaatatcatc | aaaacctgcc | gtatcttgct | ggagcagcat  | 300 |
| aatggcgagg | ttccggaaga  | tcgtgctgcg | cttgaagccc | tgcccggcgt | aggtcgtaaa  | 360 |
| acagccaacg | tcgtattaaa  | cactgcattc | ggctggccga | ctattgctgt | cgacacgcac  | 420 |
| attttccgcg | tttgtaatcg  | tactcaattt | gcgcggggga | aaaacgtcga | acaggtagaa  | 480 |
| gaaaagctac | tgaagtggt   | tccagcagag | tttaaagtcg | actgccacca | ttggttgatc  | 540 |
| ctgcacgggc | gttatacctg  | cattgccgcg | aagccccgct | gtggctcttg | tattattgaa  | 600 |
| gatcttttgt | aatacaaga   | gaaagttgac | atctga     |            |             | 636 |

&lt;210&gt; 137

&lt;211&gt; 504

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 137

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgaaaagac | ttcacaagag | gttcctgtta | gctacgtttt | gcgcgttatt | cacagcaact | 60  |
| ctccaggccg | ccgatgtcac | tatcactgtt | aatggctcgg | tagtcgctaa | accctgcact | 120 |
| attcaaacca | aagaagctaa | cgttaatctc | gggatctttt | atacgcgcaa | tctgcaacaa | 180 |

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| cctgggttctg | catctggctg | gcacaatatt | actttgtcat | taaccgattg | tccggttgaa | 240 |
| acaagtgcag  | tgacggcaat | cgtgacaggt | tcaactgaca | atacgggtta | ttacaaaaat | 300 |
| gaaggtactg  | ccgaaaatat | tcagatagag | ctgagggatg | accaggatgc | tgcgttaaaa | 360 |
| aatggcgata  | gcaaaacggt | tattgttgat | gagatcactc | gtaatgcaca | gtttccactt | 420 |
| aaggcaagag  | ctatcacggt | gaatggaaac | gcaagccagg | gaacgatcga | ggcgctaata | 480 |
| aatgtgatct  | acacctggca | ataa       |            |            |            | 504 |

&lt;210&gt; 138

&lt;211&gt; 531

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 138

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgaaataca | ataacattat | tttcctcggg | ttatgtctgg | ggttaaccac | ctattctgct | 60  |
| ttatccgcag | atagcgttat | taaaattagc | gggcgcgctc | tcgattatgg | ctgcacagtc | 120 |
| tcacgcgatt | cgcttaattt | taccgtagat | ctccaaaaaa | acagtgccag | acaatttcca | 180 |
| acgaccggta | gcacaagtc  | agccgtccct | tttcagatta | cgtaaagtga | atgcagcaaa | 240 |
| gggacaacgg | gggttcgggt | tgcatTTaac | ggatttgagg | atgcagaaaa | taatactttg | 300 |
| ttgaaactgg | atgaaggaa  | caatacggcc | tccggtttgg | gtatagaaat | attggacgca | 360 |
| aatatgcgtc | cggtgaaact | gaatgatctt | catgccggga | tgacgtggat | cccactggta | 420 |
| ccagaacaga | acaatatTTT | gccttactcc | gctcgtctga | agtcaactca | gaagtcgcgc | 480 |
| aatccgggac | tggtgagggc | ttcggcaacc | tttacccttg | aatttcaata | a          | 531 |

&lt;210&gt; 139

&lt;211&gt; 1149

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 139

|            |            |             |            |             |            |      |
|------------|------------|-------------|------------|-------------|------------|------|
| atgagtgggt | acaccgtcaa | gcctcctacc  | ggagacacca | atgagcagac  | acaattttat | 60   |
| gattatttta | atctgttcta | cagtaagcgt  | ggtcaggaa  | aaataagcat  | ctctcagcag | 120  |
| cttggaatt  | acggtacgac | atttttcagt  | gccagtcgcc | aaagttaactg | gaacacgtca | 180  |
| cgcagcgacc | agcaaatatc | atttgatta   | aatgtgccgt | ttggtgatat  | tacgacttcg | 240  |
| ctgaattaca | gctattccaa | taatatatgg  | caaaacgac  | gggatcattt  | actcgtttt  | 300  |
| acgcttaaat | ttcccttcag | tcattggatg  | cgtacagaca | gtcagtcggc  | atttcgtaat | 360  |
| tcaaaccgca | gttacagtat | gtcaaacgat  | ttgaaaggcg | gcacgaccaa  | tctatcgggg | 420  |
| gttttatggc | ctctgctgcc | ggataataac  | ctgaattata | gcgttcagggt | cggtaacacc | 480  |
| cacggagcta | atacatcgtc | tggaaccagt  | ggttacagrt | ctcttaatta  | tcgtggagct | 540  |
| tatggtaata | ctaattgtcg | ttacagtcgg  | agtgggtgac | gcagccagat  | ttattacgga | 600  |
| atgagtgggt | ggattattgc | tcattgctgat | ggcatcacct | ttggacagcc  | gctgggcgac | 660  |
| acaatgggtc | tggttaaggc | tcctgggtgt  | gataatgtca | aaatagagaa  | ccagaccgga | 720  |
| attcataccg | actggcgctg | ctatgccata  | ttaccatttg | cgacagaata  | tagagaaaa  | 780  |
| cgtgttgctc | ttaacgcgaa | ttcccttgca  | gataatgttg | aactggatga  | aaccgtggtc | 840  |
| actgtcatcc | caactcacgg | tgctattgcc  | agagcaacat | ttaatgcaca  | aatcggcggg | 900  |
| aaagtattaa | tgacgttgaa | gtacggtaat  | aagagcgttc | cattcggtgc  | aattgtcaca | 960  |
| cacggagaga | ataaaaaatg | cagcattgtc  | gcggaaaatg | gtcaggttta  | tctgactgga | 1020 |
| cttccacagt | cagggcaatt | acaggtttca  | tggggcgaa  | ataaaaaactc | aaactgtatt | 1080 |
| gtcgagtaca | agcttcctga | agtttctcct  | ggtaccttac | tgaaccagca  | gacagcaatc | 1140 |
| tgctcgctaa |            |             |            |             |            | 1149 |

&lt;210&gt; 140

&lt;211&gt; 417

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 140

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgattgcga | ttgccgacat | cttgcaagca | ggagaaaagc | taactgctgt | ggcacctttt | 60  |
| ctggcgggta | ttcagaacga | ggaacaatac | acccaggcgc | tggaactggg | agatcatctg | 120 |
| ctgctcaacg | atcctgaaaa | ccccttgctg | gatctggtgt | gtgccaaaa  | aaccgcgtgg | 180 |
| gaagaatcag | cggccgaatt | tgcggaattt | aatgccatgg | ctcaagccat | gcctggcggt | 240 |
| atagccgtga | ttcgtaccct | tatggatcaa | tatgggttaa | ccctttccga | tctgccggaa | 300 |

attggcagta aatctatggt gtcacgcggt ttgagcggga agaggaaatt aacgctggaa 360  
 caccgtaaaa aattggcaac gcgattcggc atttctcccg ccttggttat tgattaa 417

<210> 141  
 <211> 315  
 <212> DNA  
 <213> E. Coli

<400> 141  
 atgcacctga taactcaaaa agcattgaaa gatgctgcgg aaaaataccg gcaacataaa 60  
 acggagttgg tggtcttggg gaacacgatt gctaagggat atttcaaaaa acctgagtca 120  
 ttaaaagcag tattcccatc tctggataac ttcaaatatc tggataagca ttatgttttc 180  
 aatgttgggg gcaatgaatt acgtgttgta gcaatggctc tttttgaatc gcaaaagtgc 240  
 tacatacgtg aagttatgac gcataaagaa tacgatttct ttaccgctgt tcatcgctact 300  
 aaggggaaaa aatga 315

<210> 142  
 <211> 7152  
 <212> DNA  
 <213> E. Coli

<400> 142  
 ttgctatcag tatttacatt ttttcgctgt gctagaaagg gcgcatttat gttagctcgt 60  
 tcagggaagg taagcatggc tacgaagaag agaagtggag aagaaataaa tgaccgacaa 120  
 atattatgcg ggatgggaat taactacgc cgcttaactg cgggtatctg tctgataact 180  
 caacttgctg tccctatggc tgcggcagca caaggtgtgg taaacgcccg aaccacaaca 240  
 ccagttcctg cacaatttgc cattgcaaat gccaatacgg tgcctacac ccttgagcgg 300  
 ttggaatcgg cccaaagcgt tgccgaacgt ttcggtattt cgggtgctga gttacgcaa 360  
 ctcaaccagt ttcgtacgtt tgctcgaagt tttgataatg tccgccaggg tgatgaactg 420  
 gatgtcccgg cacaagttag tgaaaaaaa ttaaccccg cgccgggtaa tagcagtgc 480  
 aacctcgagc aacagatagc cagtacttca cagcaaatcg ggtctctgct cgccgaagat 540  
 atgaacacgg agcaagcggc aaatatggcg cgtggatggg cctcttctca ggcttcaggc 600  
 gcaatgacag actggttaag ccgcttcggt accgcaagaa tcacgctggg cgtggatgaa 660  
 gatttttagcc tgaagaactc ccagttcgat tttctccatc cgtggtatga aacgcctgat 720  
 aatctctttt tcagtcagca tactctccat cgtactgacg agcgtacgca gattacaac 780  
 ggcttaggtt ggctcattt cactcccaca tggatgtcgg gcatcaactt ctttttcgac 840  
 cagcatctta gccgttacca ctcccgcggc ggcattggcg cggagtactg gcgcgactat 900  
 ctaaaattaa gcagtaacgg ctatttgca ctgaccaact ggcgcagcgc acctgaactg 960  
 gacaacgatt atgaagcagc cccggccaat ggctgggatg tacgcgcaga aagctggcta 1020  
 cccgcctggc cgcaccttgg cggtaaaactg gcttatgaac agtattatgg cgatgaagtg 1080  
 gccctgttcg ataaagacga tcggcaaatg aatcctcatg ccataaccgc tggacttaac 1140  
 tataccccc tcccgtgat gaccttcagc gcggagcaac gccagggtta acagggcgaa 1200  
 aatgacaccc gttttgccgt cgattttacc tggcaacctg gcagcgcaat gcagaaacag 1260  
 cttgaccgga atgaagtgcg tgcacggcgt agccttgca gacgcccgtta tgatctggtg 1320  
 gatcgcaaca acaatatcgt tctggaatat cgcaaaaaag aactggttcg cctgacctg 1380  
 acagaccccg tgacagggaa gtcaggagaa gtgaaatcac tggtttcgtc gctacaaacc 1440  
 aaatatgccc tgaaaggcta taacgtcgaa gccaccgcac tggaaactgc cggtaggcaa 1500  
 gtggtcaca cgggttaaaga tattctggtt accctgccgg cttaccggtt caccagtacg 1560  
 ccagaaaccg ataaccctg gccgattgaa gtcaccgccc aagatgtcaa aggcaatttg 1620  
 tcgaatcgtg aacagagcat ggtggtcgtt caggcaccta cgctaagcca gaaagattcc 1680  
 tcggtatcgt taagtaccca aacattgaac gcggattccc attcaaccgc cactactgact 1740  
 tttattgcgc atgatgcagc aggtaatcct gttgtcgggc tgggtctctc gacgcgtcac 1800  
 gaaggtgttc aggacatcac cctttctgac tggaaagata atggtgacgg aagctatacc 1860  
 cagatcctga ccacaggagc gatgtctggc acgctgacgc tgatgccaca gctgaatggg 1920  
 gtggatgccc ctaagccccc cgccgtggtg aatatcattt ctgtttctgc atccccgaact 1980  
 cactcgtcaa ttaagattga taaggaccgt tatctctccg gcaatcctat cgaggtgacg 2040  
 gtagaactga gagatgaaaa tgacaaacct gtttaaggaa aaaaacagca actgaataac 2100  
 gcagtcagca tcgacaacgt gaaaccagga gtcactacag actggaaaga aaccgcagat 2160  
 ggcgtctata agcgaccta taccgcctat accaaaggca gtggacttac tgcgaagcta 2220  
 ttaatgcaaa actggaatga agatttgcac accgctggat ttatcatcga cgccaaccg 2280  
 cagtcagcga aaattgcgac attatctgcc agcaataatg gtgtgctcgc caatgagaat 2340

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| gcagcaaa    | ccgtctcggt  | caatgtcgct  | gatgaaggaa  | gcaacccaat  | caatgatcat  | 2400 |
| accgtcacgt  | ttgcggtatt  | aagcggatcg  | gcaacttctt  | tcaacaatca  | aaacaccgca  | 2460 |
| aaaacggatg  | ttaatgggtct | ggcgactttt  | gatctgaaaa  | gtagtaagca  | ggaagacaac  | 2520 |
| acggttgaag  | tcacccttga  | aaatggcgtg  | aaacaaacgt  | taatcgctcag | ttttgtcggc  | 2580 |
| gactcgagta  | ctgcgcaggt  | tgatctgcag  | aagtcgaaaa  | atgaagtggg  | tgctgacggc  | 2640 |
| aatgacagcg  | tcacaatgac  | cgcgaccgtc  | cgggatgcaa  | aaggcaacct  | gctcaatgac  | 2700 |
| gtcatggtca  | ctttcaatgt  | taattcagca  | qagggcaaac  | tgagccaaac  | cgaaagtgaat | 2760 |
| agccacgacg  | ggatcgccac  | agctacgctg  | accagtttga  | aaaatgggtga | ttatagggtt  | 2820 |
| acggcctctg  | tgagctctgg  | ttcccaggct  | aatcaacagg  | tgaattttat  | cggtgatcaa  | 2880 |
| agtactgtcg  | ccctgaccct  | cagtgtgcct  | tcagggtgata | tcaccgtcac  | caacacagct  | 2940 |
| ccgcaatata  | tgactgcaac  | cttgacggat  | aaaaatggca  | acccactaaa  | agataaagaa  | 3000 |
| atcaccttct  | ctgtgccaaa  | cgacgtcgca  | agtaagtctt  | cgattagcaa  | cgaggaaaaa  | 3060 |
| ggcatgacgg  | atagtaacgg  | ggttgcaatc  | gcctccctga  | ccggcagctt  | agcgggacag  | 3120 |
| catatgatac  | tggtctgctt  | ggctaacagc  | aatgtcagcg  | atgcacagcc  | aatgacgttt  | 3180 |
| gtggcgagata | aagacagagc  | ggttgcgtt   | ttgcaaacat  | cgaaagcgga  | aatcattggg  | 3240 |
| aatggcggtg  | atgagacaac  | tctgacagca  | acagtgaag   | atccgtcgaa  | tcatccggtg  | 3300 |
| gcggggataa  | cggtaaactt  | caccatgcc   | caggacgttg  | cggaacactt  | tacccttgaa  | 3360 |
| aataacggta  | ttgccatcac  | tcaggccaat  | ggggaagcgc  | atgtcacgct  | gaaaggtaaa  | 3420 |
| aaagcgggca  | cgcatacggt  | taccgcaacg  | ctgggtaata  | acaataccag  | tgattcgag   | 3480 |
| ccggtaacat  | ttgtggcgga  | caaagcctcg  | gtcaggttg   | tcctgcagat  | atcaaaagat  | 3540 |
| gagatcacag  | gtaattggcg  | cgatagcgca  | acgctaactg  | caacgggtta  | agatcagttc  | 3600 |
| gacaatgagg  | tgaataatct  | tccggtaaac  | ttcagctcag  | cctcttcagg  | actcaccttg  | 3660 |
| accccgagg   | taagtaatac  | caacgagtct  | ggcatcgcg   | aggccactct  | cgcaggcggt  | 3720 |
| gcctttggtg  | agaagacggt  | tactgcatca  | ctggctaata  | atgggtgccag | cgacaacaaa  | 3780 |
| actgtgcatt  | ttattggcga  | cacagcgcg   | gcaaaaatta  | tcgagttggc  | gcctgtccca  | 3840 |
| gacagcataa  | tcgcccgtac  | cccgcaagac  | agctccggca  | gcgtcatcac  | cgccacagtc  | 3900 |
| gttgataata  | atggctttcc  | ggtgaaaggt  | gtgactgtga  | acttcaccag  | caacgcagcg  | 3960 |
| acagccgaaa  | tgacgaacgg  | cggtcaagcc  | gtgacgaacg  | aacagggtta  | ggctaccgtc  | 4020 |
| acttatacca  | atacccgctc  | ctcgatagaa  | tcaggagcga  | gaccggatac  | cgttgaggcc  | 4080 |
| agtcctgaaa  | atggtagctc  | cacgcttagc  | acatcaatta  | atgtcaacgc  | tgatgcgtct  | 4140 |
| acggcacatc  | tcaccttgct  | acaggcactt  | tttgatacag  | tctccgcagg  | cgagacaacc  | 4200 |
| agtcctgtata | ttgaggtgaa  | ggataattac  | ggcaacgggtg | tccccagca   | ggaggttaacc | 4260 |
| ctcagcggtt  | caccaagtga  | aggcgtgacc  | cccagtaata  | acgctatata  | tactaccaac  | 4320 |
| cacgaacgca  | atttttacgc  | aagctttacc  | gctacaaaag  | ccgggggtta  | tcaattgacg  | 4380 |
| gcaacccctc  | aaaatggcga  | ttcgatgcaa  | caaacagtga  | cctatgtgcc  | gaacgtcgcg  | 4440 |
| aatgctgaaa  | tcacgctggc  | agcctcgaag  | gatccggtga  | ttgccgacaa  | taacgatctc  | 4500 |
| acgacactaa  | cagcaacagt  | cgctgataca  | gagggcaatg  | cgatagccaa  | cactgaggta  | 4560 |
| acatttactc  | tgccggaaga  | tgtgaaggcg  | aacttcacgc  | tgagcgatgg  | cggtaaagtg  | 4620 |
| attactgatg  | ctgaaggcaa  | agcgaaagtc  | acgctgaaag  | gtacaaaagc  | aggcgctcat  | 4680 |
| actgttacag  | catcgatgac  | tggcggtaa   | agtgaagcag  | tgggtggtgaa | ctttattgcg  | 4740 |
| gatacgtca   | ctgcgcaggt  | taatcttaac  | gttacgag    | acaattttat  | cgctaataac  | 4800 |
| gtcgggatga  | ccaggctgca  | ggcaacagtg  | actgatggaa  | acggcaaccc  | gttagccaat  | 4860 |
| gaggcggtga  | cattcacgct  | accggcagat  | gtgagcgcaa  | gctttactct  | cggaacaaggc | 4920 |
| ggttccgcca  | ttactgatat  | caacggcaag  | gctgaagtta  | cactgagcgg  | tacaaaatcc  | 4980 |
| ggcacctacc  | ccgtgacagt  | tagcgtgaac  | aattatgggt  | tcagtatac   | gaaacagggtg | 5040 |
| actttgattg  | ccgatgctgg  | taccgcaaaa  | ctagcctcct  | taacctctgt  | atactcattc  | 5100 |
| gtcgtcagca  | cgaccgaggg  | cgcaacccatg | acggcaagcg  | tcactgacgc  | taacggcaac  | 5160 |
| ccggtagaag  | gcataaaaagt | taatttccgc  | ggaacctccg  | tcacgctaag  | cagcaccagc  | 5220 |
| gttgaaacgg  | atgatcgggg  | tttcgctgaa  | attcttgtga  | caagcaccga  | ggtcggactg  | 5280 |
| aaaacagttt  | cagcctctct  | ggcagataaa  | cctactgaa   | tcactctcg   | attactgaat  | 5340 |
| gccagtgcag  | atgttaattc  | tgcgacgatt  | accagtctgg  | agataccgga  | aggtcaggta  | 5400 |
| atggtcgcac  | aagacgtagc  | agttaaagct  | cacgttaacg  | accagtttgg  | caacccgggt  | 5460 |
| gcgcataaac  | ccgtgacatt  | cagtgcagag  | ccatcctcgc  | aaatgatcat  | cagccagaat  | 5520 |
| acggtctcta  | ctaatacgca  | gggtgtagcc  | gaggtcacca  | tgacgcccga  | aagaaaacgg  | 5580 |
| tcgtatatgg  | tgaagcatc   | cctgcgcaat  | ggagcctcac  | ttgagaaaca  | actggagggt  | 5640 |
| attgatgaaa  | aactgacact  | cacggcgctc  | agtcgctta   | tcggtgtcta  | tgccctaca   | 5700 |
| ggcgctactc  | tgacggcaac  | gctaacctct  | gcaaatggca  | ctccagtgg   | gggtcaggtc  | 5760 |
| atcaacttta  | gcgtaacgcc  | agaagggcg   | acgttaagtg  | gcggaaaagt  | gagaactaac  | 5820 |
| tcctcaggtc  | aggctccagt  | cgttttgacc  | agcaataaag  | tcggtacata  | tacggtgact  | 5880 |
| gcactcttcc  | ataacggcgt  | aacaatacag  | acacagacaa  | ccgtgaaagt  | cactggcaac  | 5940 |
| tcaagcaccg  | cccatgttgc  | tagctttatc  | gctgatccat  | cgactatcgc  | cgccaccaac  | 6000 |



|            |            |             |             |            |             |      |
|------------|------------|-------------|-------------|------------|-------------|------|
| actgatttaa | gtaccttaaa | ggcaacgggt  | gaggatggca  | gtggtaacct | gatcgaaggt  | 6060 |
| ctcactgtgt | acttcgcctt | aaaaagcggc  | tctgccacat  | taacgtcatt | aacagcgggtg | 6120 |
| accgatcaaa | acggaatcgc | gacaacaagc  | gtgaaaggag  | cgatgacagg | tagcgtcacg  | 6180 |
| gtaagcgca  | tcacgaccgc | tgggtggaatg | caaacagtag  | atataacgct | ggtggctggc  | 6240 |
| ccggcagaca | cctcgagtc  | cgtccttaag  | agcaatcggg  | catcactgaa | aggggactat  | 6300 |
| accgatagtg | ctgaattacg | tcttgttctg  | cacgatatat  | caggcaatcc | gatcaaagtt  | 6360 |
| tctgaaggga | tggaaattgt | gcaatcaggt  | actaacgtgc  | cctatataaa | aattagcgca  | 6420 |
| attgattaca | gtctaataat | caacgggtgat | tacaaagcca  | ctgttacagg | agcgcgagag  | 6480 |
| ggtatcgcaa | cgtgatccc  | tgtattgaat  | ggtgttcac   | aagctggtct | gagtaccaca  | 6540 |
| atacaattca | ctcgcgcaga | agacaaaata  | atgagcggta  | cagtatcagt | caatgggtact | 6600 |
| gacctaccga | caactacatt | cccttcgcag  | gggttcaccg  | ggcggtatta | tcagttaga   | 6660 |
| aatgacaact | ttgccccagg | aaaaacggcg  | gctgattatg  | agttttcaag | ctctgcctcc  | 6720 |
| tgggtcgatg | ttgatgctac | cggtaaaagt  | acatttaaaa  | atgtcggcag | caattcggaa  | 6780 |
| aggattacgg | cgacgcca   | atcaggaggc  | cctagctatg  | tatacgaaat | ccgtgtgaag  | 6840 |
| agttgggtgg | tgaacgccg  | cgaggcttcc  | atgatataca  | gccttgctga | aaatttttgc  | 6900 |
| agcagcaatg | gctacacgct | ccccagagca  | aactatttaa  | accactgtag | ttcccagagg  | 6960 |
| atcgggtcac | tgtacagtga | atggggagat  | atggggcatt  | acacgactga | cgctggtttt  | 7020 |
| caatacaata | tgtattggtc | atctagtccc  | gcaaaactcaa | gcgaacaata | cgtagtttcc  | 7080 |
| ctggcaacag | gtgatcaaa  | cgtatttgaa  | aagcttgggt  | ttgcttatgc | gacatgttat  | 7140 |
| aaaaacctgt | ga         |             |             |            |             |      |

7152

&lt;210&gt; 143

&lt;211&gt; 186

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 143

|            |            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|------------|-----|
| atgagcaaa  | g          | gcgattata  | tgaatttaac | aatccagatc | aactgaaaat | acctctccct | 60  |
| cataaacaca | tagcgtcaac | attcaatgac | ataatgagta | aagatgttgg | ttatgcatac |            | 120 |
| gtatcattac | tctatgcctg | tcccttaaaa | acccactcat | taagactgaa | tccattcagc |            | 180 |
| aaatga     |            |            |            |            |            |            | 186 |

&lt;210&gt; 144

&lt;211&gt; 1197

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 144

|             |            |            |             |            |            |      |
|-------------|------------|------------|-------------|------------|------------|------|
| atgacaggtg  | ctgaacagcg | cattcagcta | gctgaagccc  | aggcgaaggc | agttgccact | 60   |
| caggatggtc  | cgagatcga  | cttttcggcg | gatatggagc  | ggcaaaaaat | gtcggcagaa | 120  |
| ggcttaatgg  | ggccgtttgc | tctgaacgat | ccggccgcag  | gtacgaccgg | cccggtgtac | 180  |
| accaacggta  | cttttggtct | aacggcgggc | tggcatctcg  | atatctgggg | aaagaatcgg | 240  |
| gcggaggtta  | ctgcccgcct | gggtacgggt | aaagcacggg  | cgccggaacg | cgagcaaac  | 300  |
| cgccaattgc  | tggctggcag | cgtagcccgc | ctgtactggg  | agtggcaaac | ccaggcggcg | 360  |
| ttaaacacgg  | tcttgcagca | aatagaaaaa | gagcagaaca  | ccattatcgc | gaccgatcgc | 420  |
| cagctataat  | agaacgggat | tacttcttca | gttgaagggt  | tggaaaccga | tattaatgcc | 480  |
| agcaaaaccc  | ggcagcagct | caacgatgtc | gcggggaaaa  | tgaatttat  | tgaggcacgg | 540  |
| ttaagcgcac  | ttacaaataa | ccagacaaag | tcattgaagc  | ttaaaaccgg | cgcgttgccg | 600  |
| aaagtggcaa  | gccagcttcc | tgatgaactg | gggtactcct  | tactggcccc | gcgggcagat | 660  |
| ttgcaggcgg  | cgactggta  | cgttgagtca | tgcgtaagca  | ccattgatgc | ggcaaaagcg | 720  |
| gcattttatc  | ctgacatcaa | cctgatggcc | ttcctgcaac  | aggatgcgtt | gcacttaagc | 780  |
| gatctgttcc  | gtcattccgc | gcagcaaatg | ggcggtacgg  | caggcctgac | gctaccatt  | 840  |
| ttcgtatagtg | gtcgtcttaa | cgccaatctc | gatatcgcaa  | aagccgaaag | caacttgtct | 900  |
| atcgccagct  | acaacaaagc | ggtgggtgaa | gcgggtgaatg | acgtggcgcg | ggcagccagt | 960  |
| caggttcaga  | cactggcgga | gaaaaaccag | catcaggcgc  | aaattgagcg | cgatgccttg | 1020 |
| cgtgtggtag  | gtcttgcgca | ggcgcgcttt | aacgcgggca  | tcattgctgg | ttcccgcgtc | 1080 |
| agcgaagcca  | gaatccccgc | gctgcgtgag | cgggccaatg  | gcctgttatt | gcaagggcag | 1140 |
| tggctggatg  | cctccattca | actcactggt | gcgttgggcg  | gggggtacaa | acgctga    | 1197 |

&lt;210&gt; 145

&lt;211&gt; 291

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 145

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgtattgcc | acgcgaaact | aaaaaatata | tcgcaacaca | cggtaatctc | cgcgcacctt | 60  |
| ttcttacctg | attattcccc | catgaatcgt | gattcccttt | atccagccat | cgccgtgttt | 120 |
| ccgctgttac | tgatgctggc | cggtgtgctg | cctatgcatg | aaaccgcca  | ggcgtaagc  | 180 |
| cagcaaacgc | ccgctgcaca | agttgacacc | gcattacca  | cgcgctgaa  | aatggttggc | 240 |
| cagacagcca | atggtggctg | gagtatcacg | ataatcaact | cacttcccta | a          | 291 |

&lt;210&gt; 146

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 146

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| atgcgtgtgt | tactggcacc | gatggagga  | gtgcttgact | ctctggtgctg | tgaattgctg | 60  |
| accgaagtta | acgactacga | tctgtgcata | accgagtttg | tccgctggtg  | ggatcaactg | 120 |
| ctgccggtaa | aagtctttca | tcgcatttgc | cctgagctac | aaaacgccag  | ccggacacca | 180 |
| tctggtacgc | tggtgctgct | gcagttgtta | ggtcagttcc | cacaatggct  | ggcagagaa  | 240 |
| gccgcccgtg | cggtggagtt | aggttcctgg | ggcgtggatc | tcaattgctg  | ctgcccgctg | 300 |
| aaaacggtta | acggtagcgg | cgccggggcg | acgttactca | aagatcctga  | actcatctac | 360 |
| caggggtcaa | aagcgatgct | tgaagctgta | ccggcgcat  | tgcccgtcag  | cgtgaaagt  | 420 |
| cgtctgggct | gggacagcgg | tgagaagaaa | tttgaatcgt | ccgatgctgg  | tcaacaggct | 480 |
| ggcgctacgc | agctggtggt | gcattggcgg | acgaaagagc | agggttaccg  | cgcggagcat | 540 |
| attgactggc | aggcgattgg | cgatattcgc | cagcggtcga | atattccggt  | gattgccaac | 600 |
| ggtgaaatct | gggactggca | gagcgcgcaa | caatgcattg | cgatcagcgg  | ctgcgacgca | 660 |
| gtgatgattg | gtcgcggggc | gctcaatatt | cccaacctga | gccgggtggt  | aaaatataac | 720 |
| gaaccgga   | tgccgtggcc | ggaggtggtt | gctttgctgc | aaaaatatac  | ccgtctggaa | 780 |
| aagcagggcg | ataccggggt | atatcacggt | gcgcggatta | aacagtgtgt  | gagttatttg | 840 |
| cgtaaaaat  | acgatgaagc | aacggaatta | tttcagcatg | ttcgggtgtt  | gaataattcc | 900 |
| cctgatattg | caagggctat | tcaggcaatt | gatatcgaga | aactctaa    |            | 948 |

&lt;210&gt; 147

&lt;211&gt; 891

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 147

|             |             |            |             |              |             |     |
|-------------|-------------|------------|-------------|--------------|-------------|-----|
| atgacaatat  | cgacaacttc  | cacgcccgat | gatgcgggat  | ttaaatcttt   | tttacgccat  | 60  |
| ccagacacgc  | cgcggtattt  | tattgatatt | catcttcccg  | cgccgctgctg  | caaaactgtgt | 120 |
| gatttaacga  | cgcttaaaact | ggaaccaaac | agttttattg  | atgaagacct   | gcggcaatat  | 180 |
| tattccgacc  | tcttgtggtc  | tgtgaaaacg | caggaggagag | tggtttatat   | ttatgtagt   | 240 |
| atagagcacc  | aaagtaagcc  | ggaagaatta | atggcttttc  | gcattgatgctg | ttattccatt  | 300 |
| gcggcaatgc  | aaaaccatct  | tgatgcgggc | tataaagagc  | ttccattggt   | gctcccgatg  | 360 |
| ctgtttttatc | atggtttcag  | aagtccttat | ccttattcac  | tctgctggct   | tgatgaattt  | 420 |
| gccgagcctg  | ctatagcccg  | caaaatatat | tcacggtctt  | ttccgttggg   | ggatattacc  | 480 |
| gtggtgccgg  | atgacgagat  | tatgcaacac | cgcaaaatgg  | cgctgttggg   | gttaattcag  | 540 |
| aaacatatct  | gtcagcgcca  | tctgttggga | ttagtgcacc  | aaattgtttc   | gctgctagt   | 600 |
| acagggaaca  | ctaattgacag | acagctaata | gccctgttta  | attacgtatt   | acaaacagg   | 660 |
| gatgcccagc  | gttttcgtgc  | atttattggt | gagatagcgg  | aacgcgcacc   | acaagaaaag  | 720 |
| gagaaactga  | tgaccattgc  | tgacagatta | cgtgaagaag  | gcgcaatgca   | gggcaaacac  | 780 |
| gaagaagccc  | tgccgtattgc | tcaggagatg | ctggatagag  | gtttagacag   | agagttagtt  | 840 |
| atgatggtga  | cccgaacttc  | accagacgat | cttatcgcgc  | aaagccacta   | a           | 891 |

&lt;210&gt; 148

&lt;211&gt; 1668

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 148

|            |          |            |           |            |            |    |
|------------|----------|------------|-----------|------------|------------|----|
| gtggctcaat | tcgtttat | catgcatcgt | gtcggcaaa | ttgttccgcc | gaaacgtcat | 60 |
|------------|----------|------------|-----------|------------|------------|----|

```

at tt t t g a a a a   a c a t c t c t c t   g a g t t c t c t c   c c t g g g g c a a   a a a t t g g t g t   c c t g g g t c t g   120
a a t g g c g c g g   g t a a g t c c a c   c c t g c t g c g c   a t t a t g g c g g   g c a t t g a t a a   a g a c a t c g a a   180
g g t g a a g c g c   g t c c g c a g c c   a g a c a t c a a g   a t t g g t t a t c   t g c c g c a g g a   a c c g c a g c t g   240
a a c c c g g a a c   a c a c c g t g c g   t g a g t c c a t t   g a a g a a g c g g   t t t c a g a a g t   g g t t a a c g c c   300
c t g a a a c g c c   t g g a t g a a g t   g t a t g c g c t g   t a c g c c g a t c   c g g a t g c c g a   t t t t g a c a a g   360
c t g g c c g c t g   a a c a a g g c c g   t c t g g a a g a g   a t c a t t c a g g   c t c a c g a c g g   t c a t a a t c t g   420
a a c g t a c a g c   t g g a g c g t g c   g g c g g a t g c g   c t a c g t c t g c   c g g a c t g g g a   c g c g a a a a t c   480
g c t a a c c t c t   c c g t g g t g a   a c g t c g t c g c   g t a g c g t t g t   g c c g c c t g c t   g c t g g a a a a a   540
c c a g a c a t g c   t g c t g c t c g a   c g a a c c g a c c   a a c c a c c t g g   a t g c c g a a t c   c g t g g c c t g g   600
c t g g a a c g c t   t c c t g c a c g a   c t t c g a a g g c   a c c g t t g t g g   c g a t t a c c c a   c g a c c g t t a c   660
t t c c t c g a t a   a c g t t g c a g g   c t g g a t c c t c   g a a c t t g a c c   g c g g t g a a g g   t a t t c c g t g g   720
g a a g g t a a c t   a c t c c t c c t g   g c t g g a g c a g   a a a g a t c a g c   g c c t g g c g c a   g g a a g c t t c a   780
c a a g a a g c g g   c g c g t c g t a a   g t c g a t t g a g   a a a g a g c t g g   a a t g g g t a c g   t c a a g g t a c t   840
a a a g g c c g t c   a g t c g a a a g g   t a a a g c a c g t   c t g g c g c g c t   t t g a a g a a c t   g a a c a g c a c c   900
g a a t a t c a g a   a a c g t a a c g a   a a c c a a c g a a   c t g t t t a t t c   c a c c t g g a c c   g c g t c t g g g c   960
g a t a a a g t g c   t g g a a g t c a g   c a a c t g c g t   a a a t c c t a t g   g c g a t c g t c t   g c t g a t t g a t   1020
g a c c t g a g c t   t c t c g a t c c c   g a a a g g a g c g   a t c g t c g g g a   t c a t c g g t c c   g a a c g g t g c g   1080
g g t a a a t c g a   c c c t g t t c c g   t a t g a t c t c t   g g t c a g g a a c   a g c c g g a c a g   c g g c a c c a t c   1140
a c t t t g g g t g   a a a c g g t g a a   a c t g g c g t c g   g t t g a t c a g t   t c c g t g a c t c   a a t g g a t a a c   1200
a g c a a a a c c g   t t t g g g a a g a   a g t t t c c g g c   g g g c t g g a t a   t c a t g a a g a t   c g g c a a c a c c   1260
g a g a t g c c a a   g c c g c g c c t a   c g t t g g c c g c   t t t a a c t t t a   a a g g g t t g a   t c a g g g t a a a   1320
c g c g t t g g t g   a a c t c t c c g g   t g g t g a g c g c   g g t c g t c t g c   a t c t g g c g a a   g c t g c t g c a g   1380
g t t g g c g g c a   a c a t g t g c t   g c t c g a c g a a   c c a a c c a a c y   a c c t g g a t a t   c g a a a c c c t g   1440
c g c g c g c t g g   a a a a c g c c c t   g c t g g a g t t c   c c g g g c t g t g   c g a t g g t t a t   c t c g c a c g a c   1500
c g t t g g t t c c   t c g a c c g t a t   c g c c a c g c a c   a t t c t g g a t t   a c c a g g a t g a   a g g t a a a g t t   1560
g a g t t c t t c g   a a g g t a a c t t   t a c c g a g t a c   g a a g a g t a c a   a g a a a c g c a c   g c t g g g c g c a   1620
g a c g c g c t g g   a g c c g a a g c g   t a t c a a g t a c   a a g c g t a t t g   c g a a g t a a   1668

```

<210> 149  
 <211> 522  
 <212> DNA  
 <213> E. Coli

```

<400> 149
a t g t c a a a g c   c a a a a t a c c c   t t t t g a a a g   c g c c t t g a a g   t c g t g a a t c a   c t a c t t c a c a   60
a c t g a t g a t g   g t t a c a g g a t   c a t c t c g g c a   c g t t t t g g t g   t c c c c c g a a c   c c a g g t c a g g   120
a c a t g g g t t g   c c c t c t a t g a   a a a a c a t g g a   g a a a a a g g t t   t a a t t c c c a a   a c c t a a a g g c   180
g t t a g t g c t g   a t c c a g a g t t   g c g t a t t a a g   g t c g t g a a a g   c t g t g a t c g a   g c a g c a c a t g   240
t c c c t t a a t c   a g g c t g c t g c   t c a c t t t a t g   c t t g c t g g t a   g t g g t t c t g t   a g c c a g g t g g   300
c t g a a g g t c t   a t g a a g a g c g   c g g a g a a g c t   g g t t t a c g c g   c g c t c a a g a t   t g g c a c c a a a   360
a g a a a c a t t g   c a a t a t c a g t   t g a t c c a g a a   a a a g c g g c a t   c a g c a t t g g a   g c t g t c a a a a   420
g a c c g a c g c a   t t g a g g a t c t   t g a a a g c a a   g t t c g a t t t c   t t g a a a c g c g   g c t t a t g t a t   480
c t a a a a a a g c   t g a a a g c c c t   a g c t c a t c c c   a c g a a a a a g t   g a   522

```

<210> 150  
 <211> 852  
 <212> DNA  
 <213> E. Coli

```

<400> 150
g t g a a a g t a c   t c a a c g a g c t   a a g g c a g t t t   t a t c c t c t t g   a t g a g c t t c t   c a g g g c t g c g   60
g a g a t a c c c g   g c a g t a c g t t   t t a t t a t c a t   c t a a a g g c t c   t c a g c a a g c c   t g a c a a g t a t   120
g c g g a c g t t a   a a a a g c g t a t   t a g t g a g a t t   t a t c a c g a g a   a t a g a g g c c g   a t a c g g a t a c   180
c g t a g g g t a a   c g c t g t c t c t   t c a t c g a g a a   g g g a a a c a g a   t t a a c c a t a a   a g c t g t t c a g   240
c g c c t g a t g g   g a a c c c t c t c   a c t t a a a g c a   g c g a t t a a g g   t c a a g c g a t a   c c g c t c t t a c   300
a g a g g a g a g g   t a g g g c a a a c   c g c c c c t a a t   g t t c t c c a a a   g a g a t t t c a a   g g c t a c g c g g   360
c c a a a c g a g a   a g t g g g t t a c   c g a t g t t a c t   g a a t t t g c a g   t c a a t g g g c g   c a a g c t g t a t   420
t t g t c t c c a g   t a a t a g a t c t   c t t c a a c a a c   g a a g t t a t t t   c t t a c a g c c t   t t c g g a a a g a   480
c c a g t g a t g a   a c a t g g t t g a   g a a t a t g c t c   g a t c a g g c a t   t c a a a a a g c t   t a a t c c t c a c   540
g a g c a t c c t g   t t c t g c a c t c   t g a c c a g g g a   t g g c a g t a t c   g t a t g a g a a g   a t a t c a a a a t   600

```

|   |     |
|---|-----|
| atccttaaaag aacatggtat taaacaaagc atgtccagaa aaggcaattg tctggataat  | 660 |
| gctgtggtgg agtgttttctt tggaaacctta aagtcggagt gtttttatct tgatgagttc | 720 |
| agtaataataa gcgaactgaa ggatgctgtt acggaatata ttgaataacta caacagcaga | 780 |
| agaatttagcc tgaattataa aggtctgact ccaattgaat atcggaatca gacctatatg  | 840 |
| cctcgtgttt aa   | 852 |

&lt;210&gt; 151

&lt;211&gt; 117

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 151

|   |     |
|---|-----|
| atgaaagttc gtgcttccgt caagaaatta tgccgtaact gcaaaatcgt taagcgtgat | 60  |
| gggtgcatcc gtgtgatttg cagtgcggag ccgaagcata aacagcgcca aggtctga   | 117 |

&lt;210&gt; 152

&lt;211&gt; 1332

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 152

|   |      |
|---|------|
| atggctaaac aaccgggatt agattttcaa agtgccaaag gtggccttagg cgagctgaaa  | 60   |
| cgcagactgc tgtttgttat cgggtgcgctg attgtgttcc gtattggctc ttttattccg  | 120  |
| atccctggta ttgatgccgc tgtacttgcc aaactgcttg agcaacagcg aggcaccatc   | 180  |
| attgagatgt ttaacatgtt ctctgggtgt gctctcagcc gtgcttctat ctttgctctg   | 240  |
| gggacatgc cgtatatctt ggcgtcgatc attatccagc tgctgacggg ggttcaccca    | 300  |
| acgttggcag aaattaagaa agaaggggag tctggtcgtc gtaagatcag ccagtaacac   | 360  |
| cgctacggta ctctgggtgt ggcaatattc cagtcgatcg gtattgctac cggctcgccg   | 420  |
| aatatgcctg gtatgcaagg cctgggtgatt aaccggggct ttgcatttcta cttcacggct | 480  |
| gttgtaagtc tggtcacagg aacctgttct ctgatgtggt tgggcgaaca gattactgaa   | 540  |
| cgaggtatcg gcaacgggat ttcaatcatt atcttcggcg gtattgtcgc gggactcccg   | 600  |
| ccagccattg cccatactat cgagcaagcg cgtcaaggcg acctgcactt cctcgtgttg   | 660  |
| ctgttggttg cagtattagt atttgcagtg acgttctttg ttgtatttgt tgagcgtggt   | 720  |
| caacgccgca ttgtggtaaa ctacgcgaaa cgtcagcaag gtcgtcgtgt ctatgctgca   | 780  |
| cagagcacac atttaccgct gaaagtgaat atggcggggg taatcccggc aatcttcgct   | 840  |
| tccagtatta ttctgttccc ggcgaccatc gcgtcatggt tcgggggscgg tactggttgg  | 900  |
| aactggctga caacaatttc gctgtatttg cagcctgggc aaccgcttta tgtgttactc   | 960  |
| tatgcgtctg caatcatctt cttctgttct ttctacacgg cgttgggttt caaccgcgt    | 1020 |
| gaaacagcag ataacctgaa gaagtcgggt gcatttgtac caggaaattcg tccgggagag  | 1080 |
| caaacggcga agtatatcga taaagtaatg acccgctga cctgggttgg tgcgtgtgat    | 1140 |
| attaccttta tctgcctgat cccggagtgc atgcgtgatg caatgaaagt accgttctac   | 1200 |
| ttcgggtggga cctcactgct tatcgttgtt gtcgtgatta tggactttat ggctcaagtg  | 1260 |
| caaacctctg tgatgtccag tcagtatgag tctgcattga agaaggcgaa cctgaaaggc   | 1320 |
| tacggccgat aa   | 1332 |

&lt;210&gt; 153

&lt;211&gt; 435

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 153

|   |     |
|---|-----|
| atgcgtttaa atactctgtc tccggccgaa ggctccaaaa aggcgggtaa acgcctgggt   | 60  |
| cgtgggtatcg gttctggcct cggtaaaacc ggtggtcgtg gtcacaaaagg tcagaagtct | 120 |
| cgttctggcg gtggcgtagc tcgcgggttc gaggggtggtc agatgcctct gtaccgtcgt  | 180 |
| ctgccgaaat tcgggttcac ttctcgtaaa gcagcgatta cagccgaaat tcgtctgtct   | 240 |
| gacctggcta aagtagaagg cgggttagta gacctgaaca cgctgaaaagc ggctaacatt  | 300 |
| atcggtatcc agatcgagtt cgcgaaagtg atcctggctg gcgaagtaac gactccggtg   | 360 |
| actgttcgtg gcctgcgtgt tactaaaagg gctcgtgctg ctatcgaaagc tgctggcggt  | 420 |
| aaaatcgagg aataa  | 435 |

&lt;210&gt; 154

<211> 180  
 <212> DNA  
 <213> E. Coli

<400> 154

|              |             |             |            |             |            |     |
|--------------|-------------|-------------|------------|-------------|------------|-----|
| atggcacaaga  | ctattaaaaat | tactcaaaacc | cgcaqtgcaa | tcggctcgtct | gccgaaacac | 60  |
| aaggcacaacgc | tgcttggcct  | gggtctgcgt  | cgtattggtc | acaccgtaga  | gcgcgaggat | 120 |
| actcctgcta   | ttcgcggtat  | gatcaacgcg  | gtttccttca | tggttaaaagt | tgaggagtaa | 180 |

<210> 155  
 <211> 504  
 <212> DNA  
 <213> E. Coli

<400> 155

|            |             |             |             |            |            |     |
|------------|-------------|-------------|-------------|------------|------------|-----|
| atggctcaca | tcgaaaaaca  | agctggcgaa  | ctgcaggaaa  | agctgatcgc | ggtaaacgcg | 60  |
| gtatctaaaa | ccgttaaagg  | tggtcgtatt  | ttctccttca  | cagctctgac | tgtagttggc | 120 |
| gatggtaacg | gtcgcgttgg  | ttttggttac  | ggtaaagcgc  | gtgaagtcc  | agcagcgatc | 180 |
| cagaaacgca | tggaaaaaagc | ccgtcgcaat  | atgattaacg  | tcgcgctgaa | taacggcact | 240 |
| ctgcaacacc | ctgttaaagg  | tggtcacacg  | ggttctcgcg  | tattcatgca | gccggcttcc | 300 |
| gaaggtaccg | gtatcatcgc  | cggtgggtgca | atgcgcgcgcg | ttctggaagt | cgtgggggtt | 360 |
| cataacgttc | tggtctaaagc | ctatgggtcc  | accaacccga  | tcaacgtggt | tcgtgcaact | 420 |
| attgatggcc | tggaatat    | gaattctcca  | gaaatggctg  | ctgccaaagc | tggtaaatcc | 480 |
| gttgaagaaa | ttctggggaa  | ataa        |             |            |            | 504 |

<210> 156  
 <211> 354  
 <212> DNA  
 <213> E. Coli

<400> 156

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| atggataaga  | aatctgctcg | tatccgtcgt | gcgacccgcg | cacgccgcaa  | gctccaggag | 60  |
| ctggggcgcaa | ctcgcctggg | ggtacatcgt | accccgcgtc | acatttacgc  | acaggtaatt | 120 |
| gcaccgaacg  | gttctgaagt | tctggtagct | gcttctactg | tagaaaaagc  | tatcgctgaa | 180 |
| caactgaagt  | acaccggtaa | caaagacgcg | gctgcagctg | tggtgtaaagc | tgctcgtgaa | 240 |
| cgcgctctcg  | aaaaaggcat | caaagatgta | tccttgacc  | gttccgggtt  | ccaatatcat | 300 |
| ggctcgtgtcc | aggcactggc | agatgctgcc | cgtgaagctg | gccttcagtt  | ctaa       | 354 |

<210> 157  
 <211> 534  
 <212> DNA  
 <213> E. Coli

<400> 157

|             |            |             |             |            |             |     |
|-------------|------------|-------------|-------------|------------|-------------|-----|
| atgtctcgtg  | ttgctaaagc | accggctcgtt | gttcctgcgcg | gcgttgacgt | aaaaatcaac  | 60  |
| ggtcagggtta | ttacgatcaa | aggtaaaaac  | ggcgagctga  | ctcgtactct | caacgatgct  | 120 |
| gttgaagtta  | aacatgcaga | taataacctg  | accttcggtc  | cgcgtgatgg | ttacgcagac  | 180 |
| ggttgggcac  | aggctggtag | cgcgcgtgcc  | ctgctgaact  | caatggttat | cgggtgttacc | 240 |
| gaaggcttca  | ctaagaagct | gcagctgggt  | gggtgtaggt  | accgtgcagc | gggttaaaggc | 300 |
| aatgtgatta  | acctgtctct | gggtttctct  | catcctgttg  | accatcagct | gcctgcgggt  | 360 |
| atcactgctg  | aatgtccgac | tcagactgaa  | atcgtgctga  | aaggcgtgta | taagcagggtg | 420 |
| atcggccagg  | ttgcagcgga | tctgcgcgcc  | taccgtcgtc  | ctgagcctta | taaaggcaag  | 480 |
| ggtgttcgtt  | acgccgacga | agtcgtgcgt  | accaaagagg  | ctaagaagaa | gtaa        | 534 |

<210> 158  
 <211> 393  
 <212> DNA  
 <213> E. Coli

<400> 158

|            |            |            |            |            |            |    |
|------------|------------|------------|------------|------------|------------|----|
| atgagcatgc | aagatccgat | cgcggatatg | ctgacccgta | tccgtaacgg | tcaggccgcg | 60 |
|------------|------------|------------|------------|------------|------------|----|

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| aacaaagctg | cggtcacccat | gccttcctcc | aagctgaaag | tggcaatcgc | caacgtgctg | 120 |
| aaggagaag  | gttttattga  | agattttaaa | gttgaaggcg | acaccaagcc | tgaactggaa | 180 |
| cttactctga | agtattttcca | gggcaaagct | gttgtagaaa | gcattcagcg | tgtcagccgc | 240 |
| ccaggtctgc | gcattctataa | acgtaaagat | gagctgccga | aagttatggc | gggtctgggt | 300 |
| atcgagcttg | ttttacctc   | taaaggtgtt | atgactgac  | gtgcagcgcg | ccaggctggg | 360 |
| cttgggtggc | aaattatctg  | ctacgtagcc | taa        |            |            | 393 |

&lt;210&gt; 159

&lt;211&gt; 306

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 159

|             |             |             |            |             |            |     |
|-------------|-------------|-------------|------------|-------------|------------|-----|
| atggcctaagc | aatcaatgaa  | agcacgcgaa  | gtaaaacgcg | tagcttttagc | tgataaatac | 60  |
| ttcgcgaaac  | gcgctgaact  | gaaagcgatc  | atctctgatg | tgaacgcttc  | cgacgaagat | 120 |
| cgttggaacg  | ctgtttctcaa | gctgcgagact | ctgccgcgtg | attccagccc  | gtctcgtcag | 180 |
| cgtaaccgct  | gccgtcaaac  | aggctcgtccg | catggtttcc | tgccggaagt  | cggtttgagc | 240 |
| cgtattaagg  | tccgtgaagc  | cgtatgcgc   | ggtgaaatcc | cggttctgaa  | aaaggctagc | 300 |
| tggttaa     |             |             |            |             |            | 306 |

&lt;210&gt; 160

&lt;211&gt; 540

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 160

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| atggcgaaac  | tgcatgatta | ctacaaagac  | gaagtagtta | aaaaactcat | gactgagttt | 60  |
| aactacaatt  | ctgtcatgca | agtcctctcg  | gtcgagaaga | tcacctgaa  | catgggtgtt | 120 |
| gggtgaagcga | tcgctgacaa | aaaactgctg  | gataacgcag | cagcagacct | ggcagcaatc | 180 |
| tccgggtcaaa | aaccgctgat | caccaaaagca | cgcaaatctg | ttgcaggctt | caaaatccgt | 240 |
| cagggctatc  | cgatcggctg | taaagtaact  | ctgcgtggcg | aacgcagtgt | ggagttcttt | 300 |
| gagcgctga   | tcactattgc | tgtacctctg  | atccgtgact | tccgtggcct | gtccgctaag | 360 |
| tctttcgacg  | gtcgtggtaa | ctacagcatg  | ggtgtccgtg | agcagatcat | cttccagaa  | 420 |
| atcgactacg  | ataaagtcga | ccgcgttcgt  | ggtttggata | ttaccattac | cactactgcg | 480 |
| aaatctgacg  | aagaaggccg | cgctctgctg  | gctgcctttg | acttcccgtt | ccgcaagtaa | 540 |

&lt;210&gt; 161

&lt;211&gt; 315

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 161

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| atggcagcga  | aaatccgtcg  | tgatgacgaa  | gttatcgtgt | taaccggtaa | agataaaggt | 60  |
| aaacgcggta  | aagttaagaa  | tgtcctgtct  | tccggcaagg | tcattgttga | aggtatcaac | 120 |
| ctgggttaaga | aacatcagaa  | gccgggttccg | gccctgaacc | aaccgggtgg | catcgttgaa | 180 |
| aaagaagccg  | ctattcaggt  | ttccaacgta  | gcaatcttca | atgcggcaac | cggcaaggct | 240 |
| gaccgtgtag  | gcttttagatt | cgaagacggt  | aaaaaagtc  | gtttcttcaa | gtctaacagc | 300 |
| gaaactatca  | agtaa       |             |            |            |            | 315 |

&lt;210&gt; 162

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 162

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgatccaag | aacagactat | gctgaacgtc | gccgacaact | ccggtgcacg | tcgcgtaagt | 60  |
| tgtatcaagg | ttctgggtgg | ctcgcaccgt | cgctacgcag | gcgtaggcga | catcatcaag | 120 |
| atcaccatca | aagaagcaat | tccgcgtggg | aaggtcaaaa | aaggtgatgt | gctgaaggcg | 180 |
| gtagtgggtc | gcaccaagaa | gggtgttcgt | cgcccgacg  | gttctgtcat | tcgcttcgat | 240 |
| ggtaatgctt | gtgttcttct | gaacaacaac | agcgagcagc | ctatcggtac | gcgtattttt | 300 |
| gggccggtaa | ctcgtgagct | tcgtagttag | aagttcatga | aaattatctc | tctggcacca | 360 |

gaagtactct aa

372

<210> 163  
 <211> 567  
 <212> DNA  
 <213> E. Coli

&lt;400&gt; 163

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgttttaag | gacaaaaaac | attggccgca | ctggccgtat | ctctgctgtt | cactgcacct | 60  |
| gtttatgctg | ctgatgaagg | ttctggcgaa | attcacttta | agggggaggt | tattgaagca | 120 |
| ccttgtagaa | ttcatccaga | agatattgat | aaaaacatag | atcttggaca | agtcacgaca | 180 |
| acccatataa | accgggagca | tcatagcaat | aaagtggccg | tcgacattcg | cttgatcaac | 240 |
| tgtgatctgc | ctgcttctga | caacggtagc | ggaatgccgg | tatccaaagt | tgcgctaacc | 300 |
| ttcgatagca | cggctaagac | aactgggtgt | acgcctttgt | tgagcaaac  | cagtgcaggc | 360 |
| gaagcaactg | gggtcgggtg | acgactgatg | gacaaaaatg | acggtaacat | cgtattaggt | 420 |
| tcagccgcgc | cagatcttga | cctggatgca | agctcatcag | aacagacgct | gaactttttc | 480 |
| gcctggatgg | aacaaattga | taatgcagtc | gatgtcacgg | caggtgaagt | aaccgctaac | 540 |
| gcaacctacg | tgctggatta | taaataaa   |            |            |            | 567 |

<210> 164  
 <211> 1284  
 <212> DNA  
 <213> E. Coli

&lt;400&gt; 164

|             |             |            |             |            |             |      |
|-------------|-------------|------------|-------------|------------|-------------|------|
| atggctgata  | caaaagcaaa  | actcaccctc | aacggggata  | cagctgttga | actggatgtg  | 60   |
| ctgaaaaggca | cgctgggtca  | agatgttatt | gatatccgta  | ctctcgggtc | aaaagggtgtg | 120  |
| ttcacctttg  | acccaggctt  | cacttcaacc | gcacccctcg  | aatctaaaaa | tacttttatt  | 180  |
| gatggtgatg  | aaggtatttt  | gctgcaccgc | ggtttcccg   | tcgatcagct | ggcgaccgat  | 240  |
| tctaactacc  | tggaagtgtg  | ttacatcctg | ctgaatgggtg | aaaaaccgac | tcaggaacag  | 300  |
| tatgacgaat  | taaaaactac  | ggtgaccctg | cataccatga  | tccacgagca | gattaccctg  | 360  |
| ctgttccatg  | ctttccgtcg  | cgactcgcac | ccaatggcag  | tcattgtgtg | tattaccggc  | 420  |
| gcgctggcgg  | cgcttctatca | cgactcgcgt | gatgttaaca  | atctcctgca | ccgtgaaatt  | 480  |
| gcccgcgttc  | gcctgctgtc  | gaaaatgccg | accatggccg  | cgatgtgtta | caagtattcc  | 540  |
| attggtcagc  | catttgttta  | cccgcgcaac | gatctctcct  | acgcccgtaa | cttctgaat   | 600  |
| atgatgttct  | ccacgcccgtg | cgaaccgtat | gaagttaatc  | cgattctgga | acgtgctatg  | 660  |
| gaaccgtatc  | tgatcctgca  | cgctgaccat | gaacagaacg  | cctctacctc | caccgtgcgt  | 720  |
| accgctggct  | cttcgggtgc  | gaacccgttt | gcctgtatcg  | cagcaggtat | tgcttcaactg | 780  |
| tggggacctg  | cgcacggcgg  | tgctaacgaa | ggcgcgctga  | aaatgctgga | agaaatcagc  | 840  |
| tccgttaaac  | acattccgga  | atttgttcgt | cgtcgaaaag  | acaaaaatga | ttctttccgc  | 900  |
| ctgatgggct  | tcggtcacccg | cgtgtacaaa | aattacgacc  | cgcgcgccac | cgtaatgcgt  | 960  |
| gaaacctgcc  | atgaagtgtc  | gaaagagctg | ggcacgaagg  | atgacctgct | ggaagtggct  | 1020 |
| atggagctgg  | aaaacatcgc  | gctgaacgac | ccgtacttta  | tcgagaagaa | actgtacccg  | 1080 |
| aacgtcgatt  | tctactctgg  | tatcatcctg | aaagcgatgg  | gtattccgtc | ttccatgttc  | 1140 |
| accgtcattt  | tcgcaatggc  | acgtaccgtt | ggctggatcg  | cccactggag | cgaaatgcac  | 1200 |
| agtgcgggta  | tgaagattgc  | ccgtccgcgt | cagctgtata  | caggatatga | aaaacgcgac  | 1260 |
| tttaaaagcg  | atatcaagcg  | ttaa       |             |            |             | 1284 |

<210> 165  
 <211> 1434  
 <212> DNA  
 <213> E. Coli

&lt;400&gt; 165

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| atgaaagtaa | cgctgccaga | gtttgaacgt | gcaggagtga | tggtggttgg | tgatgtgatg  | 60  |
| ctggatcgtt | actgttacgg | ccccaccagt | cgtatctcgc | cggaaagcgc | ggtgcccggtg | 120 |
| gttaaagtga | ataccatcga | agaacgtccg | ggcggcgccg | ctaactgtgg | gatgaatc    | 180 |
| gcttctctcg | gtgctaattg | acgcctggtc | gggttgacgg | gcattgacga | tgacgcgcgc  | 240 |
| gcgctgagta | aatctctggc | cgacgtcaac | gtcaaatgcg | acttcgtttc | tgtaccgacg  | 300 |
| catccgacca | ttaccaaatt | acgggtactt | tcccgcaccc | aacagctgat | ccgtctggat  | 360 |
| tttgaagaag | gtttcgaagg | tggtgatccg | cagccgctgc | acgagcggat | taatcaggcg  | 420 |

|            |            |             |            |            |             |      |
|------------|------------|-------------|------------|------------|-------------|------|
| ctgagttcga | ttggcgcgct | gggtctttct  | gactacgcca | aaggtgcgct | ggcaagcgta  | 480  |
| cagcagatga | tccaactggc | gcgtaaagcg  | gggtgtccgg | tgctgattga | tccaaaagg   | 540  |
| accgattttg | agcgctaccg | cggtcgctacg | ctgttaacgc | cgaatctctc | ggaatttgaa  | 600  |
| gctgttgctg | gtaaatgtaa | gaccgaagaa  | gagattgttg | agcgcgccat | gaaactgatt  | 660  |
| gccgattacg | aactctcggc | tctgttagtg  | acccgttccg | aacagggtat | gtcgtgctg   | 720  |
| caaccgggta | aagcgccgct | gcatacgcca  | acccaagcgc | aggaagtgtg | tgacgttacc  | 780  |
| gggtgcggcg | acacggtgat | tggtcgctctg | gcggcaacgc | tggtcagcgg | taattcgctg  | 840  |
| gaagaagcct | gcttctttgc | caatgcggcg  | gctggcggtg | tggtcggcaa | actgggaacc  | 900  |
| tccacgggtt | cgccgatcga | gctggaaaaa  | gctgtacgtg | gacgtgcaga | tacaggcttt  | 960  |
| ggcgtgatga | ccgaagagga | actgaagctg  | gccgtagcgg | cagcgcgtaa | acgtgggtgaa | 1020 |
| aaagtgggtg | tgaccaacgg | tgtctttgac  | atcctgcacg | ccgggcacgt | ctcttatctg  | 1080 |
| gcaaatgccc | gcaagctggg | tgaccgcttg  | attgttgccg | tcaacagcga | tgccctccacc | 1140 |
| aaacggctga | aaggggattc | ccgcccggta  | aaaccactcg | aacagcgatg | gattgtgctg  | 1200 |
| ggcgcaactg | aagcggtcga | ctgggttagt  | tcgtttgaag | aggacacgcc | gcagcgcttg  | 1260 |
| atcgccggga | tcttgccaga | tctgctgggt  | aaaggcggcg | actataaacc | agaagagatt  | 1320 |
| gcccggagta | aagaagctcg | ggccaacggt  | ggcgaagtgt | tggtgctcaa | ctttgaagac  | 1380 |
| ggttgctcga | cgaccaacat | catcaagaag  | atccaacagc | ataaaaaagg | ctaa        | 1434 |

&lt;210&gt; 166

&lt;211&gt; 2841

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 166

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| atgaagccgc  | tctcttcacc  | gttacagcag  | tactggcaga  | ccgttggtga | gcggctgcc   | 60   |
| gagcctttag  | ccgaggaatc  | acttagcgca  | caggcggaagt | cagtacttac | ttttagtgtg  | 120  |
| tttgtgcag   | acagcggtgat | tgcgcatcca  | gagtggtgga  | cggaactgga | aagccaaccg  | 180  |
| ccgcagggcg  | acgaatggca  | gcattacgcg  | gcattggtgc  | aggaggcgct | ctgtaatgtg  | 240  |
| agtgcagaa   | ccgggttaat  | gcgcgaagctg | cggtatttcc  | ggcgccgcat | tatggtgcgc  | 300  |
| atcgccctgg  | cgcaaacgct  | ggcactggtt  | actgaagaga  | gcataattga | gcagctcagc  | 360  |
| tatctggcgg  | agacgctgat  | tgttgccggc  | cgtgactggc  | tgtatgacgc | ctgctgccgc  | 420  |
| gagtgaggaa  | cgccgtgcaa  | tgcgccagggc | gaagcgcaac  | cgctgctgat | tttaggcattg | 480  |
| ggtaagctgg  | gcggtgggga  | gctgaatttc  | tccctcgata  | tcgatctgat | ttttgcctgg  | 540  |
| ccggaacatg  | gttgtacgca  | gggtggacgc  | cgggaaactgg | ataacgcgca | gttttttacc  | 600  |
| cgcatggggc  | agcggctgat  | ttaaagtgctg | gatcaaccaa  | cgaggatgg  | cttcgtctat  | 660  |
| cgctgggata  | tgccggctcg  | tccgtttggc  | gaaagtggcc  | cgctggtgct | gagctttgcc  | 720  |
| gcgttggaag  | attattacca  | ggagcagggg  | cgcgactggg  | agcgttacgc | gatggtcaag  | 780  |
| gcgcggatta  | tgggcgatag  | cgaaggcgctc | tatgctaacc  | agttgcgtgc | gatgctgcgc  | 840  |
| ccgtttgttt  | tccgtcggtt  | catcgatttc  | agcgtgattc  | agtcgctgcg | caacatgaaa  | 900  |
| gggtgatttg  | cccgtgaagt  | gcgtcgacgt  | ggtttgaccg  | acaatatcaa | actcggcgca  | 960  |
| ggcggcattc  | gcgaaattga  | atttatcggt  | cagggtgtcc  | agctcattcg | cggcggacgc  | 1020 |
| gaaccgctcg  | tgcaatcgcg  | ctctttactg  | ccaacgctca  | gcgccattgc | cgagctgcat  | 1080 |
| ctgctttctg  | aaaacgatgc  | tgaacaattg  | cgaagtggcg  | atctgttcc  | gcggcgctcg  | 1140 |
| gaaaaacctgc | tgcaaaagcat | taacgacgaa  | caaaaccaga  | cgcttccctc | tgatgagctt  | 1200 |
| aatcgctgcg  | ggctggcggtg | ggcgatggac  | tttgctgact  | ggccgcaact | gaccggggcg  | 1260 |
| ctgaccgcac  | atatgaccaa  | tgtgcgcggg  | gtgtttaatg  | aattgattgg | cgacgatgaa  | 1320 |
| agtgaaactc  | aggaagagtc  | gctgtcggaa  | cagtggcggtg | agctgtggca | ggatgcgttg  | 1380 |
| caggaaagtg  | acactacgcc  | agtgctggcg  | catcttagcg  | aggatgatcg | caaacagggtg | 1440 |
| ctaaccgctga | tggccgattt  | ccgcaaaagag | ctggataaag  | gcaccatcgg | gccgcgagga  | 1500 |
| cgctcaggtg  | tcgaccatct  | gatgccgcat  | ctgctaagtg  | atgtctgtgc | gcgtgaaagac | 1560 |
| gctgcgggta  | cgctgtcgcg  | cattacggcc  | ttgctgggtg  | ggattgttac | ccgcaccacc  | 1620 |
| tatttagaat  | tgtcagtgga  | attccccggc  | gcgcttaaac  | atttgatttc | tctgtgtgcc  | 1680 |
| gcgtcgccga  | tgattgccag  | ccagctggcg  | cgttatccat  | tattgctgga | tgaattgctc  | 1740 |
| gatccaaaca  | ccctttacca  | gccgacggcg  | accgatgcct  | accgcgatga | gttgcgccag  | 1800 |
| tatttgctgc  | gcgtgccgga  | agatgacgaa  | gagcaacagc  | ttgagcgctg | gcgtcagttc  | 1860 |
| aaacaggcgc  | agctgttacg  | catcgccgca  | cgggatatcg  | ccggtacgct | accggtgatg  | 1920 |
| aaagtgcgag  | atcacttaac  | ctggctggcg  | gaagccatga  | tagatgccgt | cgttcagcag  | 1980 |
| gcgtgggttc  | aaatgggtgc  | ccgctacggg  | aagccgaatc  | acctgaacga | acgcgaagg   | 2040 |
| cggtgggttc  | cggtgggtgc  | ctacggcaag  | ctggcgggct  | gggagttagg | ctacagttcc  | 2100 |
| gatcttgacc  | ttatcttcc   | ccatgattgc  | ccaatggatg  | cgatgactga | cggtgagcgg  | 2160 |
| gaaatcgacg  | ggcggcagtt  | ttatctcgct  | ctggcgcaac  | gcattatgca | tctgttcagt  | 2220 |



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PCT/US00/02200

|             |             |            |            |             |            |      |
|-------------|-------------|------------|------------|-------------|------------|------|
| acgcgtacct  | cttcggcat   | tttgatgaa  | gtggatgctc | gactgcgtcc  | gtccggggcg | 2280 |
| gcgggaatgc  | tggtagacatc | cgcagaagca | tttgccgatt | atcagaaaaa  | cgaggcctgg | 2340 |
| acgtgggaac  | atcaggcgct  | ggtgctgctg | cgtgtagtgt | acggcgatcc  | gcagctcacc | 2400 |
| gcgcactttg  | acgcagtgcg  | tcgcgagatt | atgacgctgc | cgcgtgaag   | taaaactctg | 2460 |
| caaacggaag  | tgcgggaaat  | gcgcgagaaa | atgcgcgtc  | atctcggcaa  | taaacatcgc | 2520 |
| gatcgctttg  | atatcaaaagc | tgatgaagg  | ggaattaccg | atatacgaatt | tattacccaa | 2580 |
| tatctggtgt  | tgcgctacgc  | tcatgaaaaa | ccgaagttaa | cgcgctggtc  | agacaacgtg | 2640 |
| cgtattctgt  | aactactggc  | gcaaaacgac | attatggaag | agcagggaagc | gatggcgctg | 2700 |
| accgctgctt  | acactacgct  | tcgcgatgaa | cttcacatc  | tggcattaca  | ggaattgccg | 2760 |
| ggccatgtgt  | cggaggattg  | cttcaccgca | gagcgtgaac | tggtagcgggc | aagctggcag | 2820 |
| aagtggctgtg | tggaagaatg  | a          |            |             |            | 2841 |

<210> 167  
 <211> 1302  
 <212> DNA  
 <213> E. Coli

&lt;400&gt; 167

|            |            |            |             |             |            |      |
|------------|------------|------------|-------------|-------------|------------|------|
| atggctcagg | aaatcgaatt | aaagtttatt | gttaatcaca  | gtgccgttga  | ggcgttgctg | 60   |
| gaccatctca | atacgtggg  | cggcgagcac | catgaccccg  | tgcagttgct  | gaatatttac | 120  |
| tacgaaacgc | cggataactg | gctgctggg  | cacgatatgg  | gcttacgtat  | tcgtggcgaa | 180  |
| aacggtcgct | atgagatgac | catgaaagt  | gcagggaag   | tgacaggcg   | cttacatcag | 240  |
| cgcgcggaat | ataacgtg   | gttgagcgaa | ccgacgctc   | acctggcgca  | gttacgcagc | 300  |
| gaagctctgg | cgaacggcga | attgcccgcc | gatctcgct   | cccgctgca   | gccgctgttc | 360  |
| agcaccgatt | tttatcgca  | aaaatggctg | gtggcggtcg  | atggtagcca  | aattgaaatc | 420  |
| gccctcgacc | agggggaagt | gaaagcggtg | gaatttgctg  | aacctatctg  | tgagctggaa | 480  |
| ctggaaactg | ttagcgcgca | cacgcgcgcg | gtgctgaaac  | tggcgaaacca | actggtatcg | 540  |
| caaacgggat | tacgccagg  | cagcctgagc | aaagcggcgc  | gtggctatca  | tctggcgag  | 600  |
| ggcaatccgg | cgcgtgaaat | caaacggacc | accattttgc  | atggtgcggc  | aaaagccgat | 660  |
| gtggaaacag | ggctggaagc | ggcgctcgag | ctggcggttag | cgcaatggca  | gtatcatgaa | 720  |
| gaactgtggg | tacgcggcaa | cgatgcggcg | aaagaacagg  | tgctggcagc  | cattagcctg | 780  |
| gtccgtcata | cgtgatgct  | gttcggtggt | attgtgcgc   | gtaaagcgag  | cactcactta | 840  |
| cgtgatctgc | tgactcaatg | cgaaggcagc | attgcttctg  | cgggtgtctg  | cgtgacggcg | 900  |
| gtctactcta | ccgaaacggc | aatggcgaa  | ctggcggtga  | ccgaatggtt  | ggtaagcaaa | 960  |
| gcatggcagc | catttttaga | tgccaaagcg | cagggcaaaa  | tcagcgactc  | cttcaaacgc | 1020 |
| tttgccgata | tccatctt   | ccgccatgcc | gctgaaactga | aaagcgtttt  | ctgccagccg | 1080 |
| ttaggcgatc | gttaccgtga | ccagttgcca | cgcctgacgc  | gtgatattga  | ctcaatactg | 1140 |
| ttgctggcgg | gttactatga | tcctgtcgtc | gcgcaagcct  | ggctggagaa  | ctggcagggg | 1200 |
| ctgcatcacg | ctattgcgac | cgggcaacgc | atcgaaattg  | aacattttccg | taatgaggca | 1260 |
| aaacaatcag | aaccgttctg | gttcacacag | ggaaaacgtt  | aa          |            | 1302 |

<210> 168  
 <211> 213  
 <212> DNA  
 <213> E. Coli

&lt;400&gt; 168

|            |            |             |            |             |            |     |
|------------|------------|-------------|------------|-------------|------------|-----|
| atgtccggta | aaatgactgg | tatcgtaaaa  | tggttcaacg | ctgacaaaag  | cttcggcttc | 60  |
| atcactcctg | acgatggctc | ttaaagatgtg | ttcgtaact  | tctctgctat  | ccagaacgat | 120 |
| ggttacaaat | ctctggacga | aggtcagaaa  | gtgtccttca | ccatcgaaaag | cggcgctaaa | 180 |
| ggcccgag   | ctggtaacgt | aaccagcctg  | taa        |             |            | 213 |

<210> 169  
 <211> 1572  
 <212> DNA  
 <213> E. Coli

&lt;400&gt; 169

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgagggaca | ttgtggacc  | tgtattctct | atcggtatct | catcattatg | ggatgagctg | 60  |
| cgacatatgc | cagcaggcgg | cgtctgggtg | tttaacgtcg | atcgccatga | agatgctatc | 120 |
| agtctggcga | atcaaaat   | tgcatcccag | gctgaaaccg | cacacgtcgc | ggtcattagc | 180 |

|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| atggacagcg  | atccggcgaa | aatctttcaa  | ttagatgatt  | ctcaagggcc  | ggaaaaaata  | 240  |
| aaattatatt  | caatgctaaa | tcatgaaaaa  | ggtctatact  | atgtgacccg  | tgatttgacg  | 300  |
| tggtctattg  | atccccataa | ttaccttttt  | attcttgttt  | gcgcaataa   | cgcatggcaa  | 360  |
| aacattccctg | ccgagcggct | tcgctcatgg  | ttggataaaa  | tgaataaatg  | gagcaggtta  | 420  |
| aaccattggt  | cgcttttggt | aattaatccc  | ggaaataata  | acgataaaca  | attttcattg  | 480  |
| ttgcttgagg  | aataccgttc | actttttggt  | cttgccagtt  | tgctgtttca  | gggtgaccaa  | 540  |
| catttgctgg  | atattgcctt | ctgggtgcaac | gaaaaagggg  | tcagcgcccc  | tcagcagctt  | 600  |
| agcgttcagc  | aacaaaaatg | tatctggaca  | ttagttcaaa  | gcgaagaggg  | ggagatccaa  | 660  |
| ccacgcagcg  | acgaaaaacg | cattctgagt  | aatgttgctg  | tactggaagg  | tgccgcgccg  | 720  |
| ctatcggaac  | actggcaact | gttcaacaat  | aacgaagtcc  | tggtcaatga  | agccccgtacc | 780  |
| gctcaggcgg  | cgacggtggt | cttttcttta  | cagcaaaatg  | cgcaaatcga  | gccactggcc  | 840  |
| cgacgattc   | ataccctgcg | tcgccagcgc  | ggtagtgcga  | tgaaaaatcct | cggtcgggaa  | 900  |
| aataccgcta  | gcctgcgcgc | caccgatgaa  | cggttggtat  | tgccctgctg  | tgcaaatatg  | 960  |
| gttattccgt  | ggaatgcgcc | actctcccgt  | tgtctgacga  | tgatcgaaag  | cggtcaaggg  | 1020 |
| cagaagttaa  | gtcgtatgt  | gccggaagat  | atcactacct  | tgctgtcaat  | gacccagccg  | 1080 |
| ctcaactgc   | gtgttttcca | gaagtgggat  | gtgttctgta  | atgccgtcaa  | caacatgatg  | 1140 |
| aataaccctc  | tattacctgc | ccacggtaaa  | ggcgttctgg  | ttgccctacg  | tcgggtaccg  | 1200 |
| ggtatccgcg  | ttgaacaagc | cctgacgctg  | tgctgcctta  | accgtaccgg  | cgatatcatg  | 1260 |
| accattggcg  | gtaatcggt  | ggtgctgttt  | ctctcattct  | gtcggattaa  | cgatctggat  | 1320 |
| accgcttga   | atcatatttt | ccattgcct   | actggcgaca  | ttttctcaaa  | ccgtatggtc  | 1380 |
| tggtttgaa   | atgatcaaat | cagtgcgcag  | ctgggtgcaga | tgctgttgc   | tgccccagaa  | 1440 |
| caatggggca  | tgccgctgcc | tttaacgcaa  | agttctaaac  | cggtcatcaa  | tgccgagcac  | 1500 |
| gatggtcgcc  | actggcgacg | aataaccagaa | cccatgcgac  | tggttagatga | tgctgtggag  | 1560 |
| cgctcatcat  | ga         |             |             |             |             | 1572 |

&lt;210&gt; 170

&lt;211&gt; 189

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 170

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgaccatca | gcgatatcat | tgaaattatt | gtcgtttgcy | cactgatatt | tttcccgtcg | 60  |
| ggctatctgg | cgcggcactc | tttgcgacgc | attcgcgaca | ccttacgttt | gttctttgct | 120 |
| aaacctcggt | atgttaaacc | ggccgggacg | ttacgcccga | cgaaaaaagc | cagggcaacc | 180 |
| aaaaaatga  |            |            |            |            |            | 189 |

&lt;210&gt; 171

&lt;211&gt; 1680

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 171

|            |             |            |            |            |             |      |
|------------|-------------|------------|------------|------------|-------------|------|
| atgactcaat | ttacgcaaaa  | taccgccatg | ccttcttccc | tctggcaata | ctggcgcggc  | 60   |
| ctttccggct | ggaacttcta  | ttttctgggt | aagttcggcc | tggtgtgggc | gggatattctt | 120  |
| aacttccatc | cgctcctcaa  | tttgggtgtt | gccgcgtttc | tgctgatgcc | ccttccgcgc  | 180  |
| tacagcctgc | atcgcttgcg  | ccactggatt | gccctgccga | tcggcttgcg | tttgttctgg  | 240  |
| catgacacct | ggttgccctg  | cccggaaagc | ataatgagcc | agggttcgca | ggtggcgggg  | 300  |
| ttcagtaccg | attatttaat  | cgaccttgtc | acacgcttta | ttaactggca | gatgattggg  | 360  |
| gccatttttg | ttttattagt  | ggcctgggta | ttcctgtcac | aatggattcg | cattaccggt  | 420  |
| tttgtggttg | ccatactgct  | atggctgaac | gtacttaacc | tgccgggacc | aagtttctcc  | 480  |
| ttgtgqccag | ccggacaacc  | gacgaccact | gtaacaacga | cggttggtaa | cgacgcgcca  | 540  |
| accgttgccg | cgacgggtgg  | cgacccggta | gtgggtgata | tgcccgcaca | aactgcaccg  | 600  |
| ccaacaacgg | cgaaccttaa  | cgcttggtcg | aataatttct | ataacgcgga | ggcgaaacgt  | 660  |
| aaatcgacct | tcccgtcttc  | gctgcccgct | gatgctcagc | catttgaact | actggtgatt  | 720  |
| aacatctggt | cgctttccctg | gtcggatata | gaagccgcgc | ggttgatgtc | gcattccactg | 780  |
| tggtcgcatc | tcgatattga  | gttcaagaac | tttaactccg | ccacctccta | cagtggcccg  | 840  |
| gcggcgatcc | gtttactgcg  | cgccagctgc | gggcagactt | cgcacactaa | tctgtatcaa  | 900  |
| ccggcaataa | acgactgcta  | tctgtttgat | aacctttcga | aactgggctt | taccagcac   | 960  |
| ctgatgtgg  | gacataacgg  | ccagttcggc | ggttttttga | aagaagttcg | cgaaaaatggc | 1020 |
| ggcatgcaga | gcgaattgat  | ggatcaaca  | aatctgcggg | ttattttgct | gggtttgat   | 1080 |
| ggttcgccgg | tttatgacga  | taccgctgtg | cttaaccgct | ggctggacgt | taccgaaaaa  | 1140 |

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|             |            |            |             |             |            |      |
|-------------|------------|------------|-------------|-------------|------------|------|
| gataaaaaaca | gccgtagtgc | cacgttctac | aacacgccttc | cactgcatga  | cggcaaccat | 1200 |
| tatccggggg  | tcagcaaaac | agcggattac | aaagcgcggg  | cgcagaaatt  | ctttgatgaa | 1260 |
| ctggacgcct  | tctttactga | acttgagaaa | tcgggtcgta  | aagtgatggg  | ggcgtgggtg | 1320 |
| ccggaacacg  | gcggcgcgct | gaaggcgac  | agaatgcagg  | tatctggcct  | acgtgatatc | 1380 |
| cctagcccg   | ctatcaccca | cgccccgtt  | ggggtgaaat  | tcttcggcat  | gaaggcaccg | 1440 |
| catcaggggg  | caccgattgt | catcgaacaa | ccgagcagct  | tcttcggctat | ctccgatctg | 1500 |
| gtgggttcg   | ttctcgatgg | caagattttc | accgaagaca  | atgttgactg  | gaaaaaactc | 1560 |
| accagtggtg  | tgccacaaac | agcaccggtc | tccgagaact  | caaatgcagt  | agttattcaa | 1620 |
| taccagata   | aaccgtacgt | tcgcctgaac | ggcggcgact  | gggtgcctta  | cccgcagtaa | 1680 |

<210> 172  
 <211> 384  
 <212> DNA  
 <213> E. Coli

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| <400> 172   |             |            |            |            |            |     |
| atggaagggt  | caagaatgaa  | ataccgcac  | gctttagctg | tttctctctt | tgctcttagt | 60  |
| gccggtagtt  | atgccactac  | cctgtgtcag | gaaaaggagc | aaaatatcct | taaggagatc | 120 |
| agctatgccg  | aaaaacacca  | aaaccagaat | cgtattgacg | gtctgaataa | agccctgagt | 180 |
| gaagtccggg  | ccaactgttc  | agatagccag | ctgcgtgccg | atcatcagaa | gaaaatcgca | 240 |
| aagcagaaaag | atgaggtggc  | ggaacgcgag | caagattttg | ccgagggcga | gcaaaaaggc | 300 |
| gatgccgata  | agattgccaa  | acgcgaacgg | aaactggcag | aagcgcagga | agagctgaaa | 360 |
| aagctggaag  | gcgcgcgacta | ctaa       |            |            |            | 384 |

<210> 173  
 <211> 306  
 <212> DNA  
 <213> E. Coli

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| <400> 173   |            |            |             |            |            |     |
| atgtcgaaaag | aacacactac | ggaacatctg | cgctgctgagt | tgaaatccct | ttccgatacg | 60  |
| ctggaagagg  | tgcttagctc | atctggcgag | aagtcgaaag  | aagagttgag | taagattcgt | 120 |
| agcaaaagcg  | agcaggcact | gaaacagagc | cgttatcgcc  | tgggtgaaac | cggtgatgcc | 180 |
| attgccaaaac | aaacccgtgt | cgcgcgcgcg | cgctgccgatg | agtatgtgcg | cgaaaatccg | 240 |
| tggacggggc  | tgggcattgg | cgctgcaatc | ggtgtagtgc  | tcggcgttct | gctgtcgcgt | 300 |
| cgtaa       |            |            |             |            |            | 306 |

<210> 174  
 <211> 405  
 <212> DNA  
 <213> E. Coli

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| <400> 174  |            |             |            |            |            |     |
| atggcggaca | ctcatcacgc | acaagggccc  | ggtaaaagcg | ttctgggcat | cgggcagcga | 60  |
| attgtttcta | tcatggttga | aatggtagag  | acacgtctcg | ggctggcggt | ggtggagctg | 120 |
| gaagaggaaa | aagcgaatct | ctttcaactt  | ttactgatgc | tgggcctgac | gatgcttttc | 180 |
| gctgcatttg | gtcttatgag | cctgatgggtg | ctaattattt | gggcgggttg | cccgcaatat | 240 |
| cgctgaatg  | cgatgattgc | caccaccggtg | gtgttgctgc | tactggcact | gattggcggt | 300 |
| atctggacgc | tacgtaaaac | gcgtaagtct  | acgttgctgc | gccatacacg | ccatgagtta | 360 |
| gcaaacgata | ggcagctgct | cgaggaggag  | tcccgtgagc | agtaa      |            | 405 |

<210> 175  
 <211> 300  
 <212> DNA  
 <213> E. Coli

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| <400> 175  |            |            |             |            |            |     |
| gtgagcagta | aagtcgaacg | tgaacgacgt | aaggcgcaac  | tgcttagcca | gatccagcaa | 60  |
| caacggctgg | atctttccgc | cagtcgtcgt | gaatggctgg  | agacaacagg | cgcttacgat | 120 |
| cgctcgctga | atatgtgct  | aagtctgcgc | tcctgggcgc  | tggttggcag | tagcgtgatg | 180 |
| gcgatctgga | cgattcgcca | tcctaatatg | ctgggtccgct | gggccagacg | cggttttggc | 240 |

gtatggagcg cctggcgctct gggttaaaacg accctcaagc agcaacagct tcgcggttaa 300

<210> 176  
<211> 483  
<212> DNA  
<213> E. Coli

<400> 176

atgattctct ccatcgacag caacgacgct aataccgcg c attgcacaa aaaaacaatc 60  
agcagcctga gtggcgagc ggagagtatg atgaaaaat tagaagatgt tgggtgactg 120  
gtagcgcgca ttttaatgcc gattctgttt attaccgctg gctggggaaa aattactggc 180  
tacgcggtga cccaacaata tatggaagca atggcgctcc cgggttttat gctgccactg 240  
gtgattctgc ttgagtttgg tgggtggtctg gcaatcctgt tcggtttcct gactcgcacc 300  
acagccctgt ttaactgctgg ctttacgctg ctgacggcat ttttatttca cagcaacttt 360  
gctgaaggcg tcaactcgct gatgttcacg aaaaacctga caatttctgg cggattcctg 420  
ctgctggcaa ttaccggctc gggcgcgtat agcatcgacc gcctgctgaa taaaaagtgg 480  
taa 483

<210> 177  
<211> 891  
<212> DNA  
<213> E. Coli

<400> 177

atgatcaaga agacaacgga aattgatgcc atcttgtaa atctcaataa ggctatcgat 60  
gccactacc agtggctggt gagtatgtt cacagcggtg tcgagagaga tgccagtaag 120  
ccagaaataa cggataacca ttcttatgga ctgtgccagt ttggtcgggtg gattgatcat 180  
ctggggccac tcgataacga tgaattacct tacgttcggc taatggattc tgcccatcaa 240  
catatgcata actgtggtcg ggaattaatg ctggctattg ttgaaaatca ctggcaggac 300  
gcgcatttcg acgcctttca ggaggggttg ctttctttta ctgcggcatt aaccgattac 360  
aaaatttatt tgctgacgat ccgtagcaat atggatgtt tgacgggatt gccgggtcgt 420  
cgggttcttg atgaatcctt tgatcatcag ttacgcaacg ctgagcctct gaatctttat 480  
ttaatgttgt tggatattga cggattttaa ttggttaatg atacctacgg gcattttaatc 540  
ggcgatgtag tattacgcac cctggcaact tacttagcca gttggacggc tgattacgaa 600  
acggtttatc gctacggggg cgaagaattt atcattattg tcaaaagcggc taatgatgaa 660  
gaagcatgtc gtgcagggtg cagaatttgc cagttagtcg ataaccatgc catcacacat 720  
tctgaaggcg atatcaacat taccgtgaca gcagggtgta gtcgcgcatt tctgaagag 780  
cctctgcatg tggtcatttg aagagcggac cgggcaatgt atgagggtaa gcaaaccgga 840  
agaaatcgct gcatgtttat tgacgaacaa aatgtgatta accgagttta a 891

<210> 178  
<211> 612  
<212> DNA  
<213> E. Coli

<400> 178

atgcgccttc gtgtgtgccc cgggttttatt tcaccacctc cgggcttcgg tggctcggc 60  
tataccctta cagcgagagc ttgtgttaac atttcaatac ccttacagtt gagagttatt 120  
gatagtgtg atgtatttac tccattgttg aaactttttg ctaacgagcc actcgaaga 180  
cttatgtata cgattatcat ttttgggttc actctctggc tgataccgaa agagtttact 240  
gtcgcattca atgcttatac tgaaatacct tggctctttc agattatcgt ttttgccttt 300  
tctttcgtgg tcgccatttc cttctcaaga ttgcgagcac atattcaaaa gcattattca 360  
ttactaccag agcaacgagt attgcttcgt ttatctgaga aagaaatcgc tgtatttaaa 420  
gatttcctta aaacaggaaa tcttattatc acttctcctt gccgtaacct ggttatgaaa 480  
aaattagaac ggaagggcac cattcaacat cagagtata gcgcaactg ttcttattat 540  
ctcgtcaccc aaaaatactc ccattttatg aagttattct ggaacagcag gagtagacgt 600  
tttaatcggt ag 612

<210> 179  
<211> 177  
<212> DNA

&lt;213&gt; E. Coli

&lt;400&gt; 179

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gtgcttctcc | aaccatcggc | gcgcaccagt | ttcggtttta | aatgttttgc | ttttggtata | 60  |
| cgatcatgga | gtgaacgttc | catcctgggt | ggggaacacg | ccgcacacca | gggattcggt | 120 |
| gttgccgagg | tcgatttttt | gcattttgcy | aatctcacat | cttgttgcta | cgtatag    | 177 |

&lt;210&gt; 180

&lt;211&gt; 4281

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 180

|             |            |            |             |            |             |      |
|-------------|------------|------------|-------------|------------|-------------|------|
| atgagcggaa  | aaccagcggc | gcgtcaggga | gatatgactc  | agtatggcgg | tcccatgtgc  | 60   |
| cagggttcgg  | cagggtgaag | aattggcgcg | cccaccggcg  | tggcgtgctc | ggtgtgtccg  | 120  |
| ggcgggatga  | cttcgggcaa | cccggtaaat | ccgctgctgg  | gggcgaaggt | gctgcccggc  | 180  |
| gagacggacc  | ttgcgtgcc  | cgcccgctg  | ccgttcattc  | tctcccgac  | ctacagcagc  | 240  |
| taccggacga  | agacgcctgc | accggtgggc | gttttcggcc  | ccggctggaa | agcgccttct  | 300  |
| gatatccgct  | tacagctacg | tgatgacgga | ctgataactca | acgacaaacg | cgggcgagac  | 360  |
| attcactttg  | agccgctgct | gccgggggag | gcggtgtaca  | gccgcagtga | gtcaatgtgg  | 420  |
| cttggtgcgcg | gtggaaggg  | agcacagccg | gacggccata  | cgctggcgcg | gctgtggggg  | 480  |
| gcgctgcgcg  | cgatatccg  | gttaagcccg | catctttacc  | tggcgaccaa | cagcgacacg  | 540  |
| gggcccgtgt  | ggatactggg | gtggtctgag | cggtgcccgg  | gtgctgagga | cgtactgcca  | 600  |
| gcgcgcgctgc | cgccgtaccg | ggtgcttacc | gggatggcgg  | accgcttcgg | gcggacgctg  | 660  |
| acgtaccggc  | gtgaggccgc | cggtgacctg | gccggggaaa  | tcaccggcgt | gacggacggg  | 720  |
| gccggggcgg  | agttccgtct | ggtgctgacc | acgcaggcgc  | agcgtgcgga | agaggcccg   | 780  |
| acctcttcgc  | tatcttcttc | tgacagttcc | cgccctctct  | cagcctcagc | gttccccgac  | 840  |
| acactgccc   | gtaccgaata | cgccccgac  | aggggtatcc  | gcctttcggc | ggtgtggctg  | 900  |
| atgcacgacc  | cgccataccc | ggagagcctg | cccgtctgcg  | cactggtgcg | gtacacgtat  | 960  |
| acggaagccg  | gtgaactgct | ggcggtatat | gaccgcagca  | atacgcaggt | gcgcgcttct  | 1020 |
| acgtatgacg  | cgagcacccc | gggcccggat | gtggcgaccc  | gttacgcggg | aaggccggag  | 1080 |
| atgcgctacc  | gctacgacga | tacggggcgg | gtggtggagc  | aactgaaccc | ggcagggtta  | 1140 |
| agctacogct  | atctttatga | gcaggaccgc | atcacogtca  | ccgacagcct | gaaccggcgt  | 1200 |
| gaggtgctgc  | atacagaagg | cggggcccgg | ctgaaacggg  | tggtgaaaaa | agaactggcg  | 1260 |
| gacggcagcg  | tcacgcgcag | cggttatgac | gcggcaggaa  | ggctcacggc | gcagacggac  | 1320 |
| gcggcgggac  | ggaggacaga | gtacggtctg | aatgtggtgt  | ccggcgatat | cacggacatc  | 1380 |
| accacaccgg  | acgggcccgg | gacgaaattt | tactataaac  | acgggaacca | gctgacggcg  | 1440 |
| gtggtgtccc  | cgagcgggct | ggagagccgc | cgggaaatat  | atgaaccggg | caggctggta  | 1500 |
| tcggagacat  | cgcgacgcgg | ggagacagta | cgctaccgct  | acgatgacgc | gcacagttag  | 1560 |
| ttaccggcga  | cgacaacgga | tgcgacgggc | agcaccgggc  | agatgacctg | gagccgctac  | 1620 |
| gggcagttgc  | tggcgttcac | cgactgctcg | ggctaccaga  | cccgttatga | atacagaccgc | 1680 |
| ttcgcccaga  | tgacggcggt | ccaccgcgag | gaaggcatca  | gcctttaccg | ccgctatgac  | 1740 |
| aaaccgtggc  | ggttaacctc | ggtgaaagac | gcacagggcc  | gtgaaacgcg | gtatgaatac  | 1800 |
| aacgcgcgag  | gcgacctgac | tgccgttatc | accccggaag  | gcaaccggag | cgagacacag  | 1860 |
| tacgatgcgt  | ggggaagggc | ggtcagcacc | acgcaggcgc  | ggctgacgcg | cagtatggag  | 1920 |
| tacgatgcgt  | ccggacgtgt | catcagcctg | accaacgaga  | acggcagcca | cagcgtcttc  | 1980 |
| agttacgatg  | cgctggaccg | gctggtacag | cagggcggct  | ttgacggggc | gacgcaacgt  | 2040 |
| tatcattatg  | acctgaccgg | aaaactcaca | cagagttagg  | atgagggaat | tgtcatcctc  | 2100 |
| tggtactacg  | atgaatcgga | ccgtatcact | caccgcacgg  | tgaacggcga | accggcagag  | 2160 |
| cagtggcagt  | atgatggcca | cggtggctg  | acagacatca  | gccacctgag | cgaaggccac  | 2220 |
| cggtgtgccg  | tccactatgg | ctatgacgat | aaaggccgcc  | tgaccggcga | atgccagacg  | 2280 |
| gtggagaacc  | cgagacggg  | ggaactgctg | tggcagcatg  | agacgaaaca | cgcatacaac  | 2340 |
| gagcaggggc  | tggcaaacgg | cgtcacgcgg | gacagcctgc  | cgccggtgga | gtggctgacg  | 2400 |
| tatggcagcg  | gttacctggc | gggaatgaag | ctggcgggga  | cgccgctggt | cgagtatacg  | 2460 |
| cgggacaggg  | tgaccctgga | gacggtgcgc | agcttcggca  | gcatggcagg | cagtaatgcc  | 2520 |
| gcatacgaac  | tgaccagcac | atacacccc  | gcaggccagt  | tacagagcca | gcacctgaac  | 2580 |
| agcctggtat  | atgaccgtga | ctacgggtgg | agtgacaacg  | gcgacctggt | gcgcacagc   | 2640 |
| ggcccgcgac  | agacgcggga | atacggctac | agcggccacg  | gcaggctgga | gagtggtgcg  | 2700 |
| accctcgac   | cagacctgga | catccgcac  | ccgtatgcca  | cggacccggc | gggcaaccgg  | 2760 |
| ctgcgggacc  | cgagctgca  | cccggacagt | acactcacag  | tgtggccgga | taaccgcac   | 2820 |
| gcggaggatg  | cgcactatgt | ctaccgccac | gatgaatacg  | gcaggctgac | ggagaagacg  | 2880 |

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| gaccgcatcc | cggcggtgt  | gatacggacg  | gacgacgagc  | ggacccacca  | ctaccactac  | 2940 |
| gacagccagc | accgcctggt | gttctacacg  | cggatacagc  | atggcgagcc  | actggtcgag  | 3000 |
| agccgctacc | tctacgaccc | gctgggacgg  | cgaatggcaa  | aacgggtctg  | gcggcgaggag | 3060 |
| cgtgacctga | cggggtggat | gtcgtctgctg | cgtaaaccgg  | aggtgacgtg  | gtatggctgg  | 3120 |
| gacggagaca | ggctgacgac | ggtgcagact  | gacaccacac  | gtatccagac  | ggtatacgag  | 3180 |
| ccgggaaagt | tcacgccgct | catccgggtc  | gagacagaga  | acggcgagcg  | ggaaaaagcg  | 3240 |
| cagcggcgca | gcctggcaga | gacgctccag  | caggaaggga  | gtgagaacgg  | ccacggcgtg  | 3300 |
| gtgttcccg  | ctgaactggt | gcggctgctg  | gacaggctgg  | aggaagaaat  | ccgggcagac  | 3360 |
| cgctgagca  | gtgaaagccg | ggcgtggctt  | gcgcagctcg  | ggctgacgtg  | ggagcaactg  | 3420 |
| gccagacagg | tggagccgga | atacacaccg  | gcgcgaaaag  | ctcatcttta  | tcactgcgac  | 3480 |
| caccggggag | tgcgctggc  | gcttatcagc  | gaagacggca  | atacggcgtg  | gagcgcggaa  | 3540 |
| tatgatgaat | ggggcaacca | gcttaatgag  | gagaaccgcg  | atcatgtgta  | tcagccgtac  | 3600 |
| cgtctgccag | ggcagcagca | tgatgaggaa  | tcagggtctg  | actataaccg  | tcaccggtag  | 3660 |
| tacgatccgt | tgacggggcg | gtatattact  | caggaccgga  | tggggttgaa  | agggggatgg  | 3720 |
| aatttatatc | agtatccttt | aaatccacta  | caacaaattg  | accctatggg  | attattgcag  | 3780 |
| acttgggatg | atgccagatc | tggagcatgt  | acggggggag  | tttgtggtgt  | tctttcacgt  | 3840 |
| ataataggag | caagtaaatt | tgatagtact  | gcagatgctg  | cgttagatgc  | tttgaagaaa  | 3900 |
| acgcagaata | gatctctatg | taatgatatg  | gaatactctg  | gtattgtctg  | taaagatact  | 3960 |
| aatggaaaat | attttgcacg | taaggcagaa  | actgataaatt | taagaaagga  | gtcatatcct  | 4020 |
| ctgaaaagaa | aattgtccac | aggtacagat  | agagttgctg  | cttatcatatc | tcacgggtgca | 4080 |
| gatatgcatg | gcgattatgt | tgatgaattt  | ttttcaagta  | gcgataaaaa  | tcttgtaaga  | 4140 |
| agtaaagata | ataatcttga | agcattttat  | ctcgcaacac  | ctgatggacg  | atttgaggcg  | 4200 |
| cttaataata | aaggagaata | tattttttatc | agaaatagtg  | tcccgggatt  | gagttcagta  | 4260 |
| tgcataccgt | atcatgatta | a           |             |             |             | 4281 |

<210> 181  
 <211> 369  
 <212> DNA  
 <213> E. Coli

<400> 181

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| atgaaatata  | gttcaatatt | ttcgatgctt  | tcatttttta | tactatttgc | ctgtaatgag | 60  |
| acagctgttt  | acggttctga | tgaaaaacatt | atttttatga | ggtatgtgga | aaaattacat | 120 |
| ttagataaat  | actctgttaa | aaatacggta  | aaaactgaaa | caatggcgat | acaattagct | 180 |
| gaaatataatg | ttaggtatcg | ctatggcgaa  | cggattgcag | aagaagaaaa | accatattta | 240 |
| attacggaaac | taccagatag | ttgggttgtt  | gagggagcaa | agttacctta | tgaagttgag | 300 |
| ggtgtgttat  | ttattataga | aatttaataag | aaaaatggat | gtgttttgaa | tttctacat  | 360 |
| agtaataata  |            |             |            |            |            | 369 |

<210> 182  
 <211> 711  
 <212> DNA  
 <213> E. Coli

<400> 182

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| atgctggcgc  | tgatggatgc  | ggatggaaac  | attgcgtgga | gcggggagta | tgatgagtgg | 60  |
| ggcaaccagc  | tgaatgaaga  | gaaccgcgat  | cacctgcacc | agccgtaccg | gctgccgggg | 120 |
| cagcagtatg  | ataaggagtc  | ggggctgtac  | tacaaccgga | accggtacta | cgatccgttg | 180 |
| caggggagggt | atatcactca  | ggaccgcgata | gggctggagg | ggggatggag | tctgtatgag | 240 |
| tatccgctga  | atccggtgaa  | tggtattgat  | ccattagggg | taagtccgcg | agatgtagcg | 300 |
| ctaataagaa  | gaaaagatca  | actaaaccat  | caaagagcat | gggatataat | atctgatact | 360 |
| tatgaagata  | tgaagagatt  | aaatttaggt  | gggactgacg | aatttttcca | ttgtatggca | 420 |
| ttttgtcgag  | tgtctaaatt  | aaatgacgct  | ggtgttagcc | gatcggcgaa | agggctgggt | 480 |
| tatgaaaaag  | agatttagaga | ttacgggtta  | aatctgttcg | gtatgtacgg | cagaaaagta | 540 |
| aagctatccc  | attctgaaat  | gattgaagat  | aataaaaaag | acttggctgt | aaatgacctt | 600 |
| gggttgacat  | gtccatcaac  | aacagattgc  | tcagatagat | gtagtgatta | tattaatcca | 660 |
| gagcataaaa  | aaacgataaa  | ggctttacaa  | gatgctggct | atctcaagta | a          | 711 |

<210> 183  
 <211> 261  
 <212> DNA

&lt;213&gt; E. Coli

&lt;400&gt; 183

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| atgctgggcta | tctcaagtaa | tctatcaaag | atgataatat | ttatTTTTgc | tattataatc | 60  |
| attgttgttt  | tatgcgtaat | tacttatctt | tatttataca | aagatgaatc | tcttgtaagt | 120 |
| aaacattaca  | taaactatat | ggcaatacca | gaaaatgatg | gagtttttac | atggctocca | 180 |
| gatttttttc  | cgcacgtagc | ggtgcatata | tcaatatata | caaatgtaga | agatgattat | 240 |
| ttttttctta  | ttttcccta  | a          |            |            |            | 261 |

&lt;210&gt; 184

&lt;211&gt; 192

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 184

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gtgagggcca | gggaacaagt | ggcgaaaatc | gtatcaaaga | atgatccaga | tacaaaaaaa | 60  |
| gtgtgggtga | aatatggtaa | gataccaggg | caaggggatg | gtgtaaacct | ttttttgtt  | 120 |
| ggtgaaatta | atgttacgca | ttatTTTata | acaaatattg | gagctggatt | gcctgatgct | 180 |
| tgtgcagagt | aa         |            |            |            |            | 192 |

&lt;210&gt; 185

&lt;211&gt; 504

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 185

|            |            |             |            |             |            |     |
|------------|------------|-------------|------------|-------------|------------|-----|
| atgccgggca | acagcccgca | ttatgggctg  | tgccctcaac | acgattttac  | gtcacttaaa | 60  |
| aaactcaggg | cgcagtcggt | aacctcgcgc  | atacagccgg | gcagtgacgt  | catcgtctgc | 120 |
| gcggaaatgg | acgaacagt  | gggctatgct  | ggggctaaat | cgcgccagcg  | ctggctgttt | 180 |
| tacgcgtatg | acagtctccg | gaagacgggt  | gttgccgcag | tattcggtga  | acgcactatg | 240 |
| gcgcagctgg | ggcgtcttat | gagcctgctg  | tcaccctttg | acgtgggtgat | atggatgacg | 300 |
| gatggctggc | cgctgtatga | atcccgccctg | aagggaagc  | tgacagtaat  | cagcaagcga | 360 |
| tatacgcagc | gaattgagcg | gcataacctg  | aatctgaggc | agcacctggc  | acggctggga | 420 |
| cgggaagtgc | tgtcgtttct | aaaatcggtg  | gagctgcatg | acaaagtcat  | cgggcattat | 480 |
| ctgaacataa | aacactatca | ataa        |            |             |            | 504 |

&lt;210&gt; 186

&lt;211&gt; 276

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 186

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gtggcttctg | tttctatcag | ctgtccctcc | tggtcagcta | ctgacggggg | ggtgcgtaac | 60  |
| ggcaaaagca | ccgccggaca | tcagcgctat | ctctgctctc | actgccgtaa | aacatggcaa | 120 |
| ctgcagttca | cttacaccgc | ttctcaaccc | ggtacgcacc | agaaaatcat | tgatatggcc | 180 |
| atgaatggcg | ttggatgccg | ggcaacagcc | cgcattatgg | gcgttggcct | caacacgatt | 240 |
| ttacgtcact | taaaaaactc | aggccgcagt | cggtaa     |            |            | 276 |

&lt;210&gt; 187

&lt;211&gt; 417

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 187

|             |            |             |             |            |            |     |
|-------------|------------|-------------|-------------|------------|------------|-----|
| atgatgacta  | aaacccaaat | aaataaatta  | ataaaaaatga | tgaatgattt | agactatcca | 60  |
| tttgaagcac  | cgctcaagga | atcatttatt  | gaaagtataa  | tccaaataga | atttaattot | 120 |
| aattcaacta  | attgcctgga | gaagttatgt  | aatgaagtta  | gtattctttt | taagaatcaa | 180 |
| cctgattatc  | ttactttttt | aagagcaatg  | gatggattcg  | aagttaatgg | attacgatta | 240 |
| tttagcctct  | cgattccaga | accttcagtt  | aaaaaccttt  | ttgccgtaaa | tgaattttat | 300 |
| agaaataatg  | atgatttcat | aaacccctgat | ctacaagaac  | ggttagtgat | cggggattat | 360 |
| agcattttcaa | tatttactta | tgacattaaa  | ggtgatgctg  | ccaacttact | gatttag    | 417 |

<210> 188  
 <211> 1179  
 <212> DNA  
 <213> E. Coli

<400> 188  
 atgagtaata ttgtttacct gacagtaacg ggagaacaac aaggaagcat ctccgcaggt 60  
 tgtgggactt ctgagtctac aggtaatcgt tggcagagcg ggcatgagga tgaaatattt 120  
 acattctcac tcttaataaa tattaataat acggggcttg gttcacagtt ccatgggata 180  
 acattttgta aattaatgga taaaagcact ccattattta ttaattccat taacaataat 240  
 gaacaattat ttatgggatt tgacttctat cgaataaata gatttggttag attggaaaag 300  
 tattattata tacaactaag aggcgcgtttt ttatcggtta ttcatcacca gatcattgaa 360  
 aaccaactgg atacagaaac aataactatt agttatgaat ttatcctctg tcaacatctt 420  
 atcgcaataa ccgagttcag ctatttgcca ctccctgaaa attataaccg tttgttttta 480  
 ccaaattcaa aaaaccaaac aaataatcgt ttcaaaacgt taaacagcaa agctattggc 540  
 aggcactctg ctgctggtgg cgtatacaat gggaacattg aaggattcag agatactgcy 600  
 gaaaaactgg gtggagatgc aataaaagcg tatgatcaaa tactaaatga aaaaacagcg 660  
 ggcatagcga tagcaacagc atctattctt ttaacaaagc gttctaattg tgatacatat 720  
 acagaaataa atagttactt aggcacactt agagggtcaac aaaaacttct tgatgggata 780  
 gacataatag aaataatata cattaagaga ccttcaaaag acttagctaa cttacgaaag 840  
 gagtttaata aaactgtaag aaaaaatttt cttatcaaac ttgcaaaaac ctccgaagca 900  
 tctggaagat tcaacgcgca agacctttta agaatgagaa agggcaatgt tccctctaaa 960  
 tataatgttc accataaact atctctagat gatgggtgga ctaatgattt cgaaaattta 1020  
 gtattaatcg aaaacgaacc atatcataaa gtttttacta acatgcaatc acgaatagct 1080  
 aagggaatat tagtaggtga aagcaaaatc actccctggg ccattccatc tggctcaatt 1140  
 tatctccca tgaaaaatat tatggaccac acaaaatga 1179

<210> 189  
 <211> 666  
 <212> DNA  
 <213> E. Coli

<400> 189  
 atgggtactt ctgtgaacta taatatgcac ggagttaata ttcgctcaga gaatgcagca 60  
 aaacctcata cgatgccctc tagatatctt tgcgagtata ttagaagcat tgagaaaaat 120  
 ggccacgccc ttgattttgg ctgcggaaaa cttagatatt ctgatgaatt aatcagtaaa 180  
 tttgatgaag ttacttttct agactcgaaa aggcacactt aaagagagca aattattaga 240  
 ggaattaaaa ctaaaattat tgactatgtc ccacgatatt ataaaaatgc aaatacagtt 300  
 gctttcgagg atgtcgacaa aataattggg ggttacgatt tcatcctttg ctctaattgt 360  
 ctctctgcgc ttcttgtcgc ggatacaatc gacaaaaatg ttcttagcat caagagatta 420  
 ctaaaatcag gaggtgagac tcttattgta aatcaatata aaagctcata cttcaaaaaa 480  
 tacgaaacag gaagaaaaca tctttacgga tacatttaca aaaattcaaa aagtgtttct 540  
 tactatggat tactcgatga actcgcagtg caagaaatat gttcttcaca tggccttgaa 600  
 atattaaagt cgtggagtaa agcagggaagt tcatatgtca ctgttgggag ttgtaatgca 660  
 atataa 666

<210> 190  
 <211> 705  
 <212> DNA  
 <213> E. Coli

<400> 190  
 gtgaataata tgttcgaacc ccccaaaaat tataatgaaa tgttgcccta acttcataaa 60  
 gcaactttct taaatacgcct aatatattgc atacttctag ttatttcaga atacatccct 120  
 ttaataacat taccaaccaa gtatgtccca cctattaaag atcatgagag ctttattaat 180  
 tgggcactat cttttggtat attaccttgt gcttttgcca tttttgcata ttttaattagc 240  
 ggtgcgttag acetacataa caatgcagcc aaactacttc gggtgcgata tctttgggat 300  
 aagcatctaa ttataaaacc gttatcacgg agagctggag tcaacagaaa attaaataaa 360  
 gatgaagctc acaatgtaat gagcaatcta tattaccctg aagtaagaaa aattgaagac 420  
 aaacattata ttgaactctt ctggaataaa gtatactatt tttggatatt ttttgaattt 480



|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| tcgataattg | cattaatttc | cttcctaata  | atcttttttt | gcaaacaaat | ggatattttt | 540 |
| catgttgaag | gttctttgct | gtcttttattc | ttttttgtaa | ttttatcatt | ctcagtgagt | 600 |
| ggtattatct | ttgctttgac | agttaagccc  | agaactgaaa | gtcaagtcgg | aaaaatcccc | 660 |
| gacgataaaa | taaaagaatt | tttcactaaa  | aataacatta | attga      |            | 705 |

<210> 191  
 <211> 285  
 <212> DNA  
 <213> E. Coli

<400> 191

|            |            |             |            |             |             |     |
|------------|------------|-------------|------------|-------------|-------------|-----|
| atgtttacta | tcaacgcaga | agtacgtaaa  | gagcagggta | aggggtgcgag | ccgccgcctg  | 60  |
| cgtgccgcta | acaagttccc | ggcaatcatc  | tacggtggca | aagaagcgcc  | gctggctatc  | 120 |
| gagctggatc | acgacaaagt | catgaacatg  | caagctaaag | ctgaattcta  | cagcgaagtt  | 180 |
| ctgaccatcg | ttgttgacgg | taaaagaaatc | aaagttaaa  | ctcaggacgt  | acagcgctcac | 240 |
| ccgtacaaac | cgaagctgca | gcacatcgac  | ttcgttcgcg | cttaa       |             | 285 |

<210> 192  
 <211> 1977  
 <212> DNA  
 <213> E. Coli

<400> 192

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| atggtattgt  | tttatcgggc  | acactggcgc | gactataaaa  | acgatcaagt  | gaggatcatg  | 60   |
| atgaatctga  | cgactctgac  | ccaccgcgat | gcgttggtgc  | tgaatgcgcg  | ctttaccagc  | 120  |
| cgtgaagagg  | ccatccacgc  | gttgactcaa | cgtcttgctg  | ctctggggaa  | aatttccagt  | 180  |
| actgagcaat  | ttctggaaga  | agtgtatcgc | cgtgaaaagcc | ttggcccgcg  | cgcccttaggt | 240  |
| gaaggggttg  | ctgtgcccga  | tggcaaaact | gctgcggtaa  | aagaagcggc  | gtttgcggtc  | 300  |
| gccacactca  | gcgagccgct  | tcagtgggaa | ggcgttgatg  | gcccgggaagc | agttgattta  | 360  |
| gtggtgctgc  | tggcgattcc  | ccccaatgaa | gcgggtacta  | cgcatatgca  | actgctgaca  | 420  |
| gcgctgacca  | cgccgccttc  | ggatgatgag | attcgggcgc  | gtatacagtc  | ggcgacgacg  | 480  |
| cctgatgagt  | tgctctcgcc  | gctggatgac | aaggggagca  | cgcaaccttc  | tgccctcttt  | 540  |
| tccaacgcgc  | caactatcgt  | ctgcgtaacg | gcctgtccgg  | cgggtattgc  | tcacacctat  | 600  |
| atggctgcgg  | aatatctgga  | aaaagccgga | cgcaaaactcg | gcgtaaaatg  | ttacgttgaa  | 660  |
| aaacaaggcg  | ctaacggcat  | tgaagggcgt | ttaacggcgg  | atcaactcaa  | tagtgcaacc  | 720  |
| gcctgtattt  | ttgcggctga  | agtcgccatc | aaggagagtg  | agcgttttaa  | tggcattccc  | 780  |
| gcgctttcag  | tgccctgttc  | cgagccgatt | cgccatgcag  | aagcgttgat  | ccaacaagcg  | 840  |
| cttaccctca  | agcgtagcga  | tgagacgcgt | accgtacagc  | aagatacgca  | accggtgaaa  | 900  |
| agtgctcaaaa | cggagctgaa  | acaggcactg | ttgagcggaa  | tctcttttgc  | cgtaccggtg  | 960  |
| attgtcgcgg  | ggggcacggg  | gctggcggtc | gcggtattac  | tgctgcgaaat | cttcgggcta  | 1020 |
| caagatctgt  | ttaatgaaga  | aaactcctgg | ctgtggatgt  | accgcaagct  | ggcgggcggg  | 1080 |
| ctgctcggaa  | ttttgatggg  | accggtgctc | gcggccctata | ccgcctattc  | tctggcagat  | 1140 |
| aaaccggcgt  | tagcgccagg  | ctttgcggtc | ggacttgccg  | ccaacatgat  | cggctccggg  | 1200 |
| tttctcggcg  | cggctcgttg  | cggattgata | gccggttact  | tgatgcgctg  | ggtgaaaaat  | 1260 |
| cacttgcgtc  | ttagcagtaa  | attcaatgga | ttcctgactt  | tttatctcta  | cccgggtgctc | 1320 |
| ggtacgttgg  | gagcgggcag  | tctgatgctg | tttgtgtgtg  | gggaacctgt  | cgccctggatc | 1380 |
| aataactcgc  | ttaccgcctg  | gctgaacggg | ctgtcaggaa  | gtaacgcgct  | ggtgctgggt  | 1440 |
| gccattctcg  | gttttatgtg  | ttcctttgac | cttggaaggc  | cagtgaataa  | agccgcttat  | 1500 |
| gcattctgcc  | tgggcgcaat  | ggcgaacggc | gtttacggcc  | cgtatgccaat | tttcgcctcc  | 1560 |
| gtcaaaatgg  | tttcggcatt  | taccgtaacc | gcttccacga  | tgctcgcaac  | gcgcctgttt  | 1620 |
| aaagagtttg  | aaattgagac  | cgggaaatcc | acctggctgt  | tagggctggc  | aggtattacc  | 1680 |
| gaagggggcg  | tcccgatggc  | gattgaagat | ccgctgcggg  | ttattggttc  | gtttgtgctg  | 1740 |
| ggctctatgg  | taacgggcgc  | tattgtcggt | gcgatgaata  | tcggcccttc  | gacacccggg  | 1800 |
| gccggcattt  | tctcgctctt  | tttacttcat | gataatggcg  | cgggcgggtg  | tatggcggca  | 1860 |
| attggctggt  | ttggcgcggc  | attgggtggg | gctgcaatct  | cgactgcaat  | tctcctgatg  | 1920 |
| tggcgcgctc  | acgcgggttaa | gcatggcaac | tatctgactg  | atggcgtaat  | gccataa     | 1977 |

<210> 193  
 <211> 2634  
 <212> DNA  
 <213> E. Coli

&lt;400&gt; 193

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| atgaaagcag  | tatctcgcgt  | tcacatcacc | ccgcatatgc  | actgggatcg  | agagtgggtat | 60   |
| ttcaccacccg | aagagtcaag  | tattctgctg | gtcaataata  | tggaagagat  | cctgtgccga  | 120  |
| ctggaacagg  | acaacgaata  | caaatattac | gtactcgacg  | ggcaaacggc  | gacccctcgaa | 180  |
| gattatttcg  | cggtgaaacc  | ggaaaacaaa | gaccgtgtga  | agaaacaggt  | agaagccggc  | 240  |
| aagttgatta  | tcggccctcg  | gtataccacg | accgatacca  | cgattgtttc  | tcggaatcc   | 300  |
| atcgctcgta  | atctgatgta  | cggaatgcgt | gactgcctcg  | cgtttgccga  | gccgatgaaa  | 360  |
| ataagttatt  | taccagattc  | ctttggcatg | tccgggcaac  | tgccgcataat | ctacaatgga  | 420  |
| tttggcatta  | cccgcacat   | gttctggcgc | ggatgttcgg  | agcgccacgg  | tactgataaa  | 480  |
| accgagtttt  | tgtggcaaa   | cagtgcaggt | agcgaagtga  | cgggccaggt  | gctgccgctg  | 540  |
| ggctacgcca  | tcggtaaagta | cttacctgcc | gacgaaaacg  | gattacgtaa  | acgcctcgac  | 600  |
| agttattttg  | acgtgctgga  | aaaagcgtct | gtaaccaaa   | agattttgct  | gccgaatggg  | 660  |
| catgaccaga  | tgccattgca  | gcaaaatata | ttcgaagtga  | tggataagct  | acgtgagatc  | 720  |
| taccctcaac  | gtaagtttgt  | gatgagccgc | tttgaagagg  | tatttgagaa  | gatcgaaagc  | 780  |
| cagcgagata  | atctggcaac  | cctgaaaggg | gaattttattg | atggcaataa  | tatgcgcgtg  | 840  |
| catcgaccca  | tcggttctac  | gcgtatggat | atcaaaattg  | cccacgcgcg  | tattgaaaa   | 900  |
| aagattgtta  | atctgctgga  | accgctggca | acactggcct  | ggacgttggg  | ttttgaatac  | 960  |
| caccacggct  | tgctggagaa  | aattgtgaaa | gagatcttaa  | aaaatcatgc  | ccacgacagt  | 1020 |
| atcggtgct   | gctgtagtga  | caaagttcat | cgcgaaatcg  | tcgcccgcct  | cgaactgggt  | 1080 |
| gaagacatgg  | cgataaatct  | gattcgtttc | tacatgcgca  | aaattgccga  | caacatgccg  | 1140 |
| cagagcgacg  | ccgacaaact  | cgctctgttt | aacctgatgc  | cctggccgcg  | tgaagaagtt  | 1200 |
| atcaaacacca | ctgtgcggct  | gcgcgccacg | cagtttaatt  | tcgcccgcga  | tcgcggtcag  | 1260 |
| cctgtaccgt  | attttattcg  | ccatgcccg  | gagatcgatc  | caggccaat   | cgatcggcaa  | 1320 |
| atagttcatt  | acggttaatta | cgatcccttt | atggagtttg  | atatacagat  | caaccagatt  | 1380 |
| gtcccttcta  | tgggtctatg  | cacgctttat | atcgaagcga  | atcagccctg  | caacgtaatt  | 1440 |
| gcggcaaaaa  | gtgacgctga  | aggataactg | gaaaatgctt  | tctggcaaat  | tgcgctcaat  | 1500 |
| gaggtatggt  | ctctgcaact  | ggtagataaa | gacagcggtg  | tgcgctatga  | ccgggtattg  | 1560 |
| caaatggaag  | aaagctctga  | tgatgggtat | gaatatgact  | attcaccgcg  | aaaagaagag  | 1620 |
| tggttaatta  | ccgcagcgaa  | cgcaaaacgc | caatgcgata  | ttattcatga  | agcctggcag  | 1680 |
| agcagggctg  | ttatccgcta  | tgacatggca | gtgcgcgtca  | atttgtcaga  | acgcagcgcc  | 1740 |
| cggaacacca  | ctggcagagt  | agggtgtgtg | ttggttgtoa  | ctcttagtca  | taacagcagg  | 1800 |
| cgtattgatg  | tgatatcaaa  | tcttgataac | caggctgacg  | atcatcgctt  | tcgtgtcctg  | 1860 |
| gtccctacac  | cttttaacac  | cgacagtgtt | ctggcagata  | cgcagttttg  | ttcgctaacc  | 1920 |
| cgcccgctga  | acgacagtgc  | aatgaacaac | tggcagcaag  | aaggctggaa  | agaagccggc  | 1980 |
| gttccggtat  | ggaatatgct  | caactatggt | gccttacagg  | aagggcgtaa  | cggcagtggt  | 2040 |
| gtcttttagcg | aagggttacg  | tgaatttgaa | gtcatcggtg  | aagagaagaa  | aacctttgcc  | 2100 |
| attacgttgc  | tcgctggcgt  | gggttactg  | ggcaaaagaa  | atctgctttt  | aaggcctggg  | 2160 |
| cgcccttcgg  | gaattaaaa   | gccagtcctg | gactcacaac  | tacgtggtct  | gctttcttgt  | 2220 |
| cgccctaagtt | tattgagtta  | taccggtacg | ccaaccgcg   | ctggtgtagc  | tcagcagggc  | 2280 |
| cgagcatggc  | tgactccagt  | acagtgttac | aacaaaatcc  | catgggatgt  | gatgaagctc  | 2340 |
| aacaaagccg  | gattcaacgt  | gccggaaagt | tatagtttgt  | tgaaaatgcc  | cccagtgagg  | 2400 |
| tgccctgataa | gcgcacttaa  | gaaagctgaa | gaccgacaag  | aagtgatatt  | acggctgttt  | 2460 |
| aatccggctg  | aatcagcaac  | ctgtgatgcg | actgttgctt  | tcagtcgcga  | ggtgatttct  | 2520 |
| tgctcagaaa  | cgatgatgga  | tgaacacatt | accaccgagg  | aaaatcaagg  | ttcaaatcta  | 2580 |
| tcggggcctt  | ttttaccceg  | ccagtcacgg | acgttcagtt  | accggcttgc  | ctga        | 2634 |

&lt;210&gt; 194

&lt;211&gt; 1572

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 194

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| atgatgttag | atatagtcga  | actgtcgcgc  | ttacagtttg | ccttgaccgc | gatgtaccac | 60  |
| ttcctttttg | tgccactgac  | gctcgggtatg | gcgttcctgc | tggccattat | ggaaacggtc | 120 |
| tacgtcctct | ccggcaaaaca | gatttataaa  | gatatgacca | agttctgggg | caagtgtttt | 180 |
| ggtatcaact | tcgctctggg  | tgtggctacc  | ggtctgacca | tggagttcca | gttcgggact | 240 |
| aactggtctt | actattccca  | ctatgtaggg  | gatattctcg | gtgcgcgcgt | ggcaatcgaa | 300 |
| ggtctgatgg | ccttcttcct  | cgaatccacc  | ttttaggtgc | tggtctctct | cggttgggat | 360 |
| cgctcgggta | aagttcagca  | tatgtgtgtc  | acctggctgg | tgccgctcgg | ttcaaacctg | 420 |
| tccgcactgt | ggattctggt  | tgcgaaacgc  | tggtatgaaa | acccaatcgc | gtccgatttc | 480 |

```

aactttgaaa ctatgcgtat ggagatggtg agcttctccg agctggtgct taaccgggtt 540
gctcaggatga aattcggtca cactgtagcg tctggttatg tgactggcgc gatgttcac 600
ctcgggtatca gcgcagtgta tatgctgaaa ggtcggtgact tcgccttcgc taaacgctcc 660
tttgctatcg ctgccagctt cgggtatggtg gctgttctgt ctgttattgt tctgggtgat 720
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ggcctgtata cctgttccct ggtggcagaa ttgttcttaa tgttcaagtt tgcacgcctc 1500
ggcccaagca gctgaaaaac cggtcgctat cactttgagc agtcttccac gactactcag 1560
ccggcacgct aa 1572

```

&lt;210&gt; 195

&lt;211&gt; 1140

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 195

```

atgatcgatt atgaagtatt gcgttttacc tgggtggtgc tgggtggcgt tctgctgatt 60
ggttttgtag tcaactgacgg ttctgacatg ggggtgggca tgctcaccgg ttctctcggt 120
cgtaacgaca ccgagcgctcg aattatgatt aactccattg caccacactg ggacggtaac 180
cagggtttggc tgatcaccgc gggcgccgca ctctttgctg cctggccgat ggtctatgcc 240
gctgcgttct ccggttctta tgtggcgatg atcctcgtgc tggcgctctt gtctctccgt 300
ccggtcggtt ttgactaccg ctccaagatt gaagaaaccc gctggcgtaa catgtgggac 360
tggggcatct tcattggtag ctctgctccg ccgctggtaa ttggtgtagc gttcggtaac 420
ctgtttgcagg gcgtaccggt caacgttgat gaatatctgc gtctgtacta caccggtaac 480
ttcttccagt tgcttaaccc gttcggcctg ctggcaggcg tggtagcgt agggatgac 540
attactcagg gcgcaaccta tctgcaaatg cgtaccgtgg gcgaactgca cctgcgtacc 600
cgtgcaacgg ctacagtggt tgcgctggtg acactggtct gtttcgact ggctggcgta 660
tgggtgatgt acggtatcga tgggttatgtc gtgaaatcga caatggacca ttacgcagcc 720
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aacacgccaa ttctgtgggc tattccgcca ctgggtgtgg ttctgcgcgt gctgaccate 840
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aaaatgttcg gtcgtatcac caaagaagat attgaacgta acaccactc tctgtactaa 1140

```

&lt;210&gt; 196

&lt;211&gt; 1371

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 196

```

atggaattat cctcactgac cgccgtttcc cctgtcgatg gacgctacgg cgataaagtc 60
agcgcgctgc gcgggatttt cagcgaatat ggtttgctga aattccgtgt acaagttgaa 120
gtacgttggc tgcaaaaact ggccgcgcac gcagcgatca aggaagttcc tgcttttgct 180
gccgacgcaa tcggttacct tgatgcaatc gtcgccagtt tcagcgaaga agatgcggcg 240
cgcatcaaaa ctatcgagcg taccactaac cagcagctta aagcggttga gtatttctg 300
aaagaaaaag tggcgagat cccggaactg cagcgggtt ctgaattcat ccactttgcc 360
tgtacttccg aagatatcaa taacctctcc cagcatttaa tgctgaaaac cgcgcgtgat 420
gaagtgatcc tgccatactg gcgtcaactg attgatggca ttaagatct cgcggttcag 480
tatcgcgata tcccgctgct gtctcgtacc caggttcagc cagccacgcc gtcaaccatc 540

```

WO 00/44906

PCT/US00/02200

```

ggtaaagaga tggcaaacgt cgcctaccgt atggagcgcc agtaccgcca gcttaaccag 600
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taccgggaag ttgactggca tcagttcagc gaagagttcg tcacctcgct gggatttcag 720
tggaaccggt acaccacca gatcgaaccg cagactaca ttgccgaact gtttgattgc 780
gttgcgcgct tcaacactat tctgatcgac tttgaccgtg acgtctgggg ttatatcgcc 840
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ccgtacgaga agctgaaaga gctgactcgc ggtaagcgcg ttgacgccga aggcatagaag 1260
cagtttatcg atggctctggc gttgccagaa gaagagaaa cccgcctgaa agcgatgacg 1320
cgggctaact atattggctc agctatcacg atggttgatg agctgaaata a 1371

```

<210> 197  
 <211> 186  
 <212> DNA  
 <213> E. Coli

<400> 197

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acagtttttag gggtaaaagg caaccaggta cgtattggcg taaatgcccc gaaggaaagt 120
tctgttcacc gtgaagagat ctaccagcgt atccaggctg aaaaatcccc gcagtcacgt 180
tactaa 186

```

<210> 198  
 <211> 93  
 <212> DNA  
 <213> E. Coli

<400> 198

```

ggtagaggtgg cggagaggct gaaggcgctc ccctgctaag ggagtatgcg gtcaaaagct 60
gcacccggggg ttcgaatccc cgcctcaccg cca 93

```

<210> 199  
 <211> 603  
 <212> DNA  
 <213> E. Coli

<400> 199

```

atgaagaata aggctgataa caaaaaaagg aacttctcga cccatagtga aatcgaatca 60
ctcctttaaag cagcaaatat cgggcctcat gcagcacgta attattgtct gactttgctt 120
tggtttattc atggtttccg ggcgagtga atttgtcgat tgaggatttc ggatattgat 180
cttaaggcaa agtgtatata tatccatcga ttaaaaaaag gcttttcaac aacgcacccg 240
ctattgaata aagaagttca ggctttaaaa aactggttga gtatccgtac ttcgtacccg 300
catgctgaga gcgagtgggt atttttatca cgtaaagggg atccgctttc tcggcaacag 360
ttttaccata ttatctcgac ttccgggtgt aatgccgggt tgtcactgga gattcatccg 420
cacatgttac gccattcgtg tggttttgct ttggcgaata tgggaataga tacgcgactt 480
atccaggatt atcttgggca tcgcaatatt cgtcatactg tctggtatac cgccagcaat 540
gcaggggcgtt ttacggcat ctgggataga gccagaggac gacagcgtca cgtgttttta 600
tag 603

```

<210> 200  
 <211> 597  
 <212> DNA  
 <213> E. Coli

<400> 200

```

gtgagtaaac gtcgttatct taccggtaaa gaagttcagg ccatgatgca ggcggtttgt 60
tacggggcaa cgggagccag agattattgt cttattctgt tggcatatcg gcatgggatg 120

```

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| cgtattagtg  | aactgcttga | tctgcattat | caggaccttg | accttaatga | aggtagaata | 180 |
| aatattcgcc  | gactgaagaa | cggattttct | accgttcacc | cgttacgttt | tgatgagcgt | 240 |
| gaagccgtgg  | aacgctggac | ccaggaaact | gctaactgga | aaggcgctga | ccggactgac | 300 |
| gctatatatta | tttctcgccg | cgggagtcgg | ctttctcgcc | agcaggccta | tcgcattatt | 360 |
| cgcgatgcgg  | gtattgaagc | tggaaccgta | acgcagactc | atcctcatat | gttaaggcat | 420 |
| gcttgcggtt  | atgaattggc | ggagcgtggt | gcagatactc | gtttaattca | ggattatctc | 480 |
| gggcatcgaa  | atattcgcca | tactgtgcgt | tataccgcca | gtaatgctgc | tcgttttgcc | 540 |
| ggattatggg  | aaagaataa  | tctcataaac | gaaaaattaa | aaagagaaga | ggtttga    | 597 |

<210> 201  
 <211> 549  
 <212> DNA  
 <213> E. Coli

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| <400> 201  |            |            |            |            |             |     |
| atgaaaatta | aaactctggc | aatcgttggt | ctgtcggctc | tgccctcag  | ttctacagcg  | 60  |
| gctctgccc  | ctgccacgac | ggttaatggt | gggaccgttc | actttaaagg | ggaagttggt  | 120 |
| aacgccgtt  | gcgcagttga | tgccaggtct | gttgatcaaa | ccgttcagtt | aggacaggtt  | 180 |
| cgtaccgcat | cgtgggcaca | ggaaggagca | accagttctg | ctgtcgggtt | taacattcag  | 240 |
| ctgaatgatt | gcgataccaa | tggtgcattc | aaagccgctg | ttgcctttt  | aggtacggcg  | 300 |
| attgatgcgg | gtcataccaa | cgttctggct | ctgcagagtt | cagctgcggg | tagcgcaaca  | 360 |
| aacgttgggt | tgcatatcct | ggacagaacg | ggtgctgcgc | tgacgctgga | tggtgcgaca  | 420 |
| tttagttcag | aaacaacccr | gaataacgga | accaatacca | ttccgttcca | ggcgcggtat  | 480 |
| tttgcaaccg | gggcccgaac | cccgggtgct | gctaattgcg | atgcgacctt | caagggttcag | 540 |
| tatcaataa  |            |            |            |            |             | 549 |

<210> 202  
 <211> 648  
 <212> DNA  
 <213> E. Coli

|            |            |             |             |            |             |     |
|------------|------------|-------------|-------------|------------|-------------|-----|
| <400> 202  |            |             |             |            |             |     |
| gtgctgctaa | tgccgatgcg | accttcaagg  | ttcagtatca  | ataacctacc | cagggttcagg | 60  |
| gacgtcatta | cgggcaggga | tgcccacctt  | tgtagcataa  | aaataacgat | gaaaagggaag | 120 |
| agattatttc | tattagcgtc | gttgctgcca  | atgtttgctc  | tgcccggaag | taaatggaa   | 180 |
| accacgttgc | ccggcggaag | tatgcaattt  | caggcgctca  | ttattgcgga | aacttgccgg  | 240 |
| attgaagccg | gtgataaaca | aatgacggtc  | aatatggggc  | aaatcagcag | taaccggttt  | 300 |
| catgctggtg | gggaagatag | cgcaccgggtg | ccttttggtt  | ttcatttacg | ggaatgtagc  | 360 |
| acgggtggtg | gtgaacgtgt | aggtgtggcg  | tttcacgggtg | tcgcggtatg | taaaaatccg  | 420 |
| gatgtgcttt | ccgtgggaga | ggggccaggg  | atagccacca  | atattggcgt | agcgttggtt  | 480 |
| gatgatgaag | gaaacctcgt | accgattaat  | cgtcctccag  | caaactggaa | acggccttat  | 540 |
| tcaggctcta | cttcgctaca | tttcatcgcc  | aaatatctgt  | ctaccgggag | tcgggttact  | 600 |
| ggcggcacgc | ccaatgcccc | ggcctgggtc  | tctttaacct  | atcagtaa   |             | 648 |

<210> 203  
 <211> 726  
 <212> DNA  
 <213> E. Coli

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| <400> 203  |             |            |            |            |            |     |
| gtgagtaata | aaaacgtcaa  | tgtaaggaaa | tcgcaggaaa | taacattctg | cttgctggca | 60  |
| ggtatcctga | tggtcatggc  | aatgatgggt | gccggacgcg | ctgaagcggg | agtggcctta | 120 |
| ggtgcgactc | gcgtaattta  | tccggcaggg | caaaaacaag | agcaacttgc | cgtgacaaat | 180 |
| aatgatgaaa | atagtaccta  | tttaattcaa | tcatgggtgg | aaaatgccga | tggtgtaaa  | 240 |
| gatggctggt | ttatcgtgac  | gcctcctctg | tttgcatga  | agggaaaaaa | agagaatacc | 300 |
| ttacgtattc | ttgatgcaac  | aaataaccaa | ttgccacagg | accgggaaa  | tttattctgg | 360 |
| atgaacgtta | aagcgattcc  | gtcaatggat | aatcaaaaat | tgactgagaa | tacgctacag | 420 |
| ctcgcaatta | tcagccgcat  | taaactgtac | tatcgcccgg | ctaaattagc | gttgccaccc | 480 |
| gatcaggccg | cagaaaaaatt | aagatttctg | cgtagcgcga | attctctgac | gctgattaac | 540 |
| ccgacaccct | attacctgac  | ggtaacagag | ttgaatgccg | gaaccggggt | tcttgaaaat | 600 |
| gcattggtgc | ctccaatggg  | cgaaagcacg | gttaaatgac | cttctgatgc | aggaagcaat | 660 |

attactttacc gaacaataaa tgattatggc gcactttacc ccaaaatgac gggcgtaatg 720  
gaataa 726

<210> 204  
<211> 2637  
<212> DNA  
<213> E. Coli

<400> 204

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cctttgtcat ctgccgacct ctattttaat ccgcgctttt tagcggatga tccccaggct 180  
gtggccgatt tatcgcgttt tgaataatgg caagaattac cgcacaggac gtatcgcgtc 240  
gatatctatt tgaataatgg ttatatggca acgcgtgatg tcacatttaa tacgggcgac 300  
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aataaatggc agcatatcaa tacctggcct gagcgagaca taataccggt acgttcccgg 780  
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aacattgaaa cacaggacgg agttattcag gttaaagcga aattcaccga ctattacaac 1560  
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cagagtagcg gcattgttgc ggataatggt caggtttacc tcagcggaat gcctttagcg 2520  
ggaaaagtgc aggtgaaatg gggagaagag gaaaaatgct actgtgtcgc caattatcaa 2580  
ctgccaccag agagtcagca gcagtattat acccagctat cagctgaatg tcgttaa 2637

<210> 205  
<211> 531  
<212> DNA  
<213> E. Coli

<400> 205

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|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ttggctgcgg | atagcacgat | tactatccgc | ggctatgtca | gggataacgg | ctgtagtgtg | 120 |
| gccgctgaat | caaccaat   | tactgttgat | ctgatggaaa | acgcggcgaa | gcaatttaac | 180 |
| aacattggcg | cgacgactcc | tggtgttcca | tttcgtat   | tgctgtcacc | ctgtggtaat | 240 |
| gccgtttctg | ccgtaaaggt | tgggtttact | ggcgttgca  | atagccacaa | tgccaacctg | 300 |
| cttgcaactg | aaaatacgg  | gtcagcggct | tcgggactgg | gaatacagct | tctgaatgag | 360 |
| cagcaaaatc | aaataccct  | taatgctcca | tcgtcccgcc | tttcgtggac | gaccctgacg | 420 |
| ccgggtaaac | caaatcagct | gaatttttac | gcccggttaa | tgccgacaca | ggtgcctgtc | 480 |
| actgcggggc | atatcaatgc | cacggctacc | ttcactcttg | aatatcagta | a          | 531 |

&lt;210&gt; 206

&lt;211&gt; 504

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 206

|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| atgaatggt  | gcaaacgtg  | gtatgtattg  | gcggcaatat  | tggcgctcgc | aagtgcgacg | 60  |
| atacaggcag | ccgatgtcac | catcacgggtg | aacggtaagg  | tcgtcgccaa | accgtgtacg | 120 |
| gtttccacca | ccaatgccac | ggttgatctc  | ggcgatcttt  | attctttcag | tcttatgtct | 180 |
| gccggggcgg | catcgccctg | gcatgatgtt  | gcgcttgagt  | tgactaattg | tccgggtgga | 240 |
| acgtcgaggg | tcactgccag | cttcagcggg  | gcagccgaca  | gtaccggata | ttataaaaac | 300 |
| caggggaccg | cgcaaaacat | ccagttagag  | ctacaggatg  | acagtggcaa | cacattgaat | 360 |
| actggcgcaa | ccaaaacagt | tcaggtggat  | gattccctcac | aatcagcgca | cttcccgtta | 420 |
| caggtcagag | cattgacagt | aaatggcgga  | gccactcagg  | gaaccattca | ggcagtgatt | 480 |
| agcatcacct | atacctacag | ctga        |             |            |            | 504 |

&lt;210&gt; 207

&lt;211&gt; 903

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 207

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| atgaaacgag | ttattaccct  | gtttgctgta  | ctgctgatgg | gctggctcgg | aaatgcctgg | 60  |
| tcattcgcc  | gtaaaaaccg  | caatggtacc  | gctatcccta | ttggcggtgg | cagcgccaat | 120 |
| gtttatgtaa | acccttgcgc  | cgctcgta    | gtggggcaaa | acctggctcg | ggatctttcg | 180 |
| acgcaaatct | tttgccataa  | cgattatccg  | gaaaccatta | cagactatgt | cacactgcaa | 240 |
| cgaggctcgg | cttatggcgg  | cgtgttatct  | aatttttccg | ggaccgtaaa | atatagtggc | 300 |
| agtagctatc | catttcctac  | caccagcgaa  | acgcgcgcgc | ttgtttataa | ttcgagaacg | 360 |
| gataagccgt | ggccggtggc  | gctttatttg  | acgcctgtga | gcagtgcggg | cggggtggcg | 420 |
| attaaagctg | gctcattaat  | tgcctgtcct  | attttgcgac | agaccaacaa | ctataacagc | 480 |
| gatgatttcc | agttttgtgt  | gaatatattac | gccaataatg | atgtggtggg | gcctactggc | 540 |
| ggctgcgatg | tttctgctcg  | tgatgtcacc  | gttactctgc | cggactaccc | tggttcagtg | 600 |
| ccaattcctc | ttaccgttta  | ttgtgcgaaa  | agccaaaacc | tggggtatta | cctctccggc | 660 |
| acaaccgcag | atgcggggcaa | ctcgattttc  | accaataccg | cgtcggtttc | acctgcacag | 720 |
| ggcgtcggcg | tacagttgac  | gcgcaacgg   | acgattattc | cagcgaaata | cacggtatcg | 780 |
| ttaggagcag | tagggacttc  | ggcggtgagt  | ctgggattaa | cggcaaat   | tgacagtaac | 840 |
| ggagggcagg | tgactgcagg  | gaatgtgcaa  | tcgattattg | gcgtgacttt | tgtttatcaa | 900 |
| taa        |             |             |            |            |            | 903 |

&lt;210&gt; 208

&lt;211&gt; 1631

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 208

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| gtgctgtcaa | aactaccccg | tagactccga  | tcttttcaaa | catattgcac | catccgtgta | 60  |
| catcggggtg | aggatatgaa | atcaatggat  | aagttaacaa | caggtgttgc | ctatggcaca | 120 |
| tcggcggtga | atgctggttt | ctgggcattg  | cagttactcg | ataaagtaac | tccgtcacag | 180 |
| tgggctgcaa | tcggtgtgct | gggtagcctg  | gtttttggcc | tgctgacgta | tctgacaaat | 240 |
| ctttatttca | agattaaaga | agacaggcgt  | aaggctgcga | gaggagagta | atccaatgac | 300 |
| tcaagactat | gaactggttg | tgaaaaggagt | ccgtaatttt | gagaataaag | ttacggtaac | 360 |
| tgtagcctta | caggacaaag | aacgccttga  | cggtgaaatt | tttgacctgg | atgtcgccat | 420 |

|            |            |            |            |            |             |      |
|------------|------------|------------|------------|------------|-------------|------|
| ggaccgtgtt | gaaggagctg | cgctggagtt | ttatgaggca | gcagccagaa | ggagcgtccg  | 480  |
| gcaagtcttc | ctggaagtag | cagaaaaatt | gtcagaaaaa | gttgagtcct | atctgcagca  | 540  |
| tcagtactcc | tttaagattg | aaaatcctgc | caataagcac | gagcgtccct | atcataaata  | 600  |
| tctatgaaca | caaaaatcac | atacggcctg | tcggctgccc | ttctggcgct | gattggtgct  | 660  |
| ggcgcctctg | ctcctcagat | acttgaccag | tttctggacg | aaaaagaagg | taaccacaca  | 720  |
| atggcatacc | gcatggttcc | tggcatatgg | accatctgtc | ggggtgccac | agtgggtgat  | 780  |
| ggaaaaaccg | ttttcccaa  | tatgaaactg | tcgaaggaaa | aatgcgacca | ggtcaacgcc  | 840  |
| attgagcgtg | ataaggcgct | ggcatgggtg | gagcgcaata | ttaaagtacc | actgaccgaa  | 900  |
| ccacaaaaag | cggttatcgc | gtcattttgt | ccctataaca | ttggccccgg | taagtgttcc  | 960  |
| ccgtcgacgt | tttataagcg | gctgaatgct | ggtgatcgta | aaggtgcatt | cgaagcgatt  | 1020 |
| cgctgggtgg | tttaaggatg | cggaacgcgt | tgccgcattc | gttcaataaa | ctgttacggt  | 1080 |
| caggttattc | gtcgtgacca | ggagagcgca | ttaacctgct | gggggataga | acagtgaatc  | 1140 |
| agatattcat | gggtattttt | ctcgtgttgt | caggatttat | cgctggaaat | gtctggagcg  | 1200 |
| accgaggatg | gcacaaaaaa | tgggcggaac | gtgatgctgc | cgcatatca  | caagaggtaa  | 1260 |
| atgctcaatt | tgctgctcga | ataattgaac | agggcggaac | tatagccctg | gatgaggctg  | 1320 |
| ttaaagatgc | gcaacagaaa | tctgtgaaa  | tttctgccag | ggctgcttat | ctgtctgata  | 1380 |
| gtgttaacca | gttgctgccc | gaagcaaaaa | aatatgccat | acgccttgac | gcagcgaagc  | 1440 |
| ataccgcaga | tcttcccgct | gccgtcagag | gcaaaacaac | caaaaccgcc | gaaggaatgc  | 1500 |
| tcaccaacat | gctcggagat | attgcagcag | aagctcagct | ttatgctgaa | attgctgacg  | 1560 |
| aacgctacat | cgcaggagtg | acttgtcaac | agatctatga | atctttaaga | gataaaaaagc | 1620 |
| atcaaatgta | g          |            |            |            |             | 1631 |

&lt;210&gt; 209

&lt;211&gt; 534

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 209

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgaacacaa | aaatcagata | cgccctgtcg | gctgccgttc | tggcgctgat | tggtgctggc | 60  |
| gcattctgtc | ctcagatact | tgaccagttt | ctggacgaaa | aagaaggtaa | ccacacaatg | 120 |
| gcataccgcg | atgggttctg | catatggacc | atctgtcggg | gtgccacagt | ggtggatgga | 180 |
| aaaaccgttt | ttcccaatat | gaaactgtcg | aaggaaaaat | gcgaccaggt | caacgccatt | 240 |
| gagcgtgata | aggcgtgggc | atgggtggag | cgcaatatta | aagtaccact | gaccgaacca | 300 |
| caaaaagcgg | gtatcgcgtc | attttgtccc | tataacattg | gccccggtaa | gtgtttcccg | 360 |
| tcgacgtttt | ataagcggct | gaatgctggt | gatcgtaaa  | gtgcatcgca | agcgattcgc | 420 |
| tggtggatta | aggatggcgg | acgcgattgc | cgcatctcgt | caataaactg | ttacggtcag | 480 |
| gttattcgtc | gtgaccagga | gagcgcatta | acctgctggg | ggatagaaca | gtga       | 534 |

&lt;210&gt; 210

&lt;211&gt; 312

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 210

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| atgactcaag | actatgaact | ggttgtgaaa | ggagtccgta  | atcttgagaa | taaagttacg | 60  |
| gtaactgtag | ccttacagga | caaagaacgc | tttgacgggt  | aaatttttga | cctggatgtc | 120 |
| gccatggacc | gtgttgaaag | agctgcgctg | gagttttatg  | aggcagcagc | cagaaggagc | 180 |
| gtccggcaag | tcttctctga | agtagcagaa | aaattgtcag  | aaaaagttga | gtcttatctg | 240 |
| cagcatcagt | actccttta  | gattgaaaa  | cctgccaaata | agcagcagcg | tcctcatcat | 300 |
| aaatatctat | ga         |            |             |            |            | 312 |

&lt;210&gt; 211

&lt;211&gt; 291

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 211

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gtgctgtcaa | aactaccccg | tagactccga | tcttttcaaa | catattgcac | catccgtgta | 60  |
| catcgggggt | aggatatgaa | atcaatggat | aagttaacaa | caggtgttgc | ctatggcaca | 120 |
| tcggcgggta | atgctggttt | ctgggcattg | cagttactcg | ataaagtaac | tccgtcacag | 180 |
| tgggctgcaa | tcggtgtgct | gggtagcctg | gtttttggcc | tgctgacgta | tctgacaaat | 240 |



ctttatttca agattaaaga agacaggcgt aaggctgcga gaggagagta a 291

<210> 212  
<211> 216  
<212> DNA  
<213> E. Coli

<400> 212  
atgtcaaata aaatgactgg tttagtaaaa tggtttaacg ctgataaagg ttctggcttt 60  
atttctcctg ttgatggtag taaagatgtg ttgtgcatt ttctgcgat tcagaatgat 120  
aattatcgaa ccttatttga aggtcaaaa gttaccttct ctatagagag tgggtgctaaa 180  
ggtcctgcag cagcaaatgt catcattact gattaa 216

<210> 213  
<211> 1017  
<212> DNA  
<213> E. Coli

<400> 213  
atgtttgtca tctggagcca tagaacaggg ttcacatga gtcacaaact taccttcgcc 60  
gacagtgaat tcagcagtaa gcgcgctcag accagaaaag agattttctt gtcccgcatg 120  
gagcagattc tgccatggca aaacatgggt gaagtcacg agccgtttta ccccaggct 180  
ggtaatggcc ggcgacctta tccgctggaa accatgtac gatttactg catgcagcat 240  
tggtacaacc tgagcgatgg cgcgatggaa gatgctctgt acgaaatcgc ctccatgcgt 300  
ctgtttggcc ggttatccct ggatagcgcc ttgcccggacc gcaccacat catgaatttc 360  
cgccacctgc tggagcagca tcaactggcc cgccaattgt tcaagacat caatcgctgg 420  
ctggccgaag caggcgctcat gatgactcaa ggcaccttg tcgatgccac catcattgag 480  
gcaccagct cgaccaagaa caaagagcag caacgcgatc cggagatgca tcagaccaag 540  
aaaggcaatc agtggcactt tggcatgaag gccacattg gtgtcgatgc caagagtggc 600  
ctgaccacaca gcctggctcac caccgcgcc aacgagcatg acctcaatca gctgggtaat 660  
ctgctgcatg gagaggagca atttgtctca gccgatgccg gctaccaagg ggcgccacag 720  
cgcgaggagc tggccgaggt ggatgtggac tggctgatcg ccgagcgccc cggcaaggta 780  
agaaccttga aacagcatcc acgcaagaac aaaacggcca tcaacatcga atacatgaaa 840  
gccagcatcc gggccagggt ggagcaccga ttctgcacat tcaagcgaca gttcggcttc 900  
gtgaaagcca gatacaagggt gttgctgaaa aacgataacc aactggcgat gttatttcacg 960  
ctggccaacc tgtttcgggc ggaccaaagt atacgtcagt gggagagatc tcactaa 1017

<210> 214  
<211> 474  
<212> DNA  
<213> E. Coli

<400> 214  
atggtatata taataatcgt ttcccacgga catgaagact acatcaaaaa attactcgaa 60  
aatcttaagt ctgacgatga gcaactacaag attatcgtag gcgacaacaa agactctcta 120  
ttattgaaac aaatatgcca gcattatgca ggccctggact atattagtgg aggtgtatac 180  
ggctttggtc ataataataa tattgcggtg gcgtatgtaa aggaaaaata tagaccgca 240  
gatgatgatt acattttgtt tttgaatccc gatatcatca tgaagcatga tgatttgctg 300  
acatatatta aatatgtcga aagtaagcgt tatgctttta gtacattatg cctgttccga 360  
gatgaagcga aatctttaca tgattattcc gtaagaaaat ttccgtgctt ttctgatttt 420  
atttgtctat ttatgttagg gattaaggaa ggtgcgaaca agtcctctgat atga 474

<210> 215  
<211> 1119  
<212> DNA  
<213> E. Coli

<400> 215  
atgggaaaaa gcatagtcgt tgtttctgcg gtcaatttta ccactggcgg tccattttacc 60  
attttgaaaa aatttttggc agcaactaat aataaagaaa atgtcagttt tatcgcat 120  
gtccattctg ctaaagagtt aaaagaaagt tatccatggg ttaaatcat tgagtttcc 180

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| gaggttaaag  | ggtcgtggct | aaaacgtttg | cactttgaat | atgtagtttg | taaaaaactt  | 240  |
| tcaaaagagc  | tgaatgctac | gcattggatt | tgtctgcatg | atattacggc | caatgtcgtc  | 300  |
| actaaaaaaa  | gatatgtgta | ttgtcataac | cctgcacctt | tttataaagg | aattttatct  | 360  |
| cgtgaaattc  | ttatggagcc | tagctttttc | ttatttaaaa | tgctatacgg | gctgatatat  | 420  |
| aaaataaaca  | ttaaaaaa   | tactgcagtg | tttgttcaac | aattctggat | gaaagaaaaa  | 480  |
| tttatcaaga  | aatattctat | aaataacatc | attgtcagtc | ggccagaaat | taaattatct  | 540  |
| gataaaagcc  | aacttactga | tgatgattct | caatttaaga | ataacccttc | tgagttgaca  | 600  |
| atattttacc  | ctgctgttcc | acgagtattt | aaaaattacg | agcttattat | tagtgcagca  | 660  |
| aggaaattga  | aagaacaatc | caatattaaa | tttctgctta | ctatcagttg | tacagaaaaat | 720  |
| gcgtatgcaa  | aatatattat | cagtcttgca | gaaggactgg | ataatgttca | tttctctcgg  | 780  |
| tacttggata  | aagaaaaaat | cgatcattgt | tataatattt | cagatatagt | ttgttttccc  | 840  |
| tctagggttag | aaacatgggg | attgccgttg | tctgaagcta | aagagcagag | taagtgggta  | 900  |
| ttagcatcag  | atttcccatt | tactagagaa | actcttggtg | gttatgaaaa | gaaagctttt  | 960  |
| tttgattcta  | ataacgatga | catgttagtt | aaacttatta | ttgacttcaa | aaaaggtaac  | 1020 |
| ctcaaaaaag  | atatctctga | tgcaaatctc | atttatcgta | atgaaaaatg | attagttggg  | 1080 |
| tttgatgaac  | tagttaattt | tattactgaa | gaacattga  |            |             | 1119 |

<210> 216  
 <211> 591  
 <212> DNA  
 <213> E. Coli

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| <400> 216  |            |            |            |            |            |     |
| atgatcttaa | aactcgctaa | acgatatggt | ctctgtggtt | ttattcggct | tgttagagat | 60  |
| gtcttattga | ctcgtgtatt | ttaccggaac | tgtagaatta | ttcgatttcc | ctgctatatt | 120 |
| cgcaatgatg | gtagcattaa | ttttggtgaa | aatttcacaa | gtggagtcgg | tctcaggctg | 180 |
| gatgcatttg | gacgtggcgt | gatttttttt | tccgataatg | tgcaagttaa | cgactatggt | 240 |
| catatcgctt | caattgagag | cgttacgata | ggtcgggata | cgcttattgc | aagtaaagta | 300 |
| tttattaccg | atcataatca | cggttccctt | aagcactctg | atccaatgag | ttcgccaaat | 360 |
| atacctccag | acatgcgcac | gttggaatct | tcagctgttg | taattggcca | gagggttttg | 420 |
| ttgggtgaga | atgtgacggt | tttgcttgga | acaattattg | gtaatggagt | cgtagtcggc | 480 |
| gccaatctcg | ttgttagagg | ttctattccc | gaaaatactg | tcattgcggg | agtaccagca | 540 |
| aaaatcataa | agaaatacaa | tcatgagacc | aaattatggg | aaaaagcata | g          | 591 |

<210> 217  
 <211> 993  
 <212> DNA  
 <213> E. Coli

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| <400> 217   |             |            |            |            |             |     |
| atgtattttt  | tgaatgattt  | aaatttctct | agacgcgatg | ctggatttaa | agcaagaaaa  | 60  |
| gatgcactgg  | acattgcttc  | agattatgaa | aacatttctg | ttgttaacat | tcctctatgg  | 120 |
| gggtggagtag | tcagagagaat | tattagttct | gttaagctta | gtacatttct | ctgcggtctt  | 180 |
| gaaaaataag  | atgttttaat  | tttcaatttc | cogatggcca | aaccattttg | gcatatattg  | 240 |
| tcattctttc  | accgccttct  | aaaatttaga | atagtacctc | tgattcatga | tattgatgaa  | 300 |
| ttaaagaggag | gagggggtag  | tgattctgtg | cggttgcta  | cctgtgatat | ggtcataagt  | 360 |
| cacaatccac  | aaatgacaaa  | gtaccttagt | aaatatatgt | ctcaggataa | aatcaaagac  | 420 |
| ataaaaaatat | ttgattacct  | cgtctcatct | gatgtggagc | atcgagatgt | tacggataag  | 480 |
| caacgagggg  | tcatatatgc  | tggaacctt  | tctaggcata | aatgttcttt | catatatact  | 540 |
| gaaggatgcg  | atthtactct  | ctttggtgtc | aactatgaaa | ataaagataa | tcctaaatat  | 600 |
| cttggaagtt  | ttgatgctca  | atctccggaa | aagattaacc | tcccaggcat | gcaatttgga  | 660 |
| ctcatttggg  | atggagattc  | tgctgaaacc | tgtagtggtg | cctttggcga | ctattttaaag | 720 |
| tttaataacc  | ctcataagac  | atctctttat | ctttcaatgg | aacttccagt | atttatatgg  | 780 |
| gataaagccg  | cccttgccga  | tttcattgta | gataatagaa | taggatatgc | agtgggatca  | 840 |
| atcaaagaaa  | tgcaagagat  | tggtgactcc | atgacaatag | aaacttataa | gcaaattagt  | 900 |
| gagaatacaa  | aaattatttc  | tcagaaaatt | cgaacaggaa | gtactctcag | ggatgttctt  | 960 |
| gaagaggtga  | tcgatgatct  | taaaactcgc | ttaa       |            |             | 993 |

<210> 218  
 <211> 1167  
 <212> DNA

&lt;213&gt; E. Coli

&lt;400&gt; 218

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| atgatctatc  | ttgtaattag  | tgtctttctc  | attacagcat | ttatctgttt  | atatcttaag  | 60   |
| aaggatatat  | tttatccagc  | cgtatgcgtt  | aatatcatct | tcgcactggg  | cttattggga  | 120  |
| tatgaaataa  | cgtcagatat  | atatgctttt  | cagttaaatg | acgctacgtt  | gatttttcta  | 180  |
| ctttgcaatg  | ttttgacatt  | taccctgtca  | tgtttattga | cggaaaagtgt | attagatcta  | 240  |
| aatatcagaa  | aagtcaataa  | tgcattttat  | agcataccat | cgaagaaagt  | gcataatgta  | 300  |
| ggcttggttag | ttatttcttt  | ttcgatgata  | tatatatgca | tgagggttaag | taactaccag  | 360  |
| ttcgggacta  | gcttacttag  | ctatatgaat  | ttgataagag | atgctgatgt  | tgaagacaca  | 420  |
| tcaagaaaatt | tctcagcata  | catgcagcca  | atcattctaa | ctacttttgc  | tttattttatt | 480  |
| tggtctaaaa  | aatttactaa  | tacaaaaggta | agtaaaacat | ttactttact  | tgtttttatt  | 540  |
| gtattcatct  | ttgcaattat  | actgaatact  | ggtaagcaaa | ttgtctttat  | ggttatcatc  | 600  |
| tcttatgcatt | tcattcgtagg | tgtaaataga  | gtaaaacatt | atgtttatct  | tattacagct  | 660  |
| gtagggtgttc | tattctcctt  | gtatatgctc  | tttttacgtg | gactgcctgg  | ggggatggca  | 720  |
| tattatctat  | ccatgtattt  | ggtcagccct  | ataatcgctt | ttcaggaggt  | ttattttcag  | 780  |
| caagtatcta  | actctgccag  | ttctcatgtc  | tttttggttt | ttgaaaaggct | gatggggcta  | 840  |
| ttaacagggtg | gagtcctctat | gtcgttgcat  | aaagaatttg | tgtgggtggg  | tttgccaaca  | 900  |
| aatgtttata  | ctgctttttc  | ggattatggt  | tatatctccg | cggagctaa   | ctatttgatg  | 960  |
| atgggttattc | atggctgtat  | ttcagggtgt  | ttatggagat | tgtctcgaaa  | ttacatatct  | 1020 |
| gtgaaaaatat | ttttattcata | ttttattttat | accttttctt | tcatttttta  | tcataaaagc  | 1080 |
| ttcatgacta  | atattagcag  | ttggatacaa  | ataactcttt | gtatcatagt  | attctctcaa  | 1140 |
| tttcttaagg  | cccagaaaat  | aaagtga     |            |             |             | 1167 |

&lt;210&gt; 219

&lt;211&gt; 1104

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 219

|             |             |             |            |            |            |      |
|-------------|-------------|-------------|------------|------------|------------|------|
| atgtacgatt  | atatcattgt  | tggttctggt  | ttgtttggtg | ccgtttgtgc | gaatgagtta | 60   |
| aaaaagctaa  | acaaaaaagt  | tttagtgatt  | gagaaaaaga | atcatatcgg | tggaatgctg | 120  |
| tacacagagg  | actgtgaggg  | tatccagatt  | cataaatatg | gtgcacatat | ttttcatacc | 180  |
| aatgataaat  | atataatggg  | ttacgttaat  | gatttagtag | aatttaacog | ttttactaat | 240  |
| tctccactgg  | cgaattataa  | agacaaaatta | ttcaaccttc | cttttaatat | gaatactttc | 300  |
| caccaaatgt  | ggggagttaa  | agatcctcaa  | gaagctcaaa | atatcattaa | tgctcagaaa | 360  |
| aaaaaagtatg | gtgacaagg   | acctgaaaaat | ttggaggagc | aggcgatttc | attagttggg | 420  |
| gaggacttat  | accaagcatt  | gataaagggt  | tatacgaga  | agcagtgagg | aagaagtgc  | 480  |
| aaagaattgc  | ctgcattttat | tattaagcga  | atcccagtg  | gatttacgtt | tgataacaat | 540  |
| tatttttccg  | atcgctatca  | aggtattccg  | gtgggaggct | acactaagct | tattgaaaaa | 600  |
| atgcttgaag  | gtgtggacgt  | aaaattaggc  | attgattttt | tgaaagacaa | agattctcta | 660  |
| gcgagtaaa   | cccatagaat  | catctacact  | ggacccattg | atcagtaact | cgactatagg | 720  |
| tttgagcgt   | tagaatatcg  | ctctttaaaa  | tttgagacgg | aacgccatga | atttccaaac | 780  |
| ttccaaaggga | atgcagtaat  | aaatttcact  | gatgctaatt | taccatatac | cagaataatt | 840  |
| gagcataaac  | attttgacta  | tggttgagaca | aagcatacgg | ttgttacaaa | agaatatcca | 900  |
| ttagagtgg   | aagttggcga  | cgaaccttac  | tatccagtta | atgataataa | aaacatggag | 960  |
| ctttttaaga  | aatatagaga  | gttagctagc  | agagaagaca | aggttatatt | tggcgggctg | 1020 |
| ttggccgagt  | ataaatatta  | tgatatgcat  | caagtgata  | ctgccgctct | ttatcaagt  | 1080 |
| aaaaatataa  | tgagtacgga  | ttaa        |            |            |            | 1104 |

&lt;210&gt; 220

&lt;211&gt; 1116

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 220

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| atgttcccaa | aaataatgaa | tgatgaaaac | tttttcaaaa  | aagcggcggc | gcacggggag | 60  |
| gaacctcctt | taactcctca | aaacgaacat | cagcgggtccg | ggctgcgctt | cgccccgtcg | 120 |
| gtcagactac | cccgtgcggg | tggcctggct | ggcatgttct  | taccgattgc | ttcaacgctg | 180 |
| gtttcacacc | cgcgcgggg  | ctgggtggtg | ctgggtgttg  | tcggctgggc | gttcgtctgg | 240 |
| ccgcatttag | cctggcagat | agcagcagg  | gccgtcgatc  | cgttagccg  | ggaaatttac | 300 |

|             |             |            |            |             |            |      |
|-------------|-------------|------------|------------|-------------|------------|------|
| aacttaaaaa  | ccgatgcagt  | attagcggga | atgtgggtag | gcgtaatggg  | cgtaaactg  | 360  |
| ctgccttcca  | ccgcgatgtt  | gatgattatg | tgtctgaatt | tgatgggggc  | aggcgccccc | 420  |
| cgtctgtttg  | tcgcgggtct  | ggtgttgatg | gtggtttcct | gccttgtcac  | cctcgagctg | 480  |
| acgggcatta  | ccgtgtcggt  | caatagtgcg | ccgctggaat | ggtggctctc  | ccttcccatt | 540  |
| attgtcattt  | atcctctgct  | gtttggctgg | gtcagctacc | agacggcaac  | caaactggcg | 600  |
| gaacataaac  | gcaggttgca  | ggtcatgagt | acccgcgacg | gcatgacggg  | cgtgtataac | 660  |
| cgacgtcatt  | gggaaactat  | gttacgcaat | gaatttgata | actgtcggcg  | gcataatcgc | 720  |
| gatgcaacgt  | tactgattat  | cgatatcgac | catttcaaga | gcatcaacga  | tacctggggc | 780  |
| catgatgtgg  | gcgatgaagc  | gattgtggcg | cttaccgcac | agttacaaat  | tacctgcgc  | 840  |
| ggtagcgtatg | tgatttggtcg | gtttggcgcg | gatgagtttg | cagtaatcat  | gtccggtacg | 900  |
| ccagctgaga  | gcgccattac  | cgccatgtta | cgggtgcatg | aagggtctaaa | tacattacgt | 960  |
| ttgccgaata  | cgccacaggt  | aactttacgg | attagtgtgg | gggttgccgc  | gctgaaccca | 1020 |
| caaatgagtc  | actatcgtga  | gtggttgaaa | tcggcagatt | tggcgcttta  | caaagcaaa  | 1080 |
| aaagccggac  | gtaaccgcac  | cgaagtggcg | gcctga     |             |            | 1116 |

&lt;210&gt; 221

&lt;211&gt; 1404

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 221

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| ttggatgtga  | acgttgatca  | gttcgatact  | gaagctttcc | gtactgacaa  | actggaactg  | 60   |
| accagcggca  | acatcgctga  | ccataacggt  | aacgtagtat | ctgggtgtgt  | cgatatccat  | 120  |
| agcagcgatt  | acgttctgaa  | cgctgatctg  | gtgaacgacc | gtacctggga  | tacttccaag  | 180  |
| tctaactacg  | gttacggtat  | tgttgctatg  | aactctgatg | gtcacctgac  | tatcaacggt  | 240  |
| aacggcgacg  | tagacaacgg  | tactgaactg  | gataacagct | ctgtagacaa  | tgttgttgct  | 300  |
| gcaaccggta  | actacaaagt  | tcgtatcgac  | aacgcaactg | gcgctggcgc  | tatcgctgat  | 360  |
| tacaaagata  | aagaaattat  | ctacgtaaac  | gacgtcaaca | gcaacgcgac  | cttctctgct  | 420  |
| gctaacaagg  | ctgacctggg  | tgcatacacc  | tatcaggctg | aacagcgcg   | taacaccggt  | 480  |
| gttctgcaac  | agatggagct  | gaccgactac  | gctaaccatg | cgctgagcat  | cccgtctcgc  | 540  |
| aacaccaata  | tctggaacct  | ggaaccaagac | accgttggta | ctcgrctgac  | caactctcgt  | 600  |
| catggcctgg  | ctgataacgg  | cggcgcatgg  | gtaagctact | tcggtggtaa  | cttcaacggc  | 660  |
| gacaacggca  | ccatcaacta  | tgatcaggat  | gttaacggca | tcattggtcgg | tgttgatacc  | 720  |
| aaaattgacg  | gtaacaacgc  | taagtggatc  | gtcgggtcgg | ctgcaggctt  | cgctaaagggt | 780  |
| gacatgaatg  | accgttctgg  | tcaggtggat  | caagacagcc | agactgccta  | catctactct  | 840  |
| tctgtctact  | tcgcgaacaa  | cgtctttggt  | gatggtagct | tgagctactc  | tcacttcaac  | 900  |
| aacgcctgt   | ctgcaacct   | gagcaacggt  | acttacgttg | acggtagcac  | caactccgac  | 960  |
| gcttggggct  | tcggtttgaa  | agccgggttac | gacttcaaac | tgggtgatgc  | tgggtacgtg  | 1020 |
| actccttacg  | gcagcggttc  | tggtctgttc  | cagtctgggt | atgactacca  | gctgagcaac  | 1080 |
| gacatgaaag  | ttgacgggtca | gtcttacgac  | agcatgcgtt | atgaactggg  | tgtagatgca  | 1140 |
| ggttatacct  | tcacctacag  | cgaagatcag  | gctctgactc | cgtacttcaa  | actggcttac  | 1200 |
| gtctacgacg  | actctaacaa  | cgataacgat  | gtgaacggcg | attccatcga  | taacgggtact | 1260 |
| gaagggctctg | cggtagcgtg  | tggtctgggt  | actcagttta | gcttcaccaa  | gaacttcagc  | 1320 |
| gcctataccg  | atgctaacta  | cctcgggtggt | ggtgacgtag | atcaagactg  | gtccgcgaac  | 1380 |
| gtgggtgtta  | aatatacctg  | gtaa        |            |             |             | 1404 |

&lt;210&gt; 222

&lt;211&gt; 669

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 222

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| atgcccgctca | aggatttgac | gggcattact | gcaaaggacg | cgcaaatgtt | atctgtagtt  | 60  |
| aaacctcttc  | aggaatttgg | taagctcgat | aaatgtttgt | ccagatacgg | tacgcgcttc  | 120 |
| gagttttaata | atgaaaagca | agttatat   | tccagtgatg | tcaataacga | agatactttc  | 180 |
| ggtattttag  | agggagttat | ctctctcgct | agagaagaaa | acgtacttat | cgggtattacc | 240 |
| cagggtcctt  | atattatggg | gctggctgat | ggtttaatga | aaaacgatat | accatacaaa  | 300 |
| ttaatatcag  | aaggaaattg | tacgggatat | catctaccag | ccaaacaaac | cattacgctt  | 360 |
| attgaacaaa  | atcaactctg | gcgagacgct | ttttactggt | tagcctggca | aaatagaatt  | 420 |
| ctggaattac  | gcgacgtgca | gctcattggg | cataattcct | acgaacaaat | ccgcgcaaca  | 480 |
| ttattatcaa  | tgattgactg | gaatgaagaa | ttgcgatcac | gtattggtgt | gatgaattat  | 540 |

atccatcaac gtacacgcat atcgcggttct gtcgtcgag aagttctcgc tgccttgcgt 600  
 aaaggcggct atatcgaaat gaataaaggc aaactggctg ctatcaaccg ttgccttca 660  
 gagtattaa 669

<210> 223  
 <211> 255  
 <212> DNA  
 <213> E. Coli

<400> 223  
 atgaccgata aaatccgtac tctgcaaggt cgcgttgta gcgacaaaat ggagaaatcc 60  
 attgtgttg ctatcgaaacg tttgtgaaa caccgatct acggtaaatt catcaagcgt 120  
 acgaccaaac tgcacgtaca tgacgagaac aacgaatgcg gtatcggtga cgtggttgaa 180  
 atccgcgaat gccgtccgct gtccaagact aaatcctgga cgctggttcg cgttgtagag 240  
 aaagcgggttc tgtaa 255

<210> 224  
 <211> 192  
 <212> DNA  
 <213> E. Coli

<400> 224  
 atgaaagcaa aagagctgcg tgagaagagc gttgaagagc tgaacaccga gctgctgaac 60  
 ctgctgcgtg agcagttcaa cctgcgtatg caggctgcaa gtggccagct gcaacagctct 120  
 cacctgttga agcaagtgcg tcgcgatgct gcacgcgtta agactttact gaacgagaag 180  
 gcgggtgcgt aa 192

<210> 225  
 <211> 411  
 <212> DNA  
 <213> E. Coli

<400> 225  
 atgtttacaac caaagcgtac aaaattccgt aaaatgcaca aaggccgtaa ccgcgggtctg 60  
 gcgcagggta cggatgttag cttcggcagc ttcgggtctga aagctgttgg ccgtgggtcgt 120  
 ctgactgccc gtcagatcga agcagcagct cgtgctatga cccgtgcagt taagcgtcaa 180  
 ggtaagatct ggatccgtgt gttcccggac aaaccgatca ctgaaaaagcc gctggcagtg 240  
 cgtatgggta aaggtaaagg taacgtggag tattgggttg ccttgattca gccgggtaaa 300  
 gtcctgtatg aaatggacgg tgttcggaa gagctggccc gtgaagcatt caagctggca 360  
 gcagcgaaac tgccgattaa aaccaccttt gtaactaaga cgggtgatgta a 411

<210> 226  
 <211> 702  
 <212> DNA  
 <213> E. Coli

<400> 226  
 atgggtcaga aagtacatcc taatgggtatt cgcctgggta ttgtaaaacc atggaactct 60  
 acctggtttg cgaacaccaa agaattcgct gacaacctgg acagcgattt taaagtacgt 120  
 cagtacctga ctaaggaaact ggctaaagcg tccgtatctc gtatcggtat cgagcgtccg 180  
 gctaagagca tccgtgtaac cattcacact gctcgcgccg gtatcggtat cggtaaaaaa 240  
 ggtgaagacg tagaaaaact gcgtaaggtc gtagcggaca tcgctggcgt tcctgcacag 300  
 atcaacatcg ccgaagttcg taagcctgaa ctggacgcaa aactggttgc tgacagcatc 360  
 acttctcagc tggaaacgtcg cgttatgttc cgtcgtgcta tgaagcgtgc tgtacagaac 420  
 gcaatgcgtc tgggcgctaa aggtattaaa gttgaagtta gcggccgctc gggcggcgcg 480  
 gaaatcgcac gtaccgaatg gtaccgcgaa ggtcgcgtac cgtgcacac tctgcgtgct 540  
 gacatcgact acaacacctc tgaagcgcac accacttacg gtgtaatcgg cgttaaaagt 600  
 tggatcttca aaggcgagat cctgggtggt atggctgctg ttgaacaacc ggaaaaaccg 660  
 gctgctcagc ctaaaaagca gcagcgtaaa ggccgtaaa aa 702

<210> 227

<211> 333  
 <212> DNA  
 <213> E. Coli

<400> 227  
 atggaaacta tcgctaaaca tcgccatgct cgttcttctg ctcagaaggt tcgccttgtt 60  
 gctgacctga ttcgcggtaa gaaagtgtcg caggctctgg atattttgac ctacaccaac 120  
 aagaaagcgg ctgtactggt caagaaagt ctggaatctg ccattgctaa cgctgaacac 180  
 aacgatggcg ctgacattga cgtatctgaaa gttacgaaaa ttttcgtaga cgaaggcccg 240  
 agcatgaagc gcattatgcc gcgtgcacaaa ggtcgtgcag atcgcaccc tgaagcgacc 300  
 agccacatca ctgtggtgt gtccgatcgc tga 333

<210> 228  
 <211> 279  
 <212> DNA  
 <213> E. Coli

<400> 228  
 atgccacgtt ctctcaagaa aggtcctttt attgacctgc acttgctgaa gaaggtagag 60  
 aaagcggtgg aaagcggaga caagaagccc ctgcgcactt ggtcccgtcg ttcaacgac 120  
 tttcttaaca tgatcggttt gaccatcgct gtccataatg gtcgtcagca cggtccggta 180  
 tttgtaaccg acgaaatggt tggtcacaaa ctgggtgaat tcgcaccgac tcgtacttat 240  
 cgcgccacg ctgctgataa aaaagcgag aagaataa 279

<210> 229  
 <211> 822  
 <212> DNA  
 <213> E. Coli

<400> 229  
 atggcagttg ttaaatgtaa accgacatct ccgggtcgtc gccacgtagt taaagtgtt 60  
 aaccctgagc tgcacaaggg caaacctttt gtcctgttgc tggaaaaaaa cagcaaatcc 120  
 ggtgtgctga acaacaatgg ccgtatcacc actcgtcata tcggtggtgg ccacaagcag 180  
 gcttaccgta ttgttgactt caaacgcaac aaagacggtg tcccggcagt tgttgaacgt 240  
 cttagtagac atccgaaccg ttccgcgaac atcgcgctgg ttctgtacaa agacggtgaa 300  
 cgcggttaca tcctggcccc taaaggcctg aaagctggcg accagattca gtctggcgtt 360  
 gatgctgcaa tcaaacccag taacaccctg ccgatgcgca acatcccgtt tgggttctact 420  
 gttcataacg tagaaatgaa accaggtaaa ggcggtcagc tggcacgttc cgctggtact 480  
 tacgttcaga tcgttgctcg tgatggtgct tatgtcacc tgcgtctgcg ttctggtgaa 540  
 atgctgtaag tagaagcaga ctgccgtgca actctggcg aagttggcaa tgctgagcat 600  
 atgctgcgcg ttctgggtaa agcaggtgct gcacgctggc gtggtgttcg tccgaccgtt 660  
 cgcggtaccg cgatgaaccc ggtagaccac ccacatggtg gtggtgaagg tcgtaacttt 720  
 ggtaagcacc cggtaaactc gtggggcggt cagaccaaag gtaagaagac ccgcagcaac 780  
 aagcgtactg ataaattcat cgtacgtcgc cgtagcaaat aa 822

<210> 230  
 <211> 303  
 <212> DNA  
 <213> E. Coli

<400> 230  
 atgattcgtg aagaacgtct gctgaagggt ctgcgtgcac cgcacgtttc tgaaaaagcg 60  
 tctactgcga tggaaaaatc caacaccatc gtactcaaa ttgctaaaga cgcgacccaa 120  
 gcagaaatca aagctgctgt gcagaaactg tttgaagtcg aagtcgaagt cgttaacacc 180  
 ctggtagtta aagggaaggt taaacgtcac ggacagcgta tcggtcgtcg tagcgactgg 240  
 aaaaaagctt acgtcaccc tgaagaagcg cagaatctgg acttcgttgg cggcgctgag 300  
 taa 303

<210> 231  
 <211> 630  
 <212> DNA

&lt;213&gt; E. Coli

&lt;400&gt; 231

|             |             |            |             |            |            |     |
|-------------|-------------|------------|-------------|------------|------------|-----|
| atgattgggt  | tagtcggttaa | aaaagtgggt | atgaccgta   | tcttcacaga | agacggcggt | 60  |
| tctatcccag  | taaccgtaat  | cgaagttgaa | gcaaaccgcg  | ttactcaggt | taaagacctg | 120 |
| gctaaccgatg | gctaccgtgc  | tattcaggtg | accaccggtg  | ctaaaaaagc | taaccgtgtg | 180 |
| accaagcctg  | aagctggcca  | cttcgctaaa | gctggcgtag  | aagctggccg | tggtctgtgg | 240 |
| gaattccgcc  | tggtggaag   | cgaagagttc | actgtaggtc  | agagcattag | cgttgaactg | 300 |
| tttgctgacg  | ttaaaaaagt  | tgacgtaact | ggcaccctcta | aaggtaaagg | tttcgcaggt | 360 |
| accgttaagc  | gctggaaactt | ccgtaccag  | gacgctactc  | acggtaactc | cttgtctcac | 420 |
| cgcgttcg    | gttctatcgg  | tcagaaccag | actccgggca  | aagtgttcaa | aggcaagaaa | 480 |
| atggcaggtc  | agatgggtaa  | cgaacgtgta | accgttcaga  | gccttgacgt | agtacgcgtt | 540 |
| gacgctgagc  | gcaacctgct  | gctgggttaa | ggtgctgtcc  | cgggtgcaac | cggtagcgac | 600 |
| ctgatcgta   | aaccagctgt  | gaaggcgtaa |             |            |            | 630 |

&lt;210&gt; 232

&lt;211&gt; 606

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 232

|            |            |             |             |             |             |     |
|------------|------------|-------------|-------------|-------------|-------------|-----|
| atggaattag | tattgaaaga | cgcgagagc   | gcgctgactg  | tttccgaaac  | taccttcggt  | 60  |
| cgtgatttca | acgaagcgct | ggttcaccag  | gttgttgttg  | cttatgcagc  | tggtgctcgt  | 120 |
| cagggtactc | gtgctcagaa | gactcgtgct  | gaagtaactg  | gttccggtaa  | aaaaccgtgg  | 180 |
| cgccagaaag | gcaccggccg | tgcgcggttct | ggttctatca  | agagcccgat  | ctggcggttct | 240 |
| gggtggcgta | cctttgtctg | tcgtccgcag  | gaccacagtc  | aaaaagttaa  | caagaagatg  | 300 |
| taccgcggcg | cgctgaaaaa | catcctgtcc  | gaactgggtac | gtcaggatcg  | tctgatcggt  | 360 |
| gtcgagaaat | tctctgtaga | agcgccgaaa  | actaagctgc  | tggtcacagaa | actgaaagac  | 420 |
| atggctctgg | aagatgtgct | gatcatcacc  | ggtgagctgg  | acgaaaaacct | gttcctggct  | 480 |
| gcgcgcgaac | tgacaaaggt | tgacgtacgc  | gatgcaactg  | gtatcgaccc  | ggttagcctg  | 540 |
| atgcgcttcg | acaaagtcgt | aatgactgct  | gatgctgtta  | agcaagttga  | ggagatgctg  | 600 |
| gcata      |            |             |             |             |             | 606 |

&lt;210&gt; 233

&lt;211&gt; 312

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 233

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| atgcagaacc | aaagaatccg | tatccgcctg | aaagcggttg  | atcatcgctc  | gatcgatcaa | 60  |
| gcaaccgcgg | aaatcgctga | gactgccaag | cgcaactggtg | cgcaaggtccg | tggtccgac  | 120 |
| ccgctgccga | cacgcaaaga | gcgcttcact | gttctgatct  | ccccgcacgt  | caacaaagac | 180 |
| gcgcgcgatc | agtacgaaat | ccgtactcac | ttgcgtctgg  | ttgacatcgt  | tgagccaacc | 240 |
| gagaaaaccg | ttgatgctct | gatgcgtctg | gatctggctg  | ccggtgtaga  | cgtgcagatc | 300 |
| agcctgggtt | aa         |            |             |             |            | 312 |

&lt;210&gt; 234

&lt;211&gt; 357

&lt;212&gt; DNA

&lt;213&gt; E. Coli

&lt;400&gt; 234

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| atggctcgcg | taaaaagctgg | tggtattgca | cgtgcacgtc | acaagaaaat | tttgaacaa  | 60  |
| gctaaaggct | actacggtgc  | gcgttctcgc | gtataccgcg | ttgccttcca | ggctgttatc | 120 |
| aaagctggtc | agtatgttta  | ccgtgaccgt | cgtcaacgta | agcgtcagtt | ccgtcaactg | 180 |
| tggtatgcgc | gtatcaacgc  | agcagcacgt | cagaacggtg | tttcttacag | caaattcatc | 240 |
| aatggcctga | aaaaagcctc  | tggtgaaatc | gaccgtaaga | tectggctga | tatcgagta  | 300 |
| ttcgacaaag | tagcgttcac  | cgctctggtt | gaaaaagcga | aagcagctct | ggcataa    | 357 |

&lt;210&gt; 235

&lt;211&gt; 198

<212> DNA  
<213> E. Coli

<400> 235  
atgccaaaaa ttaagaccgt acgcgggtgct gctaagcgct tcaaaaaaac cggtaaaggt 60  
ggtttttaagc acaagcacgc taacctgcgt cacattctga ccaaaaaagc gaccaaacgt 120  
aaacgtcacc tgcgtccgaa agccatggtt tccaaaggcg atctgggcct ggtaatcgcg 180  
tgcttgcgt acgcataa 198

<210> 236  
<211> 543  
<212> DNA  
<213> E. Coli

<400> 236  
attaaaggcg gaaaacgagt tcaaacggcg cgcctaacc gtatcaatgg cgaaattcgc 60  
gcccaggaag ttcgcttaac aggtctggaa ggcgagcagc ttggtattgt gagtctgaga 120  
gaagctctgg agaaagcaga agaagccgga gtagacttag tcgagatcag ccctaacgcc 180  
gagccgccgg tttgtcgtat aatggattac ggcaaatcc tctatgaaaa gagcaagtct 240  
tctaagggaac agaagaaaaa gcaaaaagtt atccaggtta aggaattaa attccgtcct 300  
ggtaacagat aaggcgacta tcaggtaaaa ctccgcagcc tgattcgctt tctcgaagag 360  
ggtgataaag ccaaaatcac gctgcgtttc cgcggctcgtg agatggcgca ccagcaaatc 420  
ggtatggaag tgcttaatcg cgtgaaagac gatttgcaag aactggcagt ggtcgaatcc 480  
ttcccaacga agatcgaagg ccgccagatg atcatggtgc tcgctcctaa gaagaaacag 540  
taa 543

<210> 237  
<211> 1929  
<212> DNA  
<213> E. Coli

<400> 237  
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aatggcgaaac tgggtgatgc ttgcgatctg attgaaaacg acgcacaact gtcgatcatt 180  
accgccaaag acgaagaagg tctggagatc attcgtcact cctgtgcgca cctgttaggg 240  
cacgcgatta aacaactttg gcgcataacc aaaatggcaa tcggcccgggt tattgacaac 300  
ggtttttatt acgacgttga tcttgaccgc acgttaaccc aggaagatgt cgaagcactc 360  
gagaagcgga tgcatgagct tgctgagaaa aactacgacg tcattaagaa gaaagtcagc 420  
tggcacgaag cgctgaaaac ttccgccaac cgtggggaga gctacaaagt ctccattctt 480  
gacgaaaaca tcgcccatga tgacaagcca ggtctgtact tccatgaaga atatgtcgat 540  
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ccgggtatgg tattctggca caacgacggc tggaccatct tccgtgaact ggaagtgttt 840  
gttcgttcta aactgaaaag gtaccagtat caggaagtta aagggtccgtt catgatggac 900  
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ttctacggtc cgaaaattga atttaccctg tatgactgcc tcgatcgtgc atggcagtgc 1440  
ggtacagtac agctggactt ctctttgcg tctcgtctga gcgcttctta tgtaggcgaa 1500  
gacaatgaac gtaaaagtacc ggtaatgatt caccgcgcaa ttctggggtc gatggaacgt 1560  
ttcatcggta tcttgaccga agagttcgtc ggtttcttcc cgacctggct tgcgccggtt 1620  
caggttggtta tcatgaatat taccgattca cagtctgaat acgttaacga attgacgcaa 1680  
aaactatcaa atgcgggcat tcgtgttaaa gcagacttga gaaatgagaa gattggcttt 1740



|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| aaaaatccgcg | agcacacttt | gcgtcgcgtc | ccatatatgc | tggctctgtg | tgataaagag | 1800 |
| gtggaatcag  | gcaaagtgc  | cggtcgcacc | cgccgtggta | aagacctggg | aagcatggac | 1860 |
| gtaaatgaag  | tgatcgagaa | gctgcaacaa | gagattcgca | gccgcagctc | taaacattg  | 1920 |
| gaggaataa   |            |            |            |            |            | 1929 |

<210> 238  
 <211> 1353  
 <212> DNA  
 <213> E. Coli

<400> 238

|            |            |             |             |            |             |      |
|------------|------------|-------------|-------------|------------|-------------|------|
| atgactaaac | actatgatta | catcgccatc  | ggcggcgcca  | gcggcggtat | cgccctccatc | 60   |
| aaccgcgcgg | ctatgtacgg | ccagaaatgt  | gcgctgattg  | aagccaaaga | gctgggcggc  | 120  |
| acctgcgtaa | atgttggctg | tgtgccgaaa  | aaagtgatgt  | ggcacgcggc | gcaaatccgt  | 180  |
| gaagcgatcc | atatgtacgg | cccggattat  | ggttttgata  | ccactatcaa | taaattcaac  | 240  |
| tgggaacgt  | tgatcgccag | ccgtaccgcc  | tatatcgacc  | gtattcatac | ttcctatgaa  | 300  |
| aacgtgctcg | gtaaaaataa | cgttgatgta  | atcaaaggct  | tgcccgcgtt | cgttgatgcc  | 360  |
| aaaacgctgg | aggtaaacgg | cgaaaccatc  | acggccgcatc | atattctgat | cgccacaggc  | 420  |
| ggtcgtccga | gccaccgcga | tattccgggc  | gtggaatacg  | gtattgattc | tgatggcttc  | 480  |
| ttcgcccttc | ctgctttgcc | agagcgcgtg  | gcggttggtg  | gcgcgggtta | catcgccgtt  | 540  |
| gagctggcgg | gcgtgattaa | cgccctcggc  | gcgaaaacgc  | atctgtttgt | gcgtaaacat  | 600  |
| gcgccctgct | gcagcttcga | cccgatgatt  | tccgaaacgc  | tggtcgaaat | gatgaacgcc  | 660  |
| gaaggccgcg | agctgcacac | caacgcctac  | ccgaaagcgg  | tagtgaaaaa | taccgatggt  | 720  |
| agcctgacgc | tgagctggga | agatggctgc  | agtgaacggg  | tggattgcct | gatttgggcg  | 780  |
| attggtcgcg | agcctgcca  | tgacaacatc  | aacctggaag  | ccgctggcgt | taaaactaac  | 840  |
| gaaaaaggct | atatcgctgt | cgataaatat  | caaaacacca  | atattgaagg | tatttacgcg  | 900  |
| gtgggcgata | acacgggtgc | agtggagctg  | acaccgggtg  | cagttgcagc | gggtcgccgt  | 960  |
| ctctctgaac | gcctgtttaa | taacaagcgg  | gatgagcatc  | tggattacag | caacattccg  | 1020 |
| accgtggtct | tcagccatcc | gccgattggt  | actgttggtt  | taacggaacc | gcaggcgccg  | 1080 |
| gagcagtatg | gcgacgatca | ggtgaaagtg  | tataaatcct  | ctttcaccgc | gatgtatacc  | 1140 |
| gccgtcacca | ctcacgcgca | gccgtgcccgc | atgaagctgg  | tgtgcgttgg | atcggaagag  | 1200 |
| aaqattgtcg | gtattcacgg | cattggcttt  | ggtatggacg  | aaatgttgca | gggcttcgcg  | 1260 |
| gtggcgctga | agatgggggc | aaccaaaaaa  | gacttcgaca  | ataccgtcgc | cattcaccca  | 1320 |
| acggcgcgag | aagagttcgt | gacaatgcgt  | ttaa        |            |             | 1353 |

<210> 239  
 <211> 2904  
 <212> DNA  
 <213> E. Coli

<400> 239

|             |            |            |             |             |             |      |
|-------------|------------|------------|-------------|-------------|-------------|------|
| aaagttaagc  | ctcacggttc | attagtagcg | gtagctcaa   | cgcatcgctg  | cgcttacaca  | 60   |
| cccgccctat  | caacgtcgtc | gtcttcaacg | ttccttcagg  | acccttaaag  | ggtcagggag  | 120  |
| aactcatctc  | ggggcaagtt | tcgtgcttag | atgctttcag  | cacttatctc  | ttccgcattt  | 180  |
| agctacccgg  | cagtgccatt | ggcatgacaa | cccgaacacc  | agtgatgcgt  | ccactccggg  | 240  |
| cctctcgtag  | taggagcagc | cccctcagt  | tctccagcgc  | ccacggcaga  | tagggaccga  | 300  |
| actgtctcac  | gacgttctaa | acccagctcg | cgtaccactt  | taaatggcga  | acagccatac  | 360  |
| ccttggggacc | tacttcagcc | ccaggatgtg | atgagccgac  | atcgaggtgc  | caaacaccgc  | 420  |
| cgctgatatg  | aactcttggg | cggtatcagc | ctgttatccc  | cggagtagct  | tttatccgtt  | 480  |
| gagcgatggc  | ccttccattc | agaaccaccg | gatcaactatg | acctgcttcc  | gcacctgctc  | 540  |
| gcgccgtcac  | gctcgagtc  | aagctggctt | atgccattgc  | actaacctcc  | tgatgtccga  | 600  |
| ccaggattag  | ccaaccttcg | tgctcctccg | ttactcttta  | ggaggagacc  | gccccagtc   | 660  |
| aactacccac  | cagacactgt | ccgcaacccg | gattacgggt  | caacgttaga  | acatcaaaaca | 720  |
| ttaaagggtg  | gtatttcaag | gtcgggtcca | tgacagactg  | cgtccacact  | tcaaagcctc  | 780  |
| ccacctatcc  | tacacatcaa | ggctcaatgt | tcagtgtcaa  | gctatagtaa  | aggttcacgg  | 840  |
| ggtctttccg  | tcttggccgg | ggtacactgc | atcttcacag  | cgagttcaat  | ttcactgagt  | 900  |
| ctcgggtgga  | gacagcctgg | ccatcattac | gccattcgtg  | caggtcggaa  | cttaccggac  | 960  |
| aaggaatttc  | gctaccttag | gaccgttata | gttacggccg  | ccgtttaccg  | gggcttcgat  | 1020 |
| caagagcttc  | gcttgcgcta | accccatcaa | ttaaccttcc  | ggcaccgggc  | aggcgctaca  | 1080 |
| ccgtatacgt  | ccactttcgt | gtttgcacag | tgctgtgttt  | ttaataaaaca | gttgacagcca | 1140 |
| gtcgttatct  | tcgactgatt | tcagctccat | ccgcgaggga  | cctcacctac  | atatcagcgt  | 1200 |

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gccttctccc gaagttacgg caccattttg cctagttcct tcaccgcagt tctctcaagc 1260
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ttttcactcc cctcgccggg gttcttttct cctttccctc acggtactgg ttcactatcg 2460
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ttagatgttt cagttccccc ggttcgcctc attaacctat ggattcagtt aatgatagtg 2760
tgtcgaaaca cactgggttt ccccatcgg aaatcgccg ttataacggt tcataccacc 2820
ttaccgacgc ttatcgcgaga ttagcacgct cttcatcgcc tctgactgcc agggcatcca 2880
ccgtgtacgc ttagtcgctt aacc 2904

```

<210> 240  
 <211> 120  
 <212> DNA  
 <213> E. Coli

```

<400> 240
atgcctggca gttccctact ctgcgatggg gagaccccac actaccatcg gcgctacggc 60
gtttcacttc tgagttcggc atggggtcag gtgggaccac cgcgctacgg cccgacggca 120

```

<210> 241  
 <211> 76  
 <212> DNA  
 <213> E. Coli

```

<400> 241
gtcccccttc tctagaggcc caggacaccg ccctttcacg gcggtaacag gggttcgaat 60
cccctagggg acgcca 76

```

<210> 242  
 <211> 1549  
 <212> DNA  
 <213> E. Coli

```

<400> 242
aaattgaaga gtttgatcat ggctcagatt gaacgctggc ggaggccta acacatgcaa 60
gtcgaacggt aacaggaagc agcttgctgc ttgctgacg agtgccggac gggtagtaaa 120
tgtctgggaa gctgcctgat ggagggggat aactactgga aacggtagct aataccgcat 180
aatgtcgcaa gaccaaagag ggggaccttc gggcctcttg ccacgcatg tgcccagatg 240
ggattagctt gttggtgggg taacggctca ccaaggcgac gatccctagc tggctcgaga 300
ggatgaccag ccacactgga actgagacac ggtccagact cctacgggag gcagcagtg 360
ggaatattgc acaatggggc caagcctgat gcagccatgc cgcgtgtatg aagaaggcct 420

```

```

tcgggttgta aagtactttc agcggggagg aaggaggtaa agttaatacc tttgctcatt 480
gacgttacct gcagaagaag caccggctaa ctccgtgccg gcagccgagg taatacggag 540
ggtgcaagcg ttaacggaa ttactggcg taaagcgac gcagcgagg tggttaagtc 600
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cgtagagggg ggtagaattc caggtgtagc ggtgaaatgc gtagagatct ggaggaatac 720
cggtggcgaa ggcggccccc tggacgaaga ctgacgctca ggtgcgaaag cgtggggagc 780
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acaaggtaac cgtaggggaa cctgcggttg gatcacctcc ttaccttaa 1549

```

&lt;210&gt; 243

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 243

```

Met Asn Val Phe Ser Gln Thr Gln Arg Tyr Lys Ala Leu Phe Trp Leu
1          5          10          15
Ser Leu Phe His Leu Leu Val Ile Thr Ser Ser Asn Tyr Leu Val Gln
20         25         30
Leu Pro Val Ser Ile Leu Gly Phe His Thr Thr Trp Gly Ala Phe Ser
35         40         45
Phe Pro Phe Ile Phe Leu Ala Thr Asp Leu Thr Val Arg Ile Phe Gly
50         55         60
Ala Pro Leu Ala Arg Arg Ile Ile Phe Ala Val Met Ile Pro Ala Leu
65         70         75         80
Leu Ile Ser Tyr Val Ile Ser Ser Leu Phe Tyr Met Gly Ser Trp Gln
85         90         95
Gly Phe Gly Ala Leu Ala His Phe Asn Leu Phe Val Ala Arg Ile Ala
100        105        110
Thr Ala Ser Phe Met Ala Tyr Ala Leu Gly Gln Ile Leu Asp Val His
115        120        125
Val Phe Asn Arg Leu Arg Gln Ser Arg Arg Trp Trp Leu Ala Pro Thr
130        135        140
Ala Ser Thr Leu Phe Gly Asn Val Ser Asp Thr Leu Ala Phe Phe Phe
145        150        155        160
Ile Ala Phe Trp Arg Ser Pro Asp Ala Phe Met Ala Glu His Trp Met
165        170        175
Glu Ile Ala Leu Val Asp Tyr Cys Phe Lys Val Leu Ile Ser Ile Val
180        185        190
Phe Phe Leu Pro Met Tyr Gly Val Leu Leu Asn Met Leu Leu Lys Arg
195        200        205
Leu Ala Asp Lys Ser Glu Ile Asn Ala Leu Gln Ala Ser
210        215        220

```

&lt;210&gt; 244

&lt;211&gt; 203

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 244

```

Met Ile Arg Trp Met Asn Glu Pro Leu Trp Pro Phe Ile Glu Arg Lys
 1      5      10      15
Lys Ser Met Arg Asn Leu Val Lys Tyr Val Gly Ile Gly Leu Leu Val
 20      25      30
Met Gly Leu Ala Ala Cys Asp Asp Lys Asp Thr Asn Ala Thr Ala Gln
 35      40      45
Gly Ser Val Ala Glu Ser Asn Ala Thr Gly Asn Pro Val Asn Leu Leu
 50      55      60
Asp Gly Lys Leu Ser Phe Ser Leu Pro Ala Asp Met Thr Asp Gln Ser
 65      70      75      80
Gly Lys Leu Gly Thr Gln Ala Asn Asn Met His Val Trp Ser Asp Ala
 85      90      95
Thr Gly Gln Lys Ala Val Ile Val Ile Met Gly Asp Asp Pro Lys Glu
100      105      110
Asp Leu Ala Val Leu Ala Lys Arg Leu Glu Asp Gln Gln Arg Ser Arg
115      120      125
Asp Pro Gln Leu Gln Val Val Thr Asn Lys Ala Ile Glu Leu Lys Gly
130      135      140
His Lys Met Gln Gln Leu Asp Ser Ile Ile Ser Ala Lys Gly Gln Thr
145      150      155      160
Ala Tyr Ser Ser Val Ile Leu Gly Asn Val Gly Asn Gln Leu Leu Thr
165      170      175
Met Gln Ile Thr Leu Pro Ala Asp Asp Gln Gln Lys Ala Gln Thr Thr
180      185      190
Ala Glu Asn Ile Ile Asn Thr Leu Val Ile Gln
195      200

```

&lt;210&gt; 245

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 245

```

Met Ala Asn Met Phe Ala Leu Ile Leu Val Ile Ala Thr Leu Val Thr
 1      5      10      15
Gly Ile Leu Trp Cys Val Asp Lys Phe Phe Ala Pro Lys Arg Arg
 20      25      30
Glu Arg Gln Ala Ala Ala Gln Ala Ala Ala Gly Asp Ser Leu Asp Lys
 35      40      45
Ala Thr Leu Lys Lys Val Ala Pro Lys Pro Gly Trp Leu Glu Thr Gly
 50      55      60
Ala Ser Val Phe Pro Val Leu Ala Ile Val Leu Ile Val Arg Ser Phe
 65      70      75      80
Ile Tyr Glu Pro Phe Gln Ile Pro Ser Gly Ser Met Met Pro Thr Leu
 85      90      95
Leu Ile Gly Asp Phe Ile Leu Val Glu Lys Phe Ala Tyr Gly Ile Lys
100      105      110
Asp Pro Ile Tyr Gln Lys Thr Leu Ile Glu Thr Gly His Pro Lys Arg
115      120      125
Gly Asp Ile Val Val Phe Lys Tyr Pro Glu Asp Pro Lys Leu Asp Tyr
130      135      140
Ile Lys Arg Ala Val Gly Leu Pro Gly Asp Lys Val Thr Tyr Asp Pro
145      150      155      160
Val Ser Lys Glu Leu Thr Ile Gln Pro Gly Cys Ser Ser Gly Gln Ala
165      170      175
Cys Glu Asn Ala Leu Pro Val Thr Tyr Ser Asn Val Glu Pro Ser Asp
180      185      190
Phe Val Gln Thr Phe Ser Arg Arg Asn Gly Gly Glu Ala Thr Ser Gly

```

```

      195      200      205
Phe Phe Glu Val Pro Lys Asn Glu Thr Lys Glu Asn Gly Ile Arg Leu
210      215      220
Ser Glu Arg Lys Glu Thr Leu Gly Asp Val Thr His Arg Ile Leu Thr
225      230      235      240
Val Pro Ile Ala Gln Asp Gln Val Gly Met Tyr Tyr Gln Gln Pro Gly
      245      250      255
Gln Gln Leu Ala Thr Trp Ile Val Pro Pro Gly Gln Tyr Phe Met Met
      260      265      270
Gly Asp Asn Arg Asp Asn Ser Ala Asp Ser Arg Tyr Trp Gly Phe Val
      275      280      285
Pro Glu Ala Asn Leu Val Gly Arg Ala Thr Ala Ile Trp Met Ser Phe
      290      295      300
Asp Lys Gln Glu Gly Glu Trp Pro Thr Gly Leu Arg Leu Ser Arg Ile
305      310      315      320
Gly Gly Ile His

```

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<210> 246
<211> 586
<212> PRT
<213> E. Coli

```

```

      <400> 246
Met Thr Ile Thr Lys Leu Ala Trp Arg Asp Leu Val Pro Asp Thr Asp
1      5      10      15
Ser Tyr Gln Glu Ile Phe Ala Gln Pro His Leu Ile Asp Glu Asn Asp
      20      25      30
Pro Leu Phe Ser Asp Thr Gln Pro Arg Leu Gln Phe Ala Leu Glu Gln
      35      40      45
Leu Leu His Thr Arg Ala Ser Ser Ser Phe Met Leu Ala Lys Ala Pro
      50      55      60
Glu Glu Ser Glu Tyr Leu Asn Leu Ile Ala Asn Ala Ala Arg Thr Leu
      65      70      75      80
Gln Ser Asp Ala Gly Gln Leu Val Gly Gly His Tyr Glu Val Ser Gly
      85      90      95
His Ser Ile Arg Leu Arg His Ala Val Ser Ala Asp Asp Asn Phe Ala
      100      105      110
Thr Leu Thr Gln Val Val Ala Ala Asp Trp Val Glu Ala Glu Gln Leu
      115      120      125
Phe Gly Cys Leu Arg Gln Phe Asn Gly Asp Ile Thr Leu Gln Pro Gly
      130      135      140
Leu Val His Gln Ala Asn Gly Gly Ile Leu Ile Ile Ser Leu Arg Thr
      145      150      155      160
Leu Leu Ala Gln Pro Leu Leu Trp Met Arg Leu Lys Asn Ile Val Asn
      165      170      175
Arg Glu Arg Phe Asp Trp Val Ala Phe Asp Glu Ser Arg Pro Leu Pro
      180      185      190
Val Ser Val Pro Ser Met Pro Leu Lys Leu Lys Val Ile Leu Val Gly
      195      200      205
Glu Arg Glu Ser Leu Ala Asp Phe Gln Glu Met Glu Pro Glu Leu Ser
      210      215      220
Glu Gln Ala Ile Tyr Ser Glu Phe Glu Asp Thr Leu Gln Ile Val Asp
      225      230      235      240
Ala Glu Ser Val Thr Gln Trp Cys Arg Trp Val Thr Phe Thr Ala Arg
      245      250      255
His Asn His Leu Pro Ala Pro Gly Ala Asp Ala Trp Pro Ile Leu Ile
      260      265      270
Arg Glu Ala Ala Arg Tyr Thr Gly Glu Gln Glu Thr Leu Pro Leu Ser

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      275      280      285
Pro Gln Trp Ile Leu Arg Gln Cys Lys Glu Val Ala Ser Leu Cys Asp
290      295      300
Gly Asp Thr Phe Ser Gly Glu Gln Leu Asn Leu Met Leu Gln Gln Arg
305      310      315      320
Glu Trp Arg Glu Gly Phe Leu Ala Glu Arg Met Gln Asp Glu Ile Leu
      325      330      335
Gln Glu Gln Ile Leu Ile Glu Thr Glu Gly Glu Arg Ile Gly Gln Ile
      340      345      350
Asn Ala Leu Ser Val Ile Glu Phe Pro Gly His Pro Arg Ala Phe Gly
355      360      365
Glu Pro Ser Arg Ile Ser Cys Val Val His Ile Gly Asp Gly Glu Phe
370      375      380
Thr Asp Ile Glu Arg Lys Ala Glu Leu Gly Gly Asn Ile His Ala Lys
385      390      395      400
Gly Met Met Ile Met Gln Ala Phe Leu Met Ser Glu Leu Gln Leu Glu
      405      410      415
Gln Gln Ile Pro Phe Ser Ala Ser Leu Thr Phe Glu Gln Ser Tyr Ser
      420      425      430
Glu Val Asp Gly Asp Ser Ala Ser Met Ala Glu Leu Cys Ala Leu Ile
435      440      445
Ser Ala Leu Ala Asp Val Pro Val Asn Gln Ser Ile Ala Ile Thr Gly
450      455      460
Ser Val Asp Gln Phe Gly Arg Ala Gln Pro Val Gly Gly Leu Asn Glu
465      470      475      480
Lys Ile Glu Gly Phe Phe Ala Ile Cys Gln Gln Arg Glu Leu Thr Gly
      485      490      495
Lys Gln Gly Val Ile Ile Pro Thr Ala Asn Val Arg His Leu Ser Leu
500      505      510
His Ser Glu Leu Val Lys Ala Val Glu Glu Gly Lys Phe Thr Ile Trp
515      520      525
Ala Val Asp Asp Val Thr Asp Ala Leu Pro Leu Leu Leu Asn Leu Val
530      535      540
Trp Asp Gly Glu Gly Gln Thr Thr Leu Met Gln Thr Ile Gln Glu Arg
545      550      555      560
Ile Ala Gln Ala Ser Gln Gln Glu Gly Arg His Arg Phe Pro Trp Pro
565      570      575
Leu Arg Trp Leu Asn Trp Phe Ile Pro Asn
580      585

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<210> 247  
 <211> 394  
 <212> PRT  
 <213> E. Coli

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      <400> 247
Met Ser Lys Glu Lys Phe Glu Arg Thr Lys Pro His Val Asn Val Gly
1      5      10      15
Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
20      25      30
Thr Thr Val Leu Ala Lys Thr Tyr Gly Gly Ala Ala Arg Ala Phe Asp
35      40      45
Gln Ile Asp Asn Ala Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn
50      55      60
Thr Ser His Val Glu Tyr Asp Thr Pro Thr Arg His Tyr Ala His Val
65      70      75      80
Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala
85      90      95
Ala Gln Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp Gly Pro
100      105      110

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Met Pro Gln Thr Arg Glu His Ile Leu Leu Gly Arg Gln Val Gly Val  
 115 120 125  
 Pro Tyr Ile Ile Val Phe Leu Asn Lys Cys Asp Met Val Asp Asp Glu  
 130 135 140  
 Glu Leu Leu Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu Ser Gln  
 145 150 155 160  
 Tyr Asp Phe Pro Gly Asp Asp Thr Pro Ile Val Arg Gly Ser Ala Leu  
 165 170 175  
 Lys Ala Leu Glu Gly Asp Ala Glu Trp Glu Ala Lys Ile Leu Glu Leu  
 180 185 190  
 Ala Gly Phe Leu Asp Ser Tyr Ile Pro Glu Pro Glu Arg Ala Ile Asp  
 195 200 205  
 Lys Pro Phe Leu Leu Pro Ile Glu Asp Val Phe Ser Ile Ser Gly Arg  
 210 215 220  
 Gly Thr Val Val Thr Gly Arg Val Glu Arg Gly Ile Ile Lys Val Gly  
 225 230 235 240  
 Glu Glu Val Glu Ile Val Gly Ile Lys Glu Thr Gln Lys Ser Thr Cys  
 245 250 255  
 Thr Gly Val Glu Met Phe Arg Lys Leu Leu Asp Glu Gly Arg Ala Gly  
 260 265 270  
 Glu Asn Val Gly Val Leu Leu Arg Gly Ile Lys Arg Glu Glu Ile Glu  
 275 280 285  
 Arg Gly Gln Val Leu Ala Lys Pro Gly Thr Ile Lys Pro His Thr Lys  
 290 295 300  
 Phe Glu Ser Glu Val Tyr Ile Leu Ser Lys Asp Glu Gly Gly Arg His  
 305 310 315 320  
 Thr Pro Phe Phe Lys Gly Tyr Arg Pro Gln Phe Tyr Phe Arg Thr Thr  
 325 330 335  
 Asp Val Thr Gly Thr Ile Glu Leu Pro Glu Gly Val Glu Met Val Met  
 340 345 350  
 Pro Gly Asp Asn Ile Lys Met Val Val Thr Leu Ile His Pro Ile Ala  
 355 360 365  
 Met Asp Asp Gly Leu Arg Phe Ala Ile Arg Glu Gly Gly Arg Thr Val  
 370 375 380  
 Gly Ala Gly Val Val Ala Lys Val Leu Gly  
 385 390

<210> 248  
 <211> 704  
 <212> PRT  
 <213> E. Coli

<400> 248  
 Met Ala Arg Thr Thr Pro Ile Ala Arg Tyr Arg Asn Ile Gly Ile Ser  
 1 5 10 15  
 Ala His Ile Asp Ala Gly Lys Thr Thr Thr Thr Glu Arg Ile Leu Phe  
 20 25 30  
 Tyr Thr Gly Val Asn His Lys Ile Gly Glu Val His Asp Gly Ala Ala  
 35 40 45  
 Thr Met Asp Trp Met Glu Gln Glu Gln Arg Gly Ile Thr Ile Thr  
 50 55 60  
 Ser Ala Ala Thr Thr Ala Phe Trp Ser Gly Met Ala Lys Gln Tyr Glu  
 65 70 75 80  
 Pro His Arg Ile Asn Ile Ile Asp Thr Pro Gly His Val Asp Phe Thr  
 85 90 95  
 Ile Glu Val Glu Arg Ser Met Arg Val Leu Asp Gly Ala Val Met Val  
 100 105 110  
 Tyr Cys Ala Val Gly Gly Val Gln Pro Gln Ser Glu Thr Val Trp Arg  
 115 120 125

Gln Ala Asn Lys Tyr Lys Val Pro Arg Ile Ala Phe Val Asn Lys Met  
 130 135 140  
 Asp Arg Met Gly Ala Asn Phe Leu Lys Val Val Asn Gln Ile Lys Thr  
 145 150 155 160  
 Arg Leu Gly Ala Asn Pro Val Pro Leu Gln Leu Ala Ile Gly Ala Glu  
 165 170 175  
 Glu His Phe Thr Gly Val Val Asp Leu Val Lys Met Lys Ala Ile Asn  
 180 185 190  
 Trp Asn Asp Ala Asp Gln Gly Val Thr Phe Glu Tyr Glu Asp Ile Pro  
 195 200 205  
 Ala Asp Met Val Glu Leu Ala Asn Glu Trp His Gln Asn Leu Ile Glu  
 210 215 220  
 Ser Ala Ala Glu Ala Ser Glu Glu Leu Met Glu Lys Tyr Leu Gly Gly  
 225 230 235 240  
 Glu Glu Leu Thr Glu Ala Glu Ile Lys Gly Ala Leu Arg Gln Arg Val  
 245 250 255  
 Leu Asn Asn Glu Ile Ile Leu Val Thr Cys Gly Ser Ala Phe Lys Asn  
 260 265 270  
 Lys Gly Val Gln Ala Met Leu Asp Ala Val Ile Asp Tyr Leu Pro Ser  
 275 280 285  
 Pro Val Asp Val Pro Ala Ile Asn Gly Ile Leu Asp Asp Gly Lys Asp  
 290 295 300  
 Thr Pro Ala Glu Arg His Ala Ser Asp Asp Glu Pro Phe Ser Ala Leu  
 305 310 315 320  
 Ala Phe Lys Ile Ala Thr Asp Pro Phe Val Gly Asn Leu Thr Phe Phe  
 325 330 335  
 Arg Val Tyr Ser Gly Val Val Asn Ser Gly Asp Thr Val Leu Asn Ser  
 340 345 350  
 Val Lys Ala Ala Arg Glu Arg Phe Gly Arg Ile Val Gln Met His Ala  
 355 360 365  
 Asn Lys Arg Glu Glu Ile Lys Glu Val Arg Ala Gly Asp Ile Ala Ala  
 370 375 380  
 Ala Ile Gly Leu Lys Asp Val Thr Thr Gly Asp Thr Leu Cys Asp Pro  
 385 390 395 400  
 Asp Ala Pro Ile Ile Leu Glu Arg Met Glu Phe Pro Glu Pro Val Ile  
 405 410 415  
 Ser Ile Ala Val Glu Pro Lys Thr Lys Ala Asp Gln Glu Lys Met Gly  
 420 425 430  
 Leu Ala Leu Gly Arg Leu Ala Lys Glu Asp Pro Ser Phe Arg Val Trp  
 435 440 445  
 Thr Asp Glu Glu Ser Asn Gln Thr Ile Ile Ala Gly Met Gly Glu Leu  
 450 455 460  
 His Leu Asp Ile Ile Val Asp Arg Met Lys Arg Glu Phe Asn Val Glu  
 465 470 475 480  
 Ala Asn Val Gly Lys Pro Gln Val Ala Tyr Arg Glu Thr Ile Arg Gln  
 485 490 495  
 Lys Val Thr Asp Val Glu Gly Lys His Ala Lys Gln Ser Gly Gly Arg  
 500 505 510  
 Gly Gln Tyr Gly His Val Val Ile Asp Met Tyr Pro Leu Glu Pro Gly  
 515 520 525  
 Ser Asn Pro Lys Gly Tyr Glu Phe Ile Asn Asp Ile Lys Gly Gly Val  
 530 535 540  
 Ile Pro Gly Glu Tyr Ile Pro Ala Val Asp Lys Gly Ile Gln Glu Gln  
 545 550 555 560  
 Leu Lys Ala Gly Pro Leu Ala Gly Tyr Pro Val Val Asp Met Gly Ile  
 565 570 575  
 Arg Leu His Phe Gly Ser Tyr His Asp Val Asp Ser Ser Glu Leu Ala  
 580 585 590  
 Phe Lys Leu Ala Ala Ser Ile Ala Phe Lys Glu Gly Phe Lys Lys Ala  
 595 600 605  
 Lys Pro Val Leu Leu Glu Pro Ile Met Lys Val Glu Val Glu Thr Pro



610                      615                      620  
 Glu Glu Asn Thr Gly Asp Val Ile Gly Asp Leu Ser Arg Arg Arg Gly  
 625                      630                      635                      640  
 Met Leu Lys Gly Gln Glu Ser Glu Val Thr Gly Val Lys Ile His Ala  
                     645                      650                      655  
 Glu Val Pro Leu Ser Glu Met Phe Gly Tyr Ala Thr Gln Leu Arg Ser  
                     660                      665                      670  
 Leu Thr Lys Gly Arg Ala Ser Tyr Thr Met Glu Phe Leu Lys Tyr Asp  
                     675                      680                      685  
 Glu Ala Pro Ser Asn Val Ala Gln Ala Val Ile Glu Ala Arg Gly Lys  
                     690                      695                      700

<210> 249  
 <211> 179  
 <212> PRT  
 <213> E. Coli

<400> 249  
 Met Pro Arg Arg Val Ile Gly Gln Arg Lys Ile Leu Pro Asp Pro  
 1                      5                      10                      15  
 Lys Phe Gly Ser Glu Leu Leu Ala Lys Phe Val Asn Ile Leu Met Val  
                     20                      25                      30  
 Asp Gly Lys Lys Ser Thr Ala Glu Ser Ile Val Tyr Ser Ala Leu Glu  
                     35                      40                      45  
 Thr Leu Ala Gln Arg Ser Gly Lys Ser Glu Leu Glu Ala Phe Glu Val  
                     50                      55                      60  
 Ala Leu Glu Asn Val Arg Pro Thr Val Glu Val Lys Ser Arg Arg Val  
                     65                      70                      75                      80  
 Gly Gly Ser Thr Tyr Gln Val Pro Val Glu Val Arg Pro Val Arg Arg  
                     85                      90                      95  
 Asn Ala Leu Ala Met Arg Trp Ile Val Glu Ala Ala Arg Lys Arg Gly  
                     100                      105                      110  
 Asp Lys Ser Met Ala Leu Arg Leu Ala Asn Glu Leu Ser Asp Ala Ala  
                     115                      120                      125  
 Glu Asn Lys Gly Thr Ala Val Lys Lys Arg Glu Asp Val His Arg Met  
                     130                      135                      140  
 Ala Glu Ala Asn Lys Ala Phe Ala His Tyr Arg Trp Leu Ser Leu Arg  
                     145                      150                      155                      160  
 Ser Phe Ser His Gln Ala Gly Ala Ser Ser Lys Gln Pro Ala Leu Gly  
                     165                      170                      175  
 Tyr Leu Asn

<210> 250  
 <211> 124  
 <212> PRT  
 <213> E. Coli

<400> 250  
 Met Ala Thr Val Asn Gln Leu Val Arg Lys Pro Arg Ala Arg Lys Val  
 1                      5                      10                      15  
 Ala Lys Ser Asn Val Pro Ala Leu Glu Ala Cys Pro Gln Lys Arg Gly  
                     20                      25                      30  
 Val Cys Thr Arg Val Tyr Thr Thr Pro Lys Lys Pro Asn Ser Ala  
                     35                      40                      45  
 Leu Arg Lys Val Cys Arg Val Arg Leu Thr Asn Gly Phe Glu Val Thr  
                     50                      55                      60  
 Ser Tyr Ile Gly Gly Glu Gly His Asn Leu Gln Glu His Ser Val Ile  
                     65                      70                      75                      80

Leu Ile Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr His  
                                     85                                    90                                    95  
 Thr Val Arg Gly Ala Leu Asp Cys Ser Gly Val Lys Asp Arg Lys Gln  
                                     100                                    105                                    110  
 Ala Arg Ser Lys Tyr Gly Val Lys Arg Pro Lys Ala  
                                     115                                    120

<210> 251  
 <211> 165  
 <212> PRT  
 <213> E. Coli

<400> 251  
 Met Ala Leu Asn Leu Gln Asp Lys Gln Ala Ile Val Ala Glu Val Ser  
   1                                    5                                    10                                    15  
 Glu Val Ala Lys Gly Ala Leu Ser Ala Val Val Ala Asp Ser Arg Gly  
                                     20                                    25                                    30  
 Val Thr Val Asp Lys Met Thr Glu Leu Arg Lys Ala Gly Arg Glu Ala  
                                     35                                    40                                    45  
 Gly Val Tyr Met Arg Val Val Arg Asn Thr Leu Leu Arg Arg Ala Val  
   50                                    55                                    60  
 Glu Gly Thr Pro Phe Glu Cys Leu Lys Asp Ala Phe Val Gly Pro Thr  
  65                                    70                                    75                                    80  
 Leu Ile Ala Tyr Ser Met Glu His Pro Gly Ala Ala Ala Arg Leu Phe  
                                     85                                    90                                    95  
 Lys Glu Phe Ala Lys Ala Asn Ala Lys Phe Glu Val Lys Ala Ala Ala  
                                     100                                    105                                    110  
 Phe Glu Gly Glu Leu Ile Pro Ala Ser Gln Ile Asp Arg Leu Ala Thr  
                                     115                                    120                                    125  
 Leu Pro Thr Tyr Glu Glu Ala Ile Ala Arg Leu Met Ala Thr Met Lys  
                                     130                                    135                                    140  
 Glu Ala Ser Ala Gly Lys Leu Val Arg Thr Leu Ala Ala Val Arg Asp  
  145                                    150                                    155                                    160  
 Ala Lys Glu Ala Ala  
                                     165

<210> 252  
 <211> 121  
 <212> PRT  
 <213> E. Coli

<400> 252  
 Met Ser Ile Thr Lys Asp Gln Ile Ile Glu Ala Val Ala Ala Met Ser  
   1                                    5                                    10                                    15  
 Val Met Asp Val Val Glu Leu Ile Ser Ala Met Glu Glu Lys Phe Gly  
                                     20                                    25                                    30  
 Val Ser Ala Ala Ala Val Ala Val Ala Ala Gly Pro Val Glu Ala  
                                     35                                    40                                    45  
 Ala Glu Glu Lys Thr Glu Phe Asp Val Ile Leu Lys Ala Ala Gly Ala  
   50                                    55                                    60  
 Asn Lys Val Ala Val Ile Lys Ala Val Arg Gly Ala Thr Gly Leu Gly  
  65                                    70                                    75                                    80  
 Leu Lys Glu Ala Lys Asp Leu Val Glu Ser Ala Pro Ala Ala Leu Lys  
                                     85                                    90                                    95  
 Glu Gly Val Ser Lys Asp Asp Ala Glu Ala Leu Lys Lys Ala Leu Glu  
                                     100                                    105                                    110  
 Glu Ala Gly Ala Glu Val Glu Val Lys  
                                     115                                    120

<210> 253  
 <211> 714  
 <212> PRT  
 <213> E. Coli

<400> 253  
 Met Ser Arg Ile Ile Met Leu Ile Pro Thr Gly Thr Ser Val Gly Leu  
 1 5 10 15  
 Thr Ser Val Ser Leu Gly Val Ile Arg Ala Met Glu Arg Lys Gly Val  
 20 25 30  
 Arg Leu Ser Val Phe Lys Pro Ile Ala Gln Pro Arg Thr Gly Gly Asp  
 35 40 45  
 Ala Pro Asp Gln Thr Thr Thr Ile Val Arg Ala Asn Ser Ser Thr Thr  
 50 55 60  
 Thr Ala Ala Glu Pro Leu Lys Met Ser Tyr Val Glu Gly Leu Leu Ser  
 65 70 75 80  
 Ser Asn Gln Lys Asp Val Leu Met Glu Glu Ile Val Ala Asn Tyr His  
 85 90 95  
 Ala Asn Thr Lys Asp Ala Glu Val Val Leu Val Glu Gly Leu Val Pro  
 100 105 110  
 Thr Arg Lys His Gln Phe Ala Gln Ser Leu Asn Tyr Glu Ile Ala Lys  
 115 120 125  
 Thr Leu Asn Ala Glu Ile Val Phe Val Met Ser Gln Gly Thr Asp Thr  
 130 135 140  
 Pro Glu Gln Leu Lys Glu Arg Ile Glu Leu Thr Arg Asn Ser Phe Gly  
 145 150 155 160  
 Gly Ala Lys Asn Thr Asn Ile Thr Gly Val Ile Val Asn Lys Leu Asn  
 165 170 175  
 Ala Pro Val Asp Glu Gln Gly Arg Thr Arg Pro Asp Leu Ser Glu Ile  
 180 185 190  
 Phe Asp Asp Ser Ser Lys Ala Lys Val Asn Asn Val Asp Pro Ala Lys  
 195 200 205  
 Leu Gln Glu Ser Ser Pro Leu Pro Val Leu Gly Ala Val Pro Trp Ser  
 210 215 220  
 Phe Asp Leu Ile Ala Thr Arg Ala Ile Asp Met Ala Arg His Leu Asn  
 225 230 235 240  
 Ala Thr Ile Ile Asn Glu Gly Asp Ile Asn Thr Arg Arg Val Lys Ser  
 245 250 255  
 Val Thr Phe Cys Ala Arg Ser Ile Pro His Met Leu Glu His Phe Arg  
 260 265 270  
 Ala Gly Ser Leu Leu Val Thr Ser Ala Asp Arg Pro Asp Val Leu Val  
 275 280 285  
 Ala Ala Cys Leu Ala Ala Met Asn Gly Val Glu Ile Gly Ala Leu Leu  
 290 295 300  
 Leu Thr Gly Gly Tyr Glu Met Asp Ala Arg Ile Ser Lys Leu Cys Glu  
 305 310 315 320  
 Arg Ala Phe Ala Thr Gly Leu Pro Val Phe Met Val Asn Thr Asn Thr  
 325 330 335  
 Trp Gln Thr Ser Leu Ser Leu Gln Ser Phe Asn Leu Glu Val Pro Val  
 340 345 350  
 Asp Asp His Glu Arg Ile Glu Lys Val Gln Glu Tyr Val Ala Asn Tyr  
 355 360 365  
 Ile Asn Ala Asp Trp Ile Glu Ser Leu Thr Ala Thr Ser Glu Arg Ser  
 370 375 380  
 Arg Arg Leu Ser Pro Pro Ala Phe Arg Tyr Gln Leu Thr Glu Leu Ala  
 385 390 395 400  
 Arg Lys Ala Gly Lys Arg Ile Val Leu Pro Glu Gly Asp Glu Pro Arg  
 405 410 415  
 Thr Val Lys Ala Ala Ile Cys Ala Glu Arg Gly Ile Ala Thr Cys  
 420 425 430

Val Leu Leu Gly Asn Pro Ala Glu Ile Asn Arg Val Ala Ala Ser Gln  
 435 440 445  
 Gly Val Glu Leu Gly Ala Gly Ile Glu Ile Val Asp Pro Glu Val Val  
 450 455 460  
 Arg Glu Ser Tyr Val Gly Arg Leu Val Glu Leu Arg Lys Asn Lys Gly  
 465 470 475 480  
 Met Thr Glu Thr Val Ala Arg Glu Gln Leu Glu Asp Asn Val Val Leu  
 485 490 495  
 Gly Thr Leu Met Leu Glu Gln Asp Glu Val Asp Gly Leu Val Ser Gly  
 500 505 510  
 Ala Val His Thr Thr Ala Asn Thr Ile Arg Pro Pro Leu Gln Leu Ile  
 515 520 525  
 Lys Thr Ala Pro Gly Ser Ser Leu Val Ser Ser Val Phe Phe Met Leu  
 530 535 540  
 Leu Pro Glu Gln Val Tyr Val Tyr Gly Asp Cys Ala Ile Asn Pro Asp  
 545 550 555 560  
 Pro Thr Ala Glu Gln Leu Ala Glu Ile Ala Ile Gln Ser Ala Asp Ser  
 565 570 575  
 Ala Ala Ala Phe Gly Ile Glu Pro Arg Val Ala Met Leu Ser Tyr Ser  
 580 585 590  
 Thr Gly Thr Ser Gly Ala Gly Ser Asp Val Glu Lys Val Arg Glu Ala  
 595 600 605  
 Thr Arg Leu Ala Gln Glu Lys Arg Pro Asp Leu Met Ile Asp Gly Pro  
 610 615 620  
 Leu Gln Tyr Asp Ala Ala Val Met Ala Asp Val Ala Lys Ser Lys Ala  
 625 630 635 640  
 Pro Asn Ser Pro Val Ala Gly Arg Ala Thr Val Phe Ile Phe Pro Asp  
 645 650 655  
 Leu Asn Thr Gly Asn Thr Thr Tyr Lys Ala Val Gln Arg Ser Ala Asp  
 660 665 670  
 Leu Ile Ser Ile Gly Pro Met Leu Gln Gly Met Arg Lys Pro Val Asn  
 675 680 685  
 Asp Leu Ser Arg Gly Ala Leu Val Asp Asp Ile Val Tyr Thr Ile Ala  
 690 695 700  
 Leu Thr Ala Ile Gln Ser Ala Gln Gln Gln  
 705 710

<210> 254  
 <211> 588  
 <212> PRT  
 <213> E. Coli

<400> 254  
 Met Asn Asn Ser Ile Asn His Lys Phe His His Ile Ser Arg Ala Glu  
 1 5 10 15  
 Tyr Gln Glu Leu Leu Ala Val Ser Arg Gly Asp Ala Val Ala Asp Tyr  
 20 25 30  
 Ile Ile Asp Asn Val Ser Ile Leu Asp Leu Ile Asn Gly Gly Glu Ile  
 35 40 45  
 Ser Gly Pro Ile Val Ile Lys Gly Arg Tyr Ile Ala Gly Val Gly Ala  
 50 55 60  
 Glu Tyr Thr Asp Ala Pro Ala Leu Gln Arg Ile Asp Ala Arg Gly Ala  
 65 70 75 80  
 Thr Ala Val Pro Gly Phe Ile Asp Ala His Leu His Ile Glu Ser Ser  
 85 90 95  
 Met Met Thr Pro Val Thr Phe Glu Thr Ala Thr Leu Pro Arg Gly Leu  
 100 105 110  
 Thr Thr Val Ile Cys Asp Pro His Glu Ile Val Asn Val Met Gly Glu  
 115 120 125  
 Ala Gly Phe Ala Trp Phe Ala Arg Cys Ala Glu Gln Ala Arg Gln Asn

|   |     |     |
|---|-----|-----|
| 130   | 135 | 140 |
| Gln Tyr Leu Gln Val Ser Ser Cys Val Pro Ala Leu Glu Gly Cys Asp |     |     |
| 145   | 150 | 155 |
| Val Asn Gly Ala Ser Phe Thr Leu Glu Gln Met Leu Ala Trp Arg Asp |     | 160 |
|   | 165 | 170 |
| His Pro Gln Val Thr Gly Leu Ala Glu Met Met Asp Tyr Pro Gly Val |     | 175 |
|   | 180 | 185 |
| Ile Ser Gly Gln Asn Ala Leu Leu Asp Lys Leu Asp Ala Phe Arg His |     | 190 |
|   | 195 | 200 |
| Leu Thr Leu Asp Gly His Cys Pro Gly Leu Gly Gly Lys Glu Leu Asn |     | 205 |
|   | 210 | 215 |
| Ala Tyr Ile Thr Ala Gly Ile Glu Asn Cys His Glu Ser Tyr Gln Leu |     | 220 |
|   | 225 | 230 |
| Glu Glu Gly Arg Arg Lys Leu Gln Leu Gly Met Ser Leu Met Ile Arg |     | 235 |
|   | 245 | 250 |
| Glu Gly Ser Ala Ala Arg Asn Leu Asn Ala Leu Ala Pro Leu Ile Asn |     | 255 |
|   | 260 | 265 |
| Glu Phe Asn Ser Pro Gln Cys Met Leu Cys Thr Asp Asp Arg Asn Pro |     | 270 |
|   | 275 | 280 |
| Trp Glu Ile Ala His Glu Gly His Ile Asp Ala Leu Ile Arg Arg Leu |     | 285 |
|   | 290 | 295 |
| Ile Glu Gln His Asn Val Pro Leu His Val Ala Tyr Arg Val Ala Ser |     | 300 |
|   | 305 | 310 |
| Trp Ser Thr Ala Arg His Phe Gly Leu Asn His Leu Gly Leu Leu Ala |     | 315 |
|   | 325 | 330 |
| Pro Gly Lys Gln Ala Asp Ile Val Leu Leu Ser Asp Ala Arg Lys Val |     | 335 |
|   | 340 | 345 |
| Thr Val Gln Gln Val Leu Val Lys Gly Glu Pro Ile Asp Ala Gln Thr |     | 350 |
|   | 355 | 360 |
| Leu Gln Ala Glu Glu Ser Ala Arg Leu Ala Gln Ser Ala Pro Pro Tyr |     | 365 |
|   | 370 | 375 |
| Gly Asn Thr Ile Ala Arg Gln Pro Val Ser Ala Ser Asp Phe Ala Leu |     | 380 |
|   | 385 | 390 |
| Gln Phe Thr Pro Gly Lys Arg Tyr Arg Val Ile Asp Val Ile His Asn |     | 395 |
|   | 405 | 410 |
| Glu Leu Ile Thr His Ser His Ser Ser Val Tyr Ser Glu Asn Gly Phe |     | 415 |
|   | 420 | 425 |
| Asp Arg Asp Asp Val Ser Phe Ile Ala Val Leu Glu Arg Tyr Gly Gln |     | 430 |
|   | 435 | 440 |
| Arg Leu Ala Pro Ala Cys Gly Leu Leu Gly Gly Phe Gly Leu Asn Glu |     | 445 |
|   | 450 | 455 |
| Gly Ala Leu Ala Ala Thr Val Ser His Asp Ser His Asn Ile Val Val |     | 460 |
|   | 465 | 470 |
| Ile Gly Arg Ser Ala Glu Glu Met Ala Leu Ala Val Asn Gln Val Ile |     | 475 |
|   | 485 | 490 |
| Gln Asp Gly Gly Leu Cys Val Val Arg Asn Gly Gln Val Gln Ser     |     | 495 |
|   | 500 | 505 |
| His Leu Pro Leu Pro Ile Ala Gly Leu Met Ser Thr Asp Thr Ala Gln |     | 510 |
|   | 515 | 520 |
| Ser Leu Ala Glu Gln Ile Asp Ala Leu Lys Ala Ala Ala Arg Glu Cys |     | 525 |
|   | 530 | 535 |
| Gly Pro Leu Pro Asp Glu Pro Phe Ile Gln Met Ala Phe Leu Ser Leu |     | 540 |
|   | 545 | 550 |
| Pro Val Ile Pro Ala Leu Lys Leu Thr Ser Gln Gly Leu Phe Asp Gly |     | 555 |
|   | 565 | 570 |
| Glu Lys Phe Ala Phe Thr Thr Leu Glu Val Thr Glu                 |     | 575 |
|   | 580 | 585 |

&lt;210&gt; 255

&lt;211&gt; 408

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 255

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Met Ala Tyr Cys Asn Pro Gly Leu Glu Ser Arg Pro Asn Lys Arg Asn
1      5      10      15
Ala Leu Arg Arg His Val Val Thr Gly Ile Gly Met Lys Ile Val Ile
20      25      30
Ala Pro Asp Ser Tyr Lys Glu Ser Leu Ser Ala Ser Glu Val Ala Gln
35      40      45
Ala Ile Glu Lys Gly Phe Arg Arg Ile Phe Pro Asp Ala Gln Tyr Val
50      55      60
Ser Val Pro Val Ala Asp Gly Gly Glu Gly Thr Val Glu Ala Met Ile
65      70      75      80
Ala Ala Thr Gln Gly Ala Glu Arg His Ala Trp Val Thr Gly Pro Leu
85      90      95
Gly Glu Lys Val Asn Ala Ser Trp Gly Ile Ser Gly Asp Gly Lys Thr
100     105     110
Ala Phe Ile Glu Met Ala Ala Ala Ser Gly Leu Glu Leu Val Pro Ala
115     120     125
Glu Lys Arg Asp Pro Leu Val Thr Thr Ser Arg Gly Thr Gly Glu Leu
130     135     140
Ile Leu Gln Ala Leu Glu Ser Gly Ala Thr Asn Ile Ile Ile Gly Ile
145     150     155     160
Gly Gly Ser Ala Thr Asn Asp Gly Gly Ala Gly Met Val Gln Ala Leu
165     170     175
Gly Ala Lys Leu Cys Asp Ala Asn Gly Asn Glu Ile Gly Phe Gly Gly
180     185     190
Gly Ser Leu Asn Thr Leu Asn Asp Ile Asp Ile Ser Gly Leu Asp Pro
195     200     205
Arg Leu Lys Asp Cys Val Ile Arg Val Ala Cys Asp Val Thr Asn Pro
210     215     220
Leu Val Gly Asp Asn Gly Ala Ser Arg Ile Phe Gly Pro Gln Lys Gly
225     230     235     240
Ala Ser Glu Ala Met Ile Val Glu Leu Asp Asn Asn Leu Ser His Tyr
245     250     255
Ala Glu Val Ile Lys Lys Ala Leu His Val Asp Val Lys Asp Val Pro
260     265     270
Gly Ala Gly Ala Ala Gly Gly Met Gly Ala Ala Leu Met Ala Phe Leu
275     280     285
Gly Ala Glu Leu Lys Ser Gly Ile Glu Ile Val Thr Thr Ala Leu Asn
290     295     300
Leu Glu Glu His Ile His Asp Cys Thr Leu Val Ile Thr Gly Glu Gly
305     310     315     320
Arg Ile Asp Ser Gln Ser Ile His Gly Lys Val Pro Ile Gly Val Ala
325     330     335
Asn Val Ala Lys Lys Tyr His Lys Pro Val Ile Gly Ile Ala Gly Ser
340     345     350
Leu Thr Asp Asp Val Gly Val Val His Gln His Gly Ile Asp Ala Val
355     360     365
Phe Ser Val Leu Thr Ser Ile Gly Thr Leu Asp Glu Ala Phe Arg Gly
370     375     380
Ala Tyr Asp Asn Ile Cys Arg Ala Ser Arg Asn Ile Ala Ala Thr Leu
385     390     395     400
Ala Ile Gly Met Arg Asn Ala Gly
405

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&lt;210&gt; 256

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 256

```

Met Ile Asp Met Thr Met Lys Val Gly Phe Ile Gly Leu Gly Ile Met
 1           5           10           15
Gly Lys Pro Met Ser Lys Asn Leu Leu Lys Ala Gly Tyr Ser Leu Val
 20           25           30
Val Ala Asp Arg Asn Pro Glu Ala Ile Ala Asp Val Ile Ala Ala Gly
 35           40           45
Ala Glu Thr Ala Ser Thr Ala Lys Ala Ile Ala Glu Gln Cys Asp Val
 50           55           60
Ile Ile Thr Met Leu Pro Asn Ser Pro His Val Lys Glu Val Ala Leu
 65           70           75           80
Gly Glu Asn Gly Ile Ile Glu Gly Ala Lys Pro Gly Thr Val Leu Ile
 85           90           95
Asp Met Ser Ser Ile Ala Pro Leu Ala Ser Arg Glu Ile Ser Glu Ala
100          105          110
Leu Lys Ala Lys Gly Ile Asp Met Leu Asp Ala Pro Val Ser Gly Gly
115          120          125
Glu Pro Lys Ala Ile Asp Gly Thr Leu Ser Val Met Val Gly Gly Asp
130          135          140
Lys Ala Ile Phe Asp Lys Tyr Tyr Asp Leu Met Lys Ala Met Ala Gly
145          150          155          160
Ser Val Val His Thr Gly Glu Ile Gly Ala Gly Asn Val Thr Lys Leu
165          170          175
Ala Asn Gln Val Ile Val Ala Leu Asn Ile Ala Ala Met Ser Glu Ala
180          185          190
Leu Thr Leu Ala Thr Lys Ala Gly Val Asn Pro Asp Leu Val Tyr Gln
195          200          205
Ala Ile Arg Gly Gly Leu Ala Gly Ser Thr Val Leu Asp Ala Lys Ala
210          215          220
Pro Met Val Met Asp Arg Asn Phe Lys Pro Gly Phe Arg Ile Asp Leu
225          230          235          240
His Ile Lys Asp Leu Ala Asn Ala Leu Asp Thr Ser His Gly Val Gly
245          250          255
Ala Gln Leu Pro Leu Thr Ala Ala Val Met Glu Met Met Gln Ala Leu
260          265          270
Arg Ala Asp Gly Leu Gly Thr Ala Asp His Ser Ala Leu Ala Cys Tyr
275          280          285
Tyr Glu Lys Leu Ala Lys Val Glu Val Thr Arg
290          295

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&lt;210&gt; 257

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 257

```

Met Asn Asn Asp Val Phe Pro Asn Lys Phe Lys Ala Ala Leu Ala Ala
 1           5           10           15
Lys Gln Val Gln Ile Gly Cys Trp Ser Ala Leu Ser Asn Pro Ile Ser
 20           25           30
Thr Glu Val Leu Gly Leu Ala Gly Phe Asp Trp Leu Val Leu Asp Gly
 35           40           45
Glu His Ala Pro Asn Asp Ile Ser Thr Phe Ile Pro Gln Leu Met Ala
 50           55           60
Leu Lys Gly Ser Ala Ser Ala Pro Val Val Arg Val Pro Thr Asn Glu
 65           70           75           80
Pro Val Ile Ile Lys Arg Leu Leu Asp Ile Gly Phe Tyr Asn Phe Leu

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      85          90          95
Ile Pro Phe Val Glu Thr Lys Glu Glu Ala Glu Leu Ala Val Ala Ser
      100          105          110
Thr Arg Tyr Pro Pro Glu Gly Ile Arg Gly Val Ser Val Ser His Arg
      115          120          125
Ala Asn Met Phe Gly Thr Val Ala Asp Tyr Phe Ala Gln Ser Asn Lys
      130          135          140
Asn Ile Thr Ile Leu Val Gln Ile Glu Ser Gln Gln Gly Val Asp Asn
      145          150          155
Val Asp Ala Ile Ala Ala Thr Glu Gly Val Asp Gly Ile Phe Val Gly
      165          170          175
Pro Ser Asp Leu Ala Ala Ala Leu Gly His Leu Gly Asn Ala Ser His
      180          185          190
Pro Asp Val Gln Lys Ala Ile Gln His Ile Phe Asn Arg Ala Ser Ala
      195          200          205
His Gly Lys Pro Ser Gly Ile Leu Ala Pro Val Glu Ala Asp Ala Arg
      210          215          220
Arg Tyr Leu Glu Trp Gly Ala Thr Phe Val Ala Val Gly Ser Asp Leu
      225          230          235
Gly Val Phe Arg Ser Ala Thr Gln Lys Leu Ala Asp Thr Phe Lys Lys
      245          250          255

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<210> 258  
 <211> 444  
 <212> PRT  
 <213> E. Coli

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      <400> 258
Met Ile Leu Asp Thr Val Asp Glu Lys Lys Lys Gly Val His Thr Arg
      5          10          15
Tyr Leu Ile Leu Leu Ile Ile Phe Ile Val Thr Ala Val Asn Tyr Ala
      20          25          30
Asp Arg Ala Thr Leu Ser Ile Ala Gly Thr Glu Val Ala Lys Glu Leu
      35          40          45
Gln Leu Ser Ala Val Ser Met Gly Tyr Ile Phe Ser Ala Phe Gly Trp
      50          55          60
Ala Tyr Leu Leu Met Gln Ile Pro Gly Gly Trp Leu Leu Asp Lys Phe
      65          70          75
Gly Ser Lys Lys Val Tyr Thr Tyr Ser Leu Phe Phe Trp Ser Leu Phe
      85          90          95
Thr Phe Leu Gln Gly Phe Val Asp Met Phe Pro Leu Ala Trp Ala Gly
      100          105          110
Ile Ser Met Phe Phe Met Arg Phe Met Leu Gly Phe Ser Glu Ala Pro
      115          120          125
Ser Phe Pro Ala Asn Ala Arg Ile Val Ala Ala Trp Phe Pro Thr Lys
      130          135          140
Glu Arg Gly Thr Ala Ser Ala Ile Phe Asn Ser Ala Gln Tyr Phe Ser
      145          150          155
Leu Ala Leu Phe Ser Pro Leu Leu Gly Trp Leu Thr Phe Ala Trp Gly
      165          170          175
Trp Glu His Val Phe Thr Val Met Gly Val Ile Gly Phe Val Leu Thr
      180          185          190
Ala Leu Trp Ile Lys Leu Ile His Asn Pro Thr Asp His Pro Arg Met
      195          200          205
Ser Ala Glu Glu Leu Lys Phe Ile Ser Glu Asn Gly Ala Val Val Asp
      210          215          220
Met Asp His Lys Lys Pro Gly Ser Ala Ala Ala Ser Gly Pro Lys Leu
      225          230          235
His Tyr Ile Lys Gln Leu Leu Ser Asn Arg Met Met Leu Gly Val Phe
      245          250          255

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Phe Gly Gln Tyr Phe Ile Asn Thr Ile Thr Trp Phe Phe Leu Thr Trp  
 260 265 270  
 Phe Pro Ile Tyr Leu Val Gln Glu Lys Gly Met Ser Ile Leu Lys Val  
 275 280 285  
 Gly Leu Val Ala Ser Ile Pro Ala Leu Cys Gly Phe Ala Gly Gly Val  
 290 295 300  
 Leu Gly Gly Val Phe Ser Asp Tyr Leu Ile Lys Arg Gly Leu Ser Leu  
 305 310 315 320  
 Thr Leu Ala Arg Lys Leu Pro Ile Val Leu Gly Met Leu Leu Ala Ser  
 325 330 335  
 Thr Ile Ile Leu Cys Asn Tyr Thr Asn Asn Thr Thr Leu Val Val Met  
 340 345 350  
 Leu Met Ala Leu Ala Phe Phe Gly Lys Gly Phe Gly Ala Leu Gly Trp  
 355 360 365  
 Pro Val Ile Ser Asp Thr Ala Pro Lys Glu Ile Val Gly Leu Cys Gly  
 370 375 380  
 Gly Val Phe Asn Val Phe Gly Asn Val Ala Ser Ile Val Thr Pro Leu  
 385 390 395 400  
 Val Ile Gly Tyr Leu Val Ser Glu Leu His Ser Phe Asn Ala Ala Leu  
 405 410 415  
 Val Phe Val Gly Cys Ser Ala Leu Met Ala Met Val Cys Tyr Leu Phe  
 420 425 430  
 Val Val Gly Asp Ile Lys Arg Met Glu Leu Gln Lys  
 435 440

<210> 259  
 <211> 511  
 <212> PRT  
 <213> E. Coli

<400> 259  
 Met Gln Thr Ser Asp Thr Arg Ala Leu Pro Leu Leu Cys Ala Arg Ser  
 1 5 10 15  
 Val Tyr Lys Gln Tyr Ser Gly Val Asn Val Leu Lys Gly Ile Asp Phe  
 20 25 30  
 Thr Leu His Gln Gly Glu Val His Ala Leu Leu Gly Gly Asn Gly Ala  
 35 40 45  
 Gly Lys Ser Thr Leu Met Lys Ile Ile Ala Gly Ile Thr Pro Ala Asp  
 50 55 60  
 Ser Gly Thr Leu Glu Ile Glu Gly Asn Asn Tyr Val Arg Leu Thr Pro  
 65 70 75 80  
 Val His Ala His Gln Leu Gly Ile Tyr Leu Val Pro Gln Glu Pro Leu  
 85 90 95  
 Leu Phe Pro Ser Leu Ser Ile Lys Glu Asn Ile Leu Phe Gly Leu Ala  
 100 105 110  
 Lys Lys Gln Leu Ser Met Gln Lys Met Lys Asn Leu Leu Ala Ala Leu  
 115 120 125  
 Gly Cys Gln Phe Asp Leu His Ser Leu Ala Gly Ser Leu Asp Val Ala  
 130 135 140  
 Asp Arg Gln Met Val Glu Ile Leu Arg Gly Leu Met Arg Asp Ser Arg  
 145 150 155 160  
 Ile Leu Ile Leu Asp Glu Pro Thr Ala Ser Leu Thr Pro Ala Glu Thr  
 165 170 175  
 Glu Arg Leu Phe Ser Arg Leu Gln Glu Leu Leu Ala Thr Gly Val Gly  
 180 185 190  
 Ile Val Phe Ile Ser His Lys Leu Pro Glu Ile Arg Gln Ile Ala Asp  
 195 200 205  
 Arg Ile Ser Val Met Arg Asp Gly Thr Ile Ala Leu Ser Gly Lys Thr  
 210 215 220  
 Ser Glu Leu Ser Thr Asp Asp Ile Ile Gln Ala Ile Thr Pro Ala Val

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225          230          235          240
Arg Glu Lys Ser Leu Ser Ala Ser Gln Lys Leu Trp Leu Glu Leu Pro
          245          250          255
Gly Asn Arg Pro Gln His Ala Ala Gly Thr Pro Val Leu Thr Leu Glu
          260          265          270
Asn Leu Thr Gly Glu Gly Phe Arg Asn Val Ser Leu Thr Leu Asn Ala
          275          280          285
Gly Glu Ile Leu Gly Leu Ala Gly Leu Val Gly Ala Gly Arg Thr Glu
          290          295          300
Leu Ala Glu Thr Leu Tyr Gly Leu Arg Thr Leu Arg Gly Gly Arg Ile
305          310          315
Met Leu Asn Gly Lys Glu Ile Asn Lys Leu Ser Thr Gly Glu Arg Leu
          325          330          335
Leu Arg Gly Leu Val Tyr Leu Pro Glu Asp Arg Gln Ser Ser Gly Leu
          340          345          350
Asn Leu Asp Ala Ser Leu Ala Trp Asn Val Cys Ala Leu Thr His Asn
          355          360          365
Leu Arg Gly Phe Trp Ala Lys Thr Ala Lys Asp Asn Ala Thr Leu Glu
          370          375          380
Arg Tyr Arg Arg Ala Leu Asn Ile Lys Phe Asn Gln Pro Glu Gln Ala
385          390          395
Ala Arg Thr Leu Ser Gly Gly Asn Gln Gln Lys Ile Leu Ile Ala Lys
          405          410          415
Cys Leu Glu Ala Ser Pro Gln Val Leu Ile Val Asp Glu Pro Thr Arg
          420          425          430
Gly Val Asp Val Ser Ala Arg Asn Asp Ile Tyr Gln Leu Leu Arg Ser
          435          440          445
Ile Ala Ala Gln Asn Val Ala Val Leu Leu Ile Ser Ser Asp Leu Glu
          450          455          460
Glu Ile Glu Leu Met Ala Asp Arg Val Tyr Val Met His Gln Gly Glu
465          470          475
Ile Thr His Ser Ala Leu Thr Glu Arg Asp Ile Asn Val Glu Thr Ile
          485          490          495
Met Arg Val Ala Phe Gly Asp Ser Gln Arg Gln Glu Ala Ser Cys
          500          505          510

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<210> 260  
<211> 342  
<212> PRT  
<213> E. Coli

```

<400> 260
Met Leu Lys Phe Ile Gln Asn Asn Arg Glu Ile Thr Ala Leu Leu Ala
1          5          10          15
Val Val Leu Leu Phe Val Leu Pro Gly Phe Leu Asp Arg Gln Tyr Leu
          20          25          30
Ser Val Gln Thr Leu Thr Met Val Tyr Ser Ser Ala Gln Ile Leu Ile
          35          40          45
Leu Leu Ala Met Gly Ala Thr Leu Val Met Leu Thr Arg Asn Ile Asp
          50          55          60
Val Ser Val Gly Ser Ile Thr Gly Met Cys Ala Val Leu Leu Gly Met
65          70          75          80
Leu Leu Asn Ala Gly Tyr Ser Leu Pro Val Ala Cys Val Ala Thr Leu
          85          90          95
Leu Leu Gly Leu Leu Ala Gly Phe Phe Asn Gly Val Leu Val Ala Trp
          100          105          110
Leu Lys Ile Pro Ala Ile Val Ala Thr Leu Gly Thr Leu Gly Leu Tyr
          115          120          125
Arg Gly Ile Met Leu Leu Trp Thr Gly Gly Lys Trp Ile Glu Gly Leu
130          135          140

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Pro Ala Glu Leu Lys Gln Leu Ser Ala Pro Leu Leu Leu Gly Val Ser  
 145 150 155 160  
 Ala Ile Gly Trp Leu Thr Ile Ile Leu Val Ala Phe Met Ala Trp Leu  
 165 170 175  
 Leu Ala Lys Thr Ala Phe Gly Arg Ser Phe Tyr Ala Thr Gly Asp Asn  
 180 185 190  
 Leu Gln Gly Ala Arg Gln Leu Gly Val Arg Thr Glu Ala Ile Arg Ile  
 195 200 205  
 Val Ala Phe Ser Leu Asn Gly Cys Met Ala Ala Leu Ala Gly Ile Val  
 210 215 220  
 Phe Ala Ser Gln Ile Gly Phe Ile Pro Asn Gln Thr Gly Thr Gly Leu  
 225 230 235 240  
 Glu Met Lys Ala Ile Ala Ala Cys Val Leu Gly Gly Ile Ser Leu Leu  
 245 250 255  
 Gly Gly Ser Gly Ala Ile Ile Gly Ala Val Leu Gly Ala Trp Phe Leu  
 260 265 270  
 Thr Gln Ile Asp Ser Val Leu Val Leu Arg Ile Pro Ala Trp Trp  
 275 280 285  
 Asn Asp Phe Ile Ala Gly Leu Val Leu Leu Ala Val Leu Val Phe Asp  
 290 295 300  
 Gly Arg Leu Arg Cys Ala Leu Glu Arg Asn Leu Arg Arg Gln Lys Tyr  
 305 310 315 320  
 Ala Arg Phe Met Thr Pro Pro Pro Ser Val Lys Pro Ala Ser Ser Gly  
 325 330 335  
 Lys Lys Arg Glu Ala Ala  
 340

<210> 261  
 <211> 330  
 <212> PRT  
 <213> E. Coli

<400> 261  
 Met Arg Ile Arg Tyr Gly Trp Glu Leu Ala Leu Ala Ala Leu Leu Val  
 1 5 10 15  
 Ile Glu Ile Val Ala Phe Gly Ala Ile Asn Pro Arg Met Leu Asp Leu  
 20 25 30  
 Asn Met Leu Leu Phe Ser Thr Ser Asp Phe Ile Cys Ile Gly Ile Val  
 35 40 45  
 Ala Leu Pro Leu Thr Met Val Ile Val Ser Gly Gly Ile Asp Ile Ser  
 50 55 60  
 Phe Gly Ser Thr Ile Gly Leu Cys Ala Ile Ala Leu Gly Val Leu Phe  
 65 70 75 80  
 Gln Ser Gly Val Pro Met Pro Leu Ala Ile Leu Leu Thr Leu Leu Leu  
 85 90 95  
 Gly Ala Leu Cys Gly Leu Ile Asn Ala Gly Leu Ile Ile Tyr Thr Lys  
 100 105 110  
 Val Asn Pro Leu Val Ile Thr Leu Gly Thr Leu Tyr Leu Phe Ala Gly  
 115 120 125  
 Ser Ala Leu Leu Ser Gly Met Ala Gly Ala Thr Gly Tyr Glu Gly  
 130 135 140  
 Ile Gly Gly Phe Pro Met Ala Phe Thr Asp Phe Ala Asn Leu Asp Val  
 145 150 155 160  
 Leu Gly Leu Pro Val Pro Leu Ile Ile Phe Leu Ile Cys Leu Leu Val  
 165 170 175  
 Phe Trp Leu Trp Leu His Lys Thr His Ala Gly Arg Asn Val Phe Leu  
 180 185 190  
 Ile Gly Gln Ser Pro Arg Val Ala Leu Tyr Ser Ala Ile Pro Val Asn  
 195 200 205  
 Arg Thr Leu Cys Ala Leu Tyr Ala Met Thr Gly Leu Ala Ser Ala Val  
 210 215 220

Ala Ala Val Leu Leu Val Ser Tyr Phe Gly Ser Ala Arg Ser Asp Leu  
 225 230 235 240  
 Gly Ala Ser Phe Leu Met Pro Ala Ile Thr Ala Val Val Leu Gly Gly  
 245 250 255  
 Ala Asn Ile Tyr Gly Gly Ser Gly Ser Ile Ile Gly Thr Ala Ile Ala  
 260 265 270  
 Val Leu Leu Val Gly Tyr Leu Gln Gln Gly Leu Gln Met Ala Gly Val  
 275 280 285  
 Pro Asn Gln Val Ser Ser Ala Leu Ser Gly Ala Leu Leu Ile Val Val  
 290 295 300  
 Val Val Gly Arg Ser Val Ser Leu His Arg Gln Gln Ile Lys Glu Trp  
 305 310 315 320  
 Leu Ala Arg Arg Ala Asn Asn Pro Leu Pro  
 325 330

<210> 262  
 <211> 340  
 <212> PRT  
 <213> E. Coli

<400> 262  
 Met Thr Leu His Arg Phe Lys Lys Ile Ala Leu Leu Ser Ala Leu Gly  
 1 5 10 15  
 Ile Ala Ala Ile Ser Met Asn Val Gln Ala Ala Glu Arg Ile Ala Phe  
 20 25 30  
 Ile Pro Lys Leu Val Gly Val Gly Phe Phe Thr Ser Gly Gly Asn Gly  
 35 40 45  
 Ala Gln Gln Ala Gly Lys Glu Leu Gly Val Asp Val Thr Tyr Asp Gly  
 50 55 60  
 Pro Thr Glu Pro Ser Val Ser Gly Gln Val Gln Leu Ile Asn Asn Phe  
 65 70 75 80  
 Val Asn Gln Gly Tyr Asn Ala Ile Ile Val Ser Ala Val Ser Pro Asp  
 85 90 95  
 Gly Leu Cys Pro Ala Leu Lys Arg Ala Met Gln Arg Gly Val Arg Val  
 100 105 110  
 Leu Thr Trp Asp Ser Asp Thr Lys Pro Glu Cys Arg Ser Tyr Tyr Ile  
 115 120 125  
 Asn Gln Gly Thr Pro Ala Gln Leu Gly Gly Met Leu Val Asp Met Ala  
 130 135 140  
 Ala Arg Gln Val Asn Lys Asp Lys Ala Lys Val Ala Phe Phe Tyr Ser  
 145 150 155 160  
 Ser Pro Thr Val Thr Asp Gln Asn Gln Trp Val Lys Glu Ala Lys Ala  
 165 170 175  
 Lys Ile Ala Lys Glu His Pro Gly Trp Glu Ile Val Thr Thr Gln Phe  
 180 185 190  
 Gly Tyr Asn Asp Ala Thr Lys Ser Leu Gln Thr Ala Glu Gly Ile Leu  
 195 200 205  
 Lys Ala Tyr Ser Asp Leu Asp Ala Ile Ile Ala Pro Asp Ala Asn Ala  
 210 215 220  
 Leu Pro Ala Ala Ala Gln Ala Ala Glu Asn Leu Lys Asn Asp Lys Val  
 225 230 235 240  
 Ala Ile Val Gly Phe Ser Thr Pro Asn Val Met Arg Pro Tyr Val Glu  
 245 250 255  
 Arg Gly Thr Val Lys Glu Phe Gly Leu Trp Asp Val Val Gln Gln Gly  
 260 265 270  
 Lys Ile Ser Val Tyr Val Ala Asp Ala Leu Leu Lys Lys Gly Ser Met  
 275 280 285  
 Lys Thr Gly Asp Lys Leu Asp Ile Lys Gly Val Gly Gln Val Glu Val

290                      295                      300  
 Ser Pro Asn Ser Val Gln Gly Tyr Asp Tyr Glu Ala Asp Gly Asn Gly  
 305                      310                      315                      320  
 Ile Val Leu Leu Pro Glu Arg Val Ile Phe Asn Lys Glu Asn Ile Gly  
                     325                      330                      335  
 Lys Tyr Asp Phe  
                     340

<210> 263  
 <211> 291  
 <212> PRT  
 <213> E. Coli

<400> 263  
 Met Ala Asp Leu Asp Asp Ile Lys Asp Gly Lys Asp Phe Arg Thr Asp  
 1                      5                      10                      15  
 Gln Pro Gln Lys Asn Ile Pro Phe Thr Leu Lys Gly Cys Gly Ala Leu  
                     20                      25                      30  
 Asp Trp Gly Met Gln Ser Arg Leu Ser Arg Ile Phe Asn Pro Lys Thr  
                     35                      40                      45  
 Gly Lys Thr Val Met Leu Ala Phe Asp His Gly Tyr Phe Gln Gly Pro  
                     50                      55                      60  
 Thr Thr Gly Leu Glu Arg Ile Asp Ile Asn Ile Ala Pro Leu Phe Glu  
 65                      70                      75                      80  
 His Ala Asp Val Leu Met Cys Thr Arg Gly Ile Leu Arg Ser Val Val  
                     85                      90                      95  
 Pro Pro Ala Thr Asn Arg Pro Val Val Leu Arg Ala Ser Gly Ala Asn  
                     100                      105                      110  
 Ser Ile Leu Ala Glu Leu Ser Asn Glu Ala Val Ala Leu Ser Met Asp  
                     115                      120                      125  
 Asp Ala Val Arg Leu Asn Ser Cys Ala Val Ala Ala Gln Val Tyr Ile  
                     130                      135                      140  
 Gly Ser Glu Tyr Glu His Gln Ser Ile Lys Asn Ile Ile Gln Leu Val  
 145                      150                      155                      160  
 Asp Ala Gly Met Lys Val Gly Met Pro Thr Met Ala Val Thr Gly Val  
                     165                      170                      175  
 Gly Lys Asp Met Val Arg Asp Gln Arg Tyr Phe Ser Leu Ala Thr Arg  
                     180                      185                      190  
 Ile Ala Ala Glu Met Gly Ala Gln Ile Ile Lys Thr Tyr Tyr Val Glu  
                     195                      200                      205  
 Lys Gly Phe Glu Arg Ile Val Ala Gly Cys Pro Val Pro Ile Val Ile  
                     210                      215                      220  
 Ala Gly Gly Lys Lys Leu Pro Glu Arg Glu Ala Leu Glu Met Cys Trp  
 225                      230                      235                      240  
 Gln Ala Ile Asp Gln Gly Ala Ser Gly Val Asp Met Gly Arg Asn Ile  
                     245                      250                      255  
 Phe Gln Ser Asp His Pro Val Ala Met Met Lys Ala Val Gln Ala Val  
                     260                      265                      270  
 Val His His Asn Glu Thr Ala Asp Arg Ala Tyr Glu Leu Tyr Leu Ser  
                     275                      280                      285  
 Glu Lys Gln  
 290

<210> 264  
 <211> 96  
 <212> PRT  
 <213> E. Coli

<400> 264

Met His Val Thr Leu Val Glu Ile Asn Val His Glu Asp Lys Val Asp  
 1 5 10 15  
 Glu Phe Ile Glu Val Phe Arg Gln Asn His Leu Gly Ser Val Gln Glu  
 20 25 30  
 Glu Gly Asn Leu Arg Phe Asp Val Leu Gln Asp Pro Glu Val Asn Ser  
 35 40 45  
 Arg Phe Tyr Ile Tyr Glu Ala Tyr Lys Asp Glu Asp Ala Val Ala Phe  
 50 55 60  
 His Lys Thr Thr Pro His Tyr Lys Thr Cys Val Ala Lys Leu Glu Ser  
 65 70 75 80  
 Leu Met Thr Gly Pro Arg Lys Lys Arg Leu Phe Asn Gly Leu Met Pro  
 85 90 95

&lt;210&gt; 265

&lt;211&gt; 383

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 265

Met Phe Glu Pro Met Glu Leu Thr Asn Asp Ala Val Ile Lys Val Ile  
 1 5 10 15  
 Gly Val Gly Gly Gly Gly Asn Ala Val Glu His Met Val Arg Glu  
 20 25 30  
 Arg Ile Glu Gly Val Glu Phe Phe Ala Val Asn Thr Asp Ala Gln Ala  
 35 40 45  
 Leu Arg Lys Thr Ala Val Gly Gln Thr Ile Gln Ile Gly Ser Gly Ile  
 50 55 60  
 Thr Lys Gly Leu Gly Ala Gly Ala Asn Pro Glu Val Gly Arg Asn Ala  
 65 70 75 80  
 Ala Asp Glu Asp Arg Asp Ala Leu Arg Ala Ala Leu Glu Gly Ala Asp  
 85 90 95  
 Met Val Phe Ile Ala Ala Gly Met Gly Gly Thr Gly Thr Gly Ala  
 100 105 110  
 Ala Pro Val Val Ala Glu Val Ala Lys Asp Leu Gly Ile Leu Thr Val  
 115 120 125  
 Ala Val Val Thr Lys Pro Phe Asn Phe Glu Gly Lys Lys Arg Met Ala  
 130 135 140  
 Phe Ala Glu Gln Gly Ile Thr Glu Leu Ser Lys His Val Asp Ser Leu  
 145 150 155 160  
 Ile Thr Ile Pro Asn Asp Lys Leu Leu Lys Val Leu Gly Arg Gly Ile  
 165 170 175  
 Ser Leu Leu Asp Ala Phe Gly Ala Ala Asn Asp Val Leu Lys Gly Ala  
 180 185 190  
 Val Gln Gly Ile Ala Glu Leu Ile Thr Arg Pro Gly Leu Met Asn Val  
 195 200 205  
 Asp Phe Ala Asp Val Arg Thr Val Met Ser Glu Met Gly Tyr Ala Met  
 210 215 220  
 Met Gly Ser Gly Val Ala Ser Gly Glu Asp Arg Ala Glu Glu Ala Ala  
 225 230 235 240  
 Glu Met Ala Ile Ser Ser Pro Leu Leu Glu Asp Ile Asp Leu Ser Gly  
 245 250 255  
 Ala Arg Gly Val Leu Val Asn Ile Thr Ala Gly Phe Asp Leu Arg Leu  
 260 265 270  
 Asp Glu Phe Glu Thr Val Gly Asn Thr Ile Arg Ala Phe Ala Ser Asp  
 275 280 285  
 Asn Ala Thr Val Val Ile Gly Thr Ser Leu Asp Pro Asp Met Asn Asp  
 290 295 300  
 Glu Leu Arg Val Thr Val Ala Thr Gly Ile Gly Met Asp Lys Arg  
 305 310 315 320  
 Pro Glu Ile Thr Leu Val Thr Asn Lys Gln Val Gln Gln Pro Val Met

325 330 335  
 Asp Arg Tyr Gln Gln His Gly Met Ala Pro Leu Thr Gln Glu Gln Lys  
 340 345 350  
 Pro Val Ala Lys Val Val Asn Asp Asn Ala Pro Gln Thr Ala Lys Glu  
 355 360 365  
 Pro Asp Tyr Leu Asp Ile Pro Ala Phe Leu Arg Lys Gln Ala Asp  
 370 375 380

<210> 266  
 <211> 1014  
 <212> PRT  
 <213> E. Coli

<400> 266  
 Met Asp Val Ser Arg Arg Gln Phe Phe Lys Ile Cys Ala Gly Gly Met  
 1 5 10 15  
 Ala Gly Thr Thr Val Ala Ala Leu Gly Phe Ala Pro Lys Gln Ala Leu  
 20 25 30  
 Ala Gln Ala Arg Asn Tyr Lys Leu Leu Arg Ala Lys Glu Ile Arg Asn  
 35 40 45  
 Thr Cys Thr Tyr Cys Ser Val Gly Cys Gly Leu Leu Met Tyr Ser Leu  
 50 55 60  
 Gly Asp Gly Ala Lys Asn Ala Arg Glu Ala Ile Tyr His Ile Glu Gly  
 65 70 75 80  
 Asp Pro Asp His Pro Val Ser Arg Gly Ala Leu Cys Pro Lys Gly Ala  
 85 90 95  
 Gly Leu Leu Asp Tyr Val Asn Ser Glu Asn Arg Leu Arg Tyr Pro Glu  
 100 105 110  
 Tyr Arg Ala Pro Gly Ser Asp Lys Trp Gln Arg Ile Ser Trp Glu Glu  
 115 120 125  
 Ala Phe Ser Arg Ile Ala Lys Leu Met Lys Ala Asp Arg Asp Ala Asn  
 130 135 140  
 Phe Ile Glu Lys Asn Glu Gln Gly Val Thr Val Asn Arg Trp Leu Ser  
 145 150 155 160  
 Thr Gly Met Leu Cys Ala Ser Gly Ala Ser Asn Glu Thr Gly Met Leu  
 165 170 175  
 Thr Gln Lys Phe Ala Arg Ser Leu Gly Met Leu Ala Val Asp Asn Gln  
 180 185 190  
 Ala Arg Val His Gly Pro Thr Val Ala Ser Leu Ala Pro Thr Phe Gly  
 195 200 205  
 Arg Gly Ala Met Thr Asn His Trp Val Asp Ile Lys Asn Ala Asn Val  
 210 215 220  
 Val Met Val Met Gly Gly Asn Ala Ala Glu Ala His Pro Val Gly Phe  
 225 230 235 240  
 Arg Trp Ala Met Glu Ala Lys Asn Asn Asn Asp Ala Thr Leu Ile Val  
 245 250 255  
 Val Asp Pro Arg Phe Thr Arg Thr Ala Ser Val Ala Asp Ile Tyr Ala  
 260 265 270  
 Pro Ile Arg Ser Gly Thr Asp Ile Thr Phe Leu Ser Gly Val Leu Arg  
 275 280 285  
 Tyr Leu Ile Glu Asn Asn Lys Ile Asn Ala Glu Tyr Val Lys His Tyr  
 290 295 300  
 Thr Asn Ala Ser Leu Leu Val Arg Asp Asp Phe Ala Phe Glu Asp Gly  
 305 310 315 320  
 Leu Phe Ser Gly Tyr Asp Ala Glu Lys Arg Gln Tyr Asp Lys Ser Ser  
 325 330 335  
 Trp Asn Tyr Gln Leu Asp Glu Asn Gly Tyr Ala Lys Arg Asp Glu Thr  
 340 345 350  
 Leu Thr His Pro Arg Cys Val Trp Asn Leu Leu Lys Glu His Val Ser  
 355 360 365

Arg Tyr Thr Pro Asp Val Val Glu Asn Ile Cys Gly Thr Pro Lys Ala  
 370 375 380  
 Asp Phe Leu Lys Val Cys Glu Val Leu Ala Ser Thr Ser Ala Pro Asp  
 385 390 395 400  
 Arg Thr Thr Thr Phe Leu Tyr Ala Leu Gly Trp Thr Gln His Thr Val  
 405 410 415  
 Gly Ala Gln Asn Ile Arg Thr Met Ala Met Ile Gln Leu Leu Leu Gly  
 420 425 430  
 Asn Met Gly Met Ala Gly Gly Gly Val Asn Ala Leu Arg Gly His Ser  
 435 440 445  
 Asn Ile Gln Gly Leu Thr Asp Leu Gly Leu Leu Ser Thr Ser Leu Pro  
 450 455 460  
 Gly Tyr Leu Thr Leu Pro Ser Glu Lys Gln Val Asp Leu Gln Ser Tyr  
 465 470 475 480  
 Leu Glu Ala Asn Thr Pro Lys Ala Thr Leu Ala Asp Gln Val Asn Tyr  
 485 490 495  
 Trp Ser Asn Tyr Pro Lys Phe Phe Val Ser Leu Met Lys Ser Phe Tyr  
 500 505 510  
 Gly Asp Ala Ala Gln Lys Glu Asn Asn Trp Gly Tyr Asp Trp Leu Pro  
 515 520 525  
 Lys Trp Asp Gln Thr Tyr Asp Val Ile Lys Tyr Phe Asn Met Met Asp  
 530 535 540  
 Glu Gly Lys Val Thr Gly Tyr Phe Cys Gln Gly Phe Asn Pro Val Ala  
 545 550 555 560  
 Ser Phe Pro Asp Lys Asn Lys Val Val Ser Cys Leu Ser Lys Leu Lys  
 565 570 575  
 Tyr Met Val Val Ile Asp Pro Leu Val Thr Glu Thr Ser Thr Phe Trp  
 580 585 590  
 Gln Asn His Gly Glu Ser Asn Asp Val Asp Pro Ala Ser Ile Gln Thr  
 595 600 605  
 Glu Val Phe Arg Leu Pro Ser Thr Cys Phe Ala Glu Glu Asp Gly Ser  
 610 615 620  
 Ile Ala Asn Ser Gly Arg Trp Leu Gln Trp His Trp Lys Gly Gln Asp  
 625 630 635 640  
 Ala Pro Gly Glu Ala Arg Asn Asp Gly Glu Ile Leu Ala Gly Ile Tyr  
 645 650 655  
 His His Leu Arg Glu Leu Tyr Gln Ser Glu Gly Gly Lys Gly Val Glu  
 660 665 670  
 Pro Leu Met Lys Met Ser Trp Asn Tyr Lys Gln Pro His Glu Pro Gln  
 675 680 685  
 Ser Asp Glu Val Ala Lys Glu Asn Asn Gly Tyr Ala Leu Glu Asp Leu  
 690 695 700  
 Tyr Asp Ala Asn Gly Val Leu Ile Ala Lys Lys Gly Gln Leu Leu Ser  
 705 710 715 720  
 Ser Phe Ala His Leu Arg Asp Asp Gly Thr Thr Ala Ser Ser Cys Trp  
 725 730 735  
 Ile Tyr Thr Gly Ser Trp Thr Glu Gln Gly Asn Gln Met Ala Asn Arg  
 740 745 750  
 Asp Asn Ser Asp Pro Ser Gly Leu Gly Asn Thr Leu Gly Trp Ala Trp  
 755 760 765  
 Ala Trp Pro Leu Asn Arg Arg Val Leu Tyr Asn Arg Ala Ser Ala Asp  
 770 775 780  
 Ile Asn Gly Lys Pro Trp Asp Pro Lys Arg Met Leu Ile Gln Trp Asn  
 785 790 795 800  
 Gly Ser Lys Trp Thr Gly Asn Asp Ile Pro Asp Phe Gly Asn Ala Ala  
 805 810 815  
 Pro Gly Thr Pro Thr Gly Pro Phe Ile Met Gln Pro Glu Gly Met Gly  
 820 825 830  
 Arg Leu Phe Ala Ile Asn Lys Met Ala Glu Gly Pro Phe Pro Glu His  
 835 840 845  
 Tyr Glu Pro Ile Glu Thr Pro Leu Gly Thr Asn Pro Leu His Pro Asn



850 855 860  
 Val Val Ser Asn Pro Val Val Arg Leu Tyr Glu Gln Asp Ala Leu Arg  
 865 870 875 880  
 Met Gly Lys Lys Glu Gln Phe Pro Tyr Val Gly Thr Thr Tyr Arg Leu  
 885 890 895  
 Thr Glu His Phe His Thr Trp Thr Lys His Ala Leu Leu Asn Ala Ile  
 900 905 910  
 Ala Gln Pro Glu Gln Phe Val Glu Ile Ser Glu Thr Leu Ala Ala Ala  
 915 920 925  
 Lys Gly Ile Asn Asn Gly Asp Arg Val Thr Val Ser Ser Lys Arg Gly  
 930 935 940  
 Phe Ile Arg Ala Val Ala Val Thr Arg Arg Leu Lys Pro Leu Asn  
 945 950 955 960  
 Val Asn Gly Gln Gln Val Glu Thr Val Gly Ile Pro Ile His Trp Gly  
 965 970 975  
 Phe Glu Gly Val Ala Arg Lys Gly Tyr Ile Ala Asn Thr Leu Thr Pro  
 980 985 990  
 Asn Val Gly Asp Ala Asn Ser Gln Thr Pro Glu Tyr Lys Ala Phe Leu  
 995 1000 1005  
 Val Asn Ile Glu Lys Ala  
 1010

<210> 267  
 <211> 294  
 <212> PRT  
 <213> E. Coli

<400> 267  
 Met Ala Met Glu Thr Gln Asp Ile Ile Lys Arg Ser Ala Thr Asn Ser  
 1 5 10 15  
 Ile Thr Pro Pro Ser Gln Val Arg Asp Tyr Lys Ala Glu Val Ala Lys  
 20 25 30  
 Leu Ile Asp Val Ser Thr Cys Ile Gly Cys Lys Ala Cys Gln Val Ala  
 35 40 45  
 Cys Ser Glu Trp Asn Asp Ile Arg Asp Glu Val Gly His Cys Val Gly  
 50 55 60  
 Val Tyr Asp Asn Pro Ala Asp Leu Ser Ala Lys Ser Trp Thr Val Met  
 65 70 75 80  
 Arg Phe Ser Glu Thr Glu Gln Asn Gly Lys Leu Glu Trp Leu Ile Arg  
 85 90 95  
 Lys Asp Gly Cys Met His Cys Glu Asp Pro Gly Cys Leu Lys Ala Cys  
 100 105 110  
 Pro Ser Ala Gly Ala Ile Ile Gln Tyr Ala Asn Gly Ile Val Asp Phe  
 115 120 125  
 Gln Ser Glu Asn Cys Ile Gly Cys Gly Tyr Cys Ile Ala Gly Cys Pro  
 130 135 140  
 Phe Asn Ile Pro Arg Leu Asn Lys Glu Asp Asn Arg Val Tyr Lys Cys  
 145 150 155 160  
 Thr Leu Cys Val Asp Arg Val Ser Val Gly Gln Glu Pro Ala Cys Val  
 165 170 175  
 Lys Thr Cys Pro Thr Gly Ala Ile His Phe Gly Thr Lys Lys Glu Met  
 180 185 190  
 Leu Glu Leu Ala Glu Gln Arg Val Ala Lys Leu Lys Ala Arg Gly Tyr  
 195 200 205  
 Glu His Ala Gly Val Tyr Asn Pro Glu Gly Val Gly Gly Thr His Val  
 210 215 220  
 Met Tyr Val Leu His His Ala Asp Gln Pro Glu Leu Tyr His Gly Leu  
 225 230 235 240  
 Pro Lys Asp Pro Lys Ile Asp Thr Ser Val Ser Leu Trp Lys Gly Ala  
 245 250 255  
 Leu Lys Pro Leu Ala Ala Ala Gly Phe Ile Ala Thr Phe Ala Gly Leu

260 265 270  
 Ile Phe His Tyr Ile Gly Ile Gly Pro Asn Lys Glu Val Asp Asp Asp  
 275 280 285  
 Glu Glu Asp His His Glu  
 290

<210> 268  
 <211> 217  
 <212> PRT  
 <213> E. Coli

<400> 268  
 Met Ser Lys Ser Lys Met Ile Val Arg Thr Lys Phe Ile Asp Arg Ala  
 1 5 10 15  
 Cys His Trp Thr Val Val Ile Cys Phe Phe Leu Val Ala Leu Ser Gly  
 20 25 30  
 Ile Ser Phe Phe Pro Thr Leu Gln Trp Leu Thr Gln Thr Phe Gly  
 35 40 45  
 Thr Pro Gln Met Gly Arg Ile Leu His Pro Phe Phe Gly Ile Ala Ile  
 50 55 60  
 Phe Val Ala Leu Met Phe Met Phe Val Arg Phe Val His His Asn Ile  
 65 70 75 80  
 Pro Asp Lys Lys Asp Ile Pro Trp Leu Leu Asn Ile Val Glu Val Leu  
 85 90 95  
 Lys Gly Asn Glu His Lys Val Ala Asp Val Gly Lys Tyr Asn Ala Gly  
 100 105 110  
 Gln Lys Met Met Phe Trp Ser Ile Met Ser Met Ile Phe Val Leu Leu  
 115 120 125  
 Val Thr Gly Val Ile Ile Trp Arg Pro Tyr Phe Ala Gln Tyr Phe Pro  
 130 135 140  
 Met Gln Val Val Arg Tyr Ser Leu Leu Ile His Ala Ala Ala Gly Ile  
 145 150 155 160  
 Ile Leu Ile His Ala Ile Leu Ile His Met Tyr Met Ala Phe Trp Val  
 165 170 175  
 Lys Gly Ser Ile Lys Gly Met Ile Glu Gly Lys Val Ser Arg Arg Trp  
 180 185 190  
 Ala Lys Lys His His Pro Arg Trp Tyr Arg Glu Ile Glu Lys Ala Glu  
 195 200 205  
 Ala Lys Lys Glu Ser Glu Glu Gly Ile  
 210 215

<210> 269  
 <211> 86  
 <212> PRT  
 <213> E. Coli

<400> 269  
 Met Ala Leu Leu Ile Thr Lys Lys Cys Ile Asn Cys Asp Met Cys\_Glu  
 1 5 10 15  
 Pro Glu Cys Pro Asn Glu Ala Ile Ser Met Gly Asp His Ile Tyr Glu  
 20 25 30  
 Ile Asn Ser Asp Lys Cys Thr Glu Cys Val Gly His Tyr Glu Thr Pro  
 35 40 45  
 Thr Cys Gln Lys Val Cys Pro Ile Pro Asn Thr Ile Val Lys Asp Pro  
 50 55 60  
 Ala His Val Glu Thr Glu Glu Gln Leu Trp Asp Lys Phe Val Leu Met  
 65 70 75 80  
 His His Ala Asp Lys Ile  
 85

<210> 270  
 <211> 400  
 <212> PRT  
 <213> E. Coli

<400> 270

```

Met Gln Ser Val Asp Val Ala Ile Val Gly Gly Gly Met Val Gly Leu
 1          5          10          15
Ala Val Ala Cys Gly Leu Gln Gly Ser Gly Leu Arg Val Ala Val Leu
      20          25          30
Glu Gln Arg Val Gln Glu Pro Leu Ala Ala Asn Ala Pro Pro Gln Leu
      35          40          45
Arg Val Ser Ala Ile Asn Ala Ala Ser Glu Lys Leu Leu Thr Arg Leu
      50          55          60
Gly Val Trp Gln Asp Ile Leu Ser Arg Arg Ala Ser Cys Tyr His Gly
65          70          75          80
Met Glu Val Trp Asp Lys Asp Ser Phe Gly His Ile Ser Phe Asp Asp
      85          90          95
Gln Ser Met Gly Tyr Ser His Leu Gly His Ile Val Glu Asn Ser Val
      100          105          110
Ile His Tyr Ala Leu Trp Asn Lys Ala His Gln Ser Ser Asp Ile Thr
      115          120          125
Leu Leu Ala Pro Ala Glu Leu Gln Gln Val Ala Trp Gly Glu Asn Glu
      130          135          140
Thr Phe Leu Thr Leu Lys Asp Gly Ser Met Leu Thr Ala Arg Leu Val
145          150          155          160
Ile Gly Ala Asp Gly Ala Asn Ser Trp Leu Arg Asn Lys Ala Asp Ile
      165          170          175
Pro Leu Thr Phe Trp Asp Tyr Gln His His Ala Leu Val Ala Thr Ile
      180          185          190
Arg Thr Glu Glu Pro His Asp Ala Val Ala Arg Gln Val Phe His Gly
      195          200          205
Glu Gly Ile Leu Ala Phe Leu Pro Leu Ser Asp Pro His Leu Cys Ser
      210          215          220
Ile Val Trp Ser Leu Ser Pro Glu Glu Ala Gln Arg Met Gln Gln Ala
225          230          235          240
Ser Glu Asp Glu Phe Asn Arg Ala Leu Asn Ile Ala Phe Asp Asn Arg
      245          250          255
Leu Gly Leu Cys Lys Val Glu Ser Ala Arg Gln Val Phe Pro Leu Thr
      260          265          270
Gly Arg Tyr Ala Arg Gln Phe Ala Ser His Arg Leu Ala Leu Val Gly
      275          280          285
Asp Ala Ala His Thr Ile His Pro Leu Ala Gly Gln Gly Val Asn Leu
      290          295          300
Gly Phe Met Asp Ala Ala Glu Leu Ile Ala Glu Leu Lys Arg Leu His
305          310          315          320
Arg Gln Gly Lys Asp Ile Gly Gln Tyr Ile Tyr Leu Arg Arg Tyr Glu
      325          330          335
Arg Ser Arg Lys His Ser Ala Ala Leu Met Leu Ala Gly Met Gln Gly
      340          345          350
Phe Arg Asp Leu Phe Ser Gly Thr Asn Pro Ala Lys Lys Leu Leu Arg
      355          360          365
Asp Ile Gly Leu Lys Leu Ala Asp Thr Leu Pro Gly Val Lys Pro Gln
      370          375          380
Leu Ile Arg Gln Ala Met Gly Leu Asn Asp Leu Pro Glu Trp Leu Arg
385          390          395          400

```

<210> 271

<211> 392  
 <212> PRT  
 <213> E. Coli

<400> 271

```

Met Ser Val Ile Ile Val Gly Gly Gly Met Ala Gly Ala Thr Leu Ala
 1           5           10           15
Leu Ala Ile Ser Arg Leu Ser His Gly Ala Leu Pro Val His Leu Ile
 20           25           30
Glu Ala Thr Ala Pro Glu Ser His Ala His Pro Gly Phe Asp Gly Arg
 35           40           45
Ala Ile Ala Leu Ala Ala Gly Thr Cys Gln Gln Leu Ala Arg Ile Gly
 50           55           60
Val Trp Gln Ser Leu Ala Asp Cys Ala Thr Ala Ile Thr Thr Val His
 65           70           75           80
Val Ser Asp Arg Gly His Ala Gly Phe Val Thr Leu Ala Ala Glu Asp
 85           90           95
Tyr Gln Leu Ala Ala Leu Gly Gln Val Val Glu Leu His Asn Val Gly
100           105           110
Gln Arg Leu Phe Ala Leu Leu Arg Lys Ala Pro Gly Val Thr Leu His
115           120           125
Cys Pro Asp Arg Val Ala Asn Val Ala Arg Thr Gln Ser His Val Glu
130           135           140
Val Thr Leu Glu Ser Gly Glu Thr Leu Thr Gly Arg Val Leu Val Ala
145           150           155           160
Ala Asp Gly Thr His Ser Ala Leu Ala Thr Ala Cys Gly Val Asp Trp
165           170           175
Gln Gln Glu Pro Tyr Glu Gln Leu Ala Val Ile Ala Asn Val Ala Thr
180           185           190
Ser Val Ala His Glu Gly Arg Ala Phe Glu Arg Phe Thr Gln His Gly
195           200           205
Pro Leu Ala Met Leu Pro Met Ser Asp Gly Arg Cys Ser Leu Val Trp
210           215           220
Cys His Pro Leu Glu Arg Arg Glu Glu Val Leu Ser Trp Ser Asp Glu
225           230           235           240
Lys Phe Cys Arg Glu Leu Gln Ser Ala Phe Gly Trp Arg Leu Gly Lys
245           250           255
Ile Thr His Ala Gly Lys Arg Ser Ala Tyr Pro Leu Ala Leu Thr His
260           265           270
Ala Ala Arg Ser Ile Thr His Arg Thr Val Leu Val Gly Asn Ala Ala
275           280           285
Gln Thr Leu His Pro Ile Ala Gly Gln Gly Phe Asn Leu Gly Met Arg
290           295           300
Asp Val Met Ser Leu Ala Glu Thr Leu Thr Gln Ala Gln Glu Arg Gly
305           310           315           320
Glu Asp Met Gly Asp Tyr Gly Val Leu Cys Arg Tyr Gln Gln Arg Arg
325           330           335
Gln Ser Asp Arg Glu Ala Thr Ile Gly Val Thr Asp Ser Leu Val His
340           345           350
Leu Phe Ala Asn Arg Trp Ala Pro Leu Val Val Gly Arg Asn Ile Gly
355           360           365
Leu Met Thr Met Glu Leu Phe Thr Pro Ala Arg Asp Val Leu Ala Gln
370           375           380
Arg Thr Leu Gly Trp Val Ala Arg
385           390

```

<210> 272  
 <211> 441  
 <212> PRT  
 <213> E. Coli

&lt;400&gt; 272

```

Met Ser Glu Ile Ser Arg Gln Glu Phe Gln Arg Arg Arg Gln Ala Leu
 1      5      10      15
Val Glu Gln Met Gln Pro Gly Ser Ala Ala Leu Ile Phe Ala Ala Pro
      20      25      30
Glu Val Thr Arg Ser Ala Asp Ser Glu Tyr Pro Tyr Arg Gln Asn Ser
 35      40      45
Asp Phe Trp Tyr Phe Thr Gly Phe Asn Glu Pro Glu Ala Val Leu Val
 50      55      60
Leu Ile Lys Ser Asp Asp Thr His Asn His Ser Val Leu Phe Asn Arg
 65      70      75      80
Val Arg Asp Leu Thr Ala Glu Ile Trp Phe Gly Arg Arg Leu Gly Gln
      85      90      95
Asp Ala Ala Pro Glu Lys Leu Gly Val Asp Arg Ala Leu Ala Phe Ser
 100      105      110
Glu Ile Asn Gln Gln Leu Tyr Gln Leu Leu Asn Gly Leu Asp Val Val
 115      120      125
Tyr His Ala Gln Gly Glu Tyr Ala Tyr Ala Asp Val Ile Val Asn Ser
 130      135      140
Ala Leu Glu Lys Leu Arg Lys Gly Ser Arg Gln Asn Leu Thr Ala Pro
 145      150      155      160
Ala Thr Met Ile Asp Trp Arg Pro Val Val His Glu Met Arg Leu Phe
      165      170      175
Lys Ser Pro Glu Glu Ile Ala Val Leu Arg Arg Ala Gly Glu Ile Thr
 180      185      190
Ala Met Ala His Thr Arg Ala Met Glu Lys Cys Arg Pro Gly Met Phe
 195      200      205
Glu Tyr His Leu Glu Gly Glu Ile His His Glu Phe Asn Arg His Gly
 210      215      220
Ala Arg Tyr Pro Ser Tyr Asn Thr Ile Val Gly Ser Gly Glu Asn Gly
 225      230      235      240
Cys Ile Leu His Tyr Thr Glu Asn Glu Cys Glu Met Arg Asp Gly Asp
      245      250      255
Leu Val Leu Ile Asp Ala Gly Cys Glu Tyr Lys Gly Tyr Ala Gly Asp
 260      265      270
Ile Thr Arg Thr Phe Pro Val Asn Gly Lys Phe Thr Gln Ala Gln Arg
 275      280      285
Glu Ile Tyr Asp Ile Val Leu Glu Ser Leu Glu Thr Ser Leu Arg Leu
 290      295      300
Tyr Arg Pro Gly Thr Ser Ile Leu Glu Val Thr Gly Glu Val Val Arg
 305      310      315      320
Ile Met Val Ser Gly Leu Val Lys Leu Gly Ile Leu Lys Gly Asp Val
      325      330      335
Asp Glu Leu Ile Ala Gln Asn Ala His Arg Pro Phe Phe Met His Gly
 340      345      350
Leu Ser His Trp Leu Gly Leu Asp Val His Asp Val Gly Val Tyr Gly
 355      360      365
Gln Asp Arg Ser Arg Ile Leu Glu Pro Gly Met Val Leu Thr Val Glu
 370      375      380
Pro Gly Leu Tyr Ile Ala Pro Asp Ala Glu Val Pro Glu Gln Tyr Arg
 385      390      395      400
Gly Ile Gly Ile Arg Ile Glu Asp Asp Ile Val Ile Thr Glu Thr Gly
      405      410      415
Asn Glu Asn Leu Thr Ala Ser Val Val Lys Lys Pro Glu Glu Ile Glu
 420      425      430
Ala Leu Met Val Ala Ala Arg Lys Gln
 435      440

```

&lt;210&gt; 273

<211> 194  
 <212> PRT  
 <213> E. Coli

<400> 273

```

Met Leu Met Ser Ile Gln Asn Glu Met Pro Gly Tyr Asn Glu Met Asn
 1          5          10          15
Gln Tyr Leu Asn Gln Gln Gly Thr Gly Leu Thr Pro Ala Glu Met His
      20          25          30
Gly Leu Ile Ser Gly Met Ile Cys Gly Gly Asn Asp Asp Ser Ser Trp
      35          40          45
Leu Pro Leu Leu His Asp Leu Thr Asn Glu Gly Met Ala Phe Gly His
      50          55          60
Glu Leu Ala Gln Ala Leu Arg Lys Met His Ser Ala Thr Ser Asp Ala
65          70          75          80
Leu Gln Asp Asp Gly Phe Leu Phe Gln Leu Tyr Leu Pro Asp Gly Asp
      85          90          95
Asp Val Ser Val Phe Asp Arg Ala Asp Ala Leu Ala Gly Trp Val Asn
      100          105          110
His Phe Leu Leu Gly Leu Gly Val Thr Gln Pro Lys Leu Asp Lys Val
      115          120          125
Thr Gly Glu Thr Gly Glu Ala Ile Asp Asp Leu Arg Asn Ile Ala Gln
      130          135          140
Leu Gly Tyr Asp Glu Asp Glu Asp Gln Glu Glu Leu Glu Met Ser Leu
145          150          155          160
Glu Glu Ile Ile Glu Tyr Val Arg Val Ala Ala Leu Leu Cys His Asp
      165          170          175
Thr Phe Thr His Pro Gln Pro Thr Ala Pro Glu Val Gln Lys Pro Thr
      180          185          190
Leu His

```

<210> 274  
 <211> 120  
 <212> PRT  
 <213> E. Coli

<400> 274

```

Met Leu Lys Leu Phe Ala Lys Tyr Thr Ser Ile Gly Val Leu Asn Thr
 1          5          10          15
Leu Ile His Trp Val Val Phe Gly Val Cys Ile Tyr Val Ala His Thr
      20          25          30
Asn Gln Ala Leu Ala Asn Phe Ala Gly Phe Val Val Ala Val Ser Phe
      35          40          45
Ser Phe Phe Ala Asn Ala Lys Phe Thr Phe Lys Ala Ser Thr Thr Thr
      50          55          60
Met Arg Tyr Met Leu Tyr Val Gly Phe Met Gly Thr Leu Ser Ala Thr
65          70          75          80
Val Gly Trp Ala Ala Asp Arg Cys Ala Leu Pro Pro Met Ile Thr Leu
      85          90          95
Val Thr Phe Ser Ala Ile Ser Leu Val Cys Gly Phe Val Tyr Ser Lys
      100          105          110
Phe Ile Val Phe Arg Asp Ala Lys
      115          120

```

<210> 275  
 <211> 306  
 <212> PRT  
 <213> E. Coli

&lt;400&gt; 275

```

Met Lys Ile Ser Leu Val Val Pro Val Phe Asn Glu Glu Glu Ala Ile
 1          5          10          15
Pro Ile Phe Tyr Lys Thr Val Arg Glu Phe Glu Glu Leu Lys Ser Tyr
 20          25          30
Glu Val Glu Ile Val Phe Ile Asn Asp Gly Ser Lys Asp Ala Thr Glu
 35          40          45
Ser Ile Ile Asn Ala Leu Ala Val Ser Asp Pro Leu Val Val Pro Leu
 50          55          60
Ser Phe Thr Arg Asn Phe Gly Lys Glu Pro Ala Leu Phe Ala Gly Leu
 65          70          75          80
Asp His Ala Thr Gly Asp Ala Ile Ile Pro Ile Asp Val Asp Leu Gln
 85          90          95
Asp Pro Ile Glu Val Ile Pro His Leu Ile Glu Lys Trp Gln Ala Gly
100          105          110
Ala Asp Met Val Leu Ala Lys Arg Ser Asp Arg Ser Thr Asp Gly Arg
115          120          125
Leu Lys Arg Lys Thr Ala Glu Trp Phe Tyr Lys Leu His Asn Lys Ile
130          135          140
Ser Asn Pro Lys Ile Glu Asn Val Gly Asp Phe Arg Leu Met Ser
145          150          155          160
Arg Asp Val Val Glu Asn Ile Lys Leu Met Pro Glu Arg Asn Leu Phe
165          170          175
Met Lys Gly Ile Leu Ser Trp Val Gly Gly Lys Thr Asp Ile Val Glu
180          185          190
Tyr Val Arg Ala Glu Arg Ile Ala Gly Asp Thr Lys Phe Asn Gly Trp
195          200          205
Lys Leu Trp Asn Leu Ala Leu Glu Gly Ile Thr Ser Phe Ser Thr Phe
210          215          220
Pro Leu Arg Ile Trp Thr Tyr Ile Gly Leu Val Ala Ser Val Ala
225          230          235          240
Phe Ile Tyr Gly Ala Trp Met Ile Leu Asp Thr Ile Ile Phe Gly Asn
245          250          255
Ala Val Arg Gly Tyr Pro Ser Leu Leu Val Ser Ile Leu Phe Leu Gly
260          265          270
Gly Ile Gln Met Ile Gly Ile Gly Val Leu Gly Glu Tyr Ile Gly Arg
275          280          285
Thr Tyr Ile Glu Thr Lys Lys Arg Pro Lys Tyr Ile Ile Lys Arg Val
290          295          300
Lys Lys
305

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&lt;210&gt; 276

&lt;211&gt; 443

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 276

```

Met Asn Lys Ala Ile Lys Val Ser Leu Tyr Ile Ser Phe Val Leu Ile
 1          5          10          15
Ile Cys Ala Leu Ser Lys Asn Ile Met Met Leu Asn Thr Ser Asp Phe
 20          25          30
Gly Arg Ala Ile Lys Pro Leu Ile Glu Asp Ile Pro Ala Phe Thr Tyr
 35          40          45
Asp Leu Pro Leu Leu Tyr Lys Leu Lys Gly His Ile Asp Ser Ile Asp
 50          55          60
Ser Tyr Glu Tyr Ile Ser Ser Tyr Ser Tyr Ile Leu Tyr Thr Tyr Val
 65          70          75          80
Leu Phe Ile Ser Ile Phe Thr Glu Tyr Leu Asp Ala Arg Val Leu Ser
 85          90          95

```

```

Leu Phe Leu Lys Val Ile Tyr Ile Tyr Ser Leu Tyr Ala Ile Phe Thr
      100      105      110
Ser Tyr Ile Lys Thr Glu Arg Tyr Val Thr Leu Phe Thr Phe Phe Ile
      115      120      125
Leu Ala Phe Leu Met Cys Ser Ser Ser Thr Leu Ser Met Phe Ala Ser
      130      135      140
Phe Tyr Gln Glu Gln Ile Val Ile Ile Phe Leu Pro Phe Leu Val Tyr
145      150      155      160
Ser Leu Thr Cys Lys Asn Asn Lys Ser Met Leu Leu Leu Phe Phe Ser
      165      170      175
Leu Leu Ile Ile Ser Thr Ala Lys Asn Gln Phe Ile Leu Thr Pro Leu
      180      185      190
Ile Val Tyr Ser Tyr Tyr Ile Phe Phe Asp Arg His Lys Leu Ile Ile
      195      200      205
Lys Ser Val Ile Cys Val Val Cys Leu Leu Ala Ser Ile Phe Ala Ile
      210      215      220
Ser Tyr Ser Lys Gly Val Val Glu Leu Asn Lys Tyr His Ala Thr Tyr
225      230      235      240
Phe Gly Ser Tyr Leu Tyr Met Lys Asn Asn Gly Tyr Lys Met Pro Ser
      245      250      255
Tyr Val Asp Asp Lys Cys Val Gly Leu Asp Ala Trp Gly Asn Lys Phe
      260      265      270
Asp Ile Ser Phe Gly Ala Thr Pro Thr Glu Val Gly Thr Glu Cys Phe
      275      280      285
Glu Ser His Lys Asp Glu Thr Phe Ser Asn Ala Leu Phe Leu Leu Val
      290      295      300
Ser Lys Pro Ser Thr Ile Phe Lys Leu Pro Phe Asp Asp Gly Val Met
305      310      315      320
Ser Gln Tyr Lys Glu Asn Tyr Phe His Val Tyr Lys Lys Leu His Val
      325      330      335
Ile Tyr Gly Glu Ser Asn Ile Leu Thr Thr Ile Thr Asn Ile Lys Asp
      340      345      350
Asn Ile Phe Lys Asn Ile Arg Phe Ile Ser Leu Leu Leu Phe Phe Ile
      355      360      365
Ala Ser Ile Phe Ile Arg Asn Asn Lys Ile Lys Ala Ser Leu Phe Val
      370      375      380
Val Ser Leu Phe Gly Ile Ser Gln Phe Tyr Val Ser Phe Phe Gly Glu
385      390      395      400
Gly Tyr Arg Asp Leu Ser Lys His Leu Phe Gly Met Tyr Phe Ser Phe
      405      410      415
Asp Leu Cys Leu Tyr Ile Thr Val Val Phe Leu Ile Tyr Lys Ile Ile
      420      425      430
Gln Arg Asn Gln Asp Asn Ser Asp Val Lys His
      435      440

```

<210> 277  
 <211> 82  
 <212> PRT  
 <213> E. Coli

<400> 277

```

Met Gly Ile Leu Ser Trp Ile Ile Phe Gly Leu Ile Ala Gly Ile Leu
  1      5      10      15
Ala Lys Trp Ile Met Pro Gly Lys Asp Gly Gly Gly Phe Phe Met Thr
      20      25      30
Ile Leu Leu Gly Ile Val Gly Ala Val Val Gly Gly Trp Ile Ser Thr
      35      40      45
Leu Phe Gly Phe Gly Lys Val Asp Gly Phe Asn Phe Gly Ser Phe Val
  50      55      60

```



Val Ala Val Ile Gly Ala Ile Val Val Leu Phe Ile Tyr Arg Lys Ile  
 65 70 75 80  
 Lys Ser

<210> 278  
 <211> 60  
 <212> PRT  
 <213> E. Coli

<400> 278  
 Met Gly Lys Ala Thr Tyr Thr Val Thr Val Thr Asn Asn Ser Asn Gly  
 1 5 10 15  
 Val Ser Val Asp Tyr Glu Thr Glu Thr Pro Met Thr Leu Leu Val Pro  
 20 25 30  
 Glu Val Ala Ala Glu Val Ile Lys Asp Leu Val Asn Thr Val Arg Ser  
 35 40 45  
 Tyr Asp Thr Glu Asn Glu His Asp Val Cys Gly Trp  
 50 55 60

<210> 279  
 <211> 119  
 <212> PRT  
 <213> E. Coli

<400> 279  
 Met Leu Gln Ile Pro Gln Asn Tyr Ile His Thr Arg Ser Thr Pro Phe  
 1 5 10 15  
 Trp Asn Lys Gln Thr Ala Pro Ala Gly Ile Phe Glu Arg His Leu Asp  
 20 25 30  
 Lys Gly Thr Arg Pro Gly Val Tyr Pro Arg Leu Ser Val Met His Gly  
 35 40 45  
 Ala Val Lys Tyr Leu Gly Tyr Ala Asp Glu His Ser Ala Glu Pro Asp  
 50 55 60  
 Gln Val Ile Leu Ile Glu Ala Gly Gln Phe Ala Val Phe Pro Pro Glu  
 65 70 75 80  
 Lys Trp His Asn Ile Glu Ala Met Thr Asp Asp Thr Tyr Phe Asn Ile  
 85 90 95  
 Asp Phe Phe Val Ala Pro Glu Val Leu Met Glu Gly Ala Gln Gln Arg  
 100 105 110  
 Lys Val Ile His Asn Gly Lys  
 115

<210> 280  
 <211> 246  
 <212> PRT  
 <213> E. Coli

<400> 280  
 Met Lys Phe Lys Val Ile Ala Leu Ala Ala Leu Met Gly Ile Ser Gly  
 1 5 10 15  
 Met Ala Ala Gln Ala Asn Glu Leu Pro Asp Gly Pro His Ile Val Thr  
 20 25 30  
 Ser Gly Thr Ala Ser Val Asp Ala Val Pro Asp Ile Ala Thr Leu Ala  
 35 40 45  
 Ile Glu Val Asn Val Ala Lys Asp Ala Ala Thr Ala Lys Lys Gln  
 50 55 60  
 Ala Asp Glu Arg Val Ala Gln Tyr Ile Ser Phe Leu Glu Leu Asn Gln

```

65          70          75          80
Ile Ala Lys Lys Asp Ile Ser Ser Ala Asn Leu Arg Thr Gln Pro Asp
      85          90          95
Tyr Asp Tyr Gln Asp Gly Lys Ser Ile Leu Lys Gly Tyr Arg Ala Val
      100          105          110
Arg Thr Val Glu Val Thr Leu Arg Gln Leu Asp Lys Leu Asn Ser Leu
      115          120          125
Leu Asp Gly Ala Leu Lys Ala Gly Leu Asn Glu Ile Arg Ser Val Ser
      130          135          140
Leu Gly Val Ala Gln Pro Asp Ala Tyr Lys Asp Lys Ala Arg Lys Ala
      145          150          155          160
Ala Ile Asp Asn Ala Ile His Gln Ala Gln Glu Leu Ala Asn Gly Phe
      165          170          175
His Arg Lys Leu Gly Pro Val Tyr Ser Val Arg Tyr His Val Ser Asn
      180          185          190
Tyr Gln Pro Ser Pro Met Val Arg Met Met Lys Ala Asp Ala Ala Pro
      195          200          205
Val Ser Ala Gln Glu Thr Tyr Glu Gln Ala Ala Ile Gln Phe Asp Asp
      210          215          220
Gln Val Asp Val Val Phe Gln Leu Glu Pro Val Asp Gln Gln Pro Ala
      225          230          235          240
Lys Thr Pro Ala Ala Gln
      245

```

<210> 281  
 <211> 464  
 <212> PRT  
 <213> E. Coli

```

<400> 281
Met Leu Leu Leu Asp Ala Cys Ser Gln Met Cys Pro Ser Phe Arg Arg
  1          5          10          15
Phe Gln Thr Val Phe His Asn Ser Ser Ile Phe Leu Pro Tyr Trp Leu
      20          25          30
Ala Thr Leu Val Ser Phe Arg Glu Thr Phe Gln Glu Glu Lys Leu Leu
      35          40          45
Thr Met Lys Gly Ser Tyr Lys Ser Arg Trp Val Ile Val Ile Val Val
      50          55          60
Val Ile Ala Ala Ile Ala Ala Phe Trp Phe Trp Gln Gly Arg Asn Asp
      65          70          75          80
Ser Arg Ser Ala Ala Pro Gly Ala Thr Lys Gln Ala Gln Gln Ser Pro
      85          90          95
Ala Gly Gly Arg Arg Gly Met Arg Ser Gly Pro Leu Ala Pro Val Gln
      100          105          110
Ala Ala Thr Ala Val Glu Gln Ala Val Pro Arg Tyr Leu Thr Gly Leu
      115          120          125
Gly Thr Ile Thr Ala Ala Asn Thr Val Thr Val Arg Ser Arg Val Asp
      130          135          140
Gly Gln Leu Ile Ala Leu His Phe Gln Glu Gly Gln Gln Val Lys Ala
      145          150          155          160
Gly Asp Leu Leu Ala Glu Ile Asp Pro Ser Gln Phe Lys Val Ala Leu
      165          170          175
Ala Gln Ala Gln Gly Gln Leu Ala Lys Asp Lys Ala Thr Leu Ala Asn
      180          185          190
Ala Arg Arg Asp Leu Ala Arg Tyr Gln Gln Leu Ala Lys Thr Asn Leu
      195          200          205
Val Ser Arg Gln Glu Leu Asp Ala Gln Gln Ala Leu Val Ser Glu Thr
      210          215          220
Glu Gly Thr Ile Lys Ala Asp Glu Ala Ser Val Ala Ser Ala Gln Leu
      225          230          235          240

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Gln Leu Asp Trp Ser Arg Ile Thr Ala Pro Val Asp Gly Arg Val Gly  
 245 250 255  
 Leu Lys Gln Val Asp Val Gly Asn Gln Ile Ser Ser Gly Asp Thr Thr  
 260 265 270  
 Gly Ile Val Val Ile Thr Gln Thr His Pro Ile Asp Leu Val Phe Thr  
 275 280 285  
 Leu Pro Glu Ser Asp Ile Ala Thr Val Val Gln Ala Gln Lys Ala Gly  
 290 295 300  
 Lys Pro Leu Val Val Glu Ala Trp Asp Arg Thr Asn Ser Lys Lys Leu  
 305 310 315 320  
 Ser Glu Gly Thr Leu Leu Ser Leu Asp Asn Gln Ile Asp Ala Thr Thr  
 325 330 335  
 Gly Thr Ile Lys Val Lys Ala Arg Phe Asn Asn Gln Asp Asp Ala Leu  
 340 345 350  
 Phe Pro Asn Gln Phe Val Asn Ala Arg Met Leu Val Asp Thr Glu Gln  
 355 360 365  
 Asn Ala Val Val Ile Pro Thr Ala Ala Leu Gln Met Gly Asn Glu Gly  
 370 375 380  
 His Phe Val Trp Val Leu Asn Ser Glu Asn Lys Val Ser Lys His Leu  
 385 390 395 400  
 Val Thr Pro Gly Ile Gln Asp Ser Gln Lys Val Val Ile Arg Ala Gly  
 405 410 415  
 Ile Ser Ala Gly Asp Arg Val Val Thr Asp Gly Ile Asp Arg Leu Thr  
 420 425 430  
 Glu Gly Ala Lys Val Glu Val Val Glu Ala Gln Ser Ala Thr Thr Pro  
 435 440 445  
 Glu Glu Lys Ala Thr Ser Arg Glu Tyr Ala Lys Lys Gly Ala Arg Ser  
 450 455 460

&lt;210&gt; 282

&lt;211&gt; 1040

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 282

Met Gln Val Leu Pro Ser Ser Thr Gly Gly Pro Ser Arg Leu Phe  
 1 5 10 15  
 Ile Met Arg Pro Val Ala Thr Thr Leu Leu Met Val Ala Ile Leu Leu  
 20 25 30  
 Ala Gly Ile Ile Gly Tyr Arg Ala Leu Pro Val Ser Ala Leu Pro Glu  
 35 40 45  
 Val Asp Tyr Pro Thr Ile Gln Val Val Thr Leu Tyr Pro Gly Ala Ser  
 50 55 60  
 Pro Asp Val Met Thr Ser Ala Val Thr Ala Pro Leu Glu Arg Gln Phe  
 65 70 75 80  
 Gly Gln Met Ser Gly Leu Lys Gln Met Ser Ser Gln Ser Ser Gly Gly  
 85 90 95  
 Ala Ser Val Ile Thr Leu Gln Phe Gln Leu Thr Leu Pro Leu Asp Val  
 100 105 110  
 Ala Glu Gln Glu Val Gln Ala Ala Ile Asn Ala Ala Thr Asn Leu Leu  
 115 120 125  
 Pro Ser Asp Leu Pro Asn Pro Pro Val Tyr Ser Lys Val Asn Pro Ala  
 130 135 140  
 Asp Pro Pro Ile Met Thr Leu Ala Val Thr Ser Thr Ala Met Pro Met  
 145 150 155 160  
 Thr Gln Val Glu Asp Met Val Glu Thr Arg Val Ala Gln Lys Ile Ser  
 165 170 175  
 Gln Ile Ser Gly Val Gly Leu Val Thr Leu Ser Gly Gly Gln Arg Pro  
 180 185 190  
 Ala Val Arg Val Lys Leu Asn Ala Gln Ala Ile Ala Ala Leu Gly Leu

|   |     |     |
|---|-----|-----|
| 195   | 200 | 205 |
| Thr Ser Glu Thr Val Arg Thr Ala Ile Thr Gly Ala Asn Val Asn Ser |     |     |
| 210   | 215 | 220 |
| Ala Lys Gly Ser Leu Asp Gly Pro Ser Arg Ala Val Thr Leu Ser Ala |     |     |
| 225   | 230 | 235 |
| Asn Asp Gln Met Gln Ser Ala Glu Glu Tyr Arg Gln Leu Ile Ile Ala |     |     |
| 245   | 250 | 255 |
| Tyr Gln Asn Gly Ala Pro Ile Arg Leu Gly Asp Val Ala Thr Val Glu |     |     |
| 260   | 265 | 270 |
| Gln Gly Ala Glu Asn Ser Trp Leu Gly Ala Trp Ala Asn Lys Glu Gln |     |     |
| 275   | 280 | 285 |
| Ala Ile Val Met Asn Val Gln Arg Gln Pro Gly Ala Asn Ile Ile Ser |     |     |
| 290   | 295 | 300 |
| Thr Ala Asp Ser Ile Arg Gln Met Leu Pro Gln Leu Thr Glu Ser Leu |     |     |
| 305   | 310 | 315 |
| Pro Lys Ser Val Lys Val Thr Val Leu Ser Asp Arg Thr Thr Asn Ile |     |     |
| 325   | 330 | 335 |
| Arg Ala Ser Val Asp Asp Thr Gln Phe Glu Leu Met Met Ala Ile Ala |     |     |
| 340   | 345 | 350 |
| Leu Val Val Met Ile Ile Tyr Leu Phe Leu Arg Asn Ile Pro Ala Thr |     |     |
| 355   | 360 | 365 |
| Ile Ile Pro Gly Val Ala Val Pro Leu Ser Leu Ile Gly Thr Phe Ala |     |     |
| 370   | 375 | 380 |
| Val Met Val Phe Leu Asp Phe Ser Ile Asn Asn Leu Thr Leu Met Ala |     |     |
| 385   | 390 | 395 |
| Leu Thr Ile Ala Thr Gly Phe Val Val Asp Asp Ala Ile Val Val Ile |     |     |
| 405   | 410 | 415 |
| Glu Asn Ile Ser Arg Tyr Ile Glu Lys Gly Glu Lys Pro Leu Ala Ala |     |     |
| 420   | 425 | 430 |
| Ala Leu Lys Gly Ala Gly Glu Ile Gly Phe Thr Ile Ile Ser Leu Thr |     |     |
| 435   | 440 | 445 |
| Phe Ser Leu Ile Ala Val Leu Ile Pro Leu Leu Phe Met Gly Asp Ile |     |     |
| 450   | 455 | 460 |
| Val Gly Arg Leu Phe Arg Glu Phe Ala Ile Thr Leu Ala Val Ala Ile |     |     |
| 465   | 470 | 475 |
| Leu Ile Ser Ala Val Val Ser Leu Thr Leu Thr Pro Met Met Cys Ala |     |     |
| 485   | 490 | 495 |
| Arg Met Leu Ser Gln Glu Ser Leu Arg Lys Gln Asn Arg Phe Ser Arg |     |     |
| 500   | 505 | 510 |
| Ala Ser Glu Lys Met Phe Asp Arg Ile Ile Ala Ala Tyr Gly Arg Gly |     |     |
| 515   | 520 | 525 |
| Leu Ala Lys Val Leu Asn His Pro Trp Leu Thr Leu Ser Val Ala Leu |     |     |
| 530   | 535 | 540 |
| Ser Thr Leu Leu Leu Ser Val Leu Leu Trp Val Phe Ile Pro Lys Gly |     |     |
| 545   | 550 | 555 |
| Phe Phe Pro Val Gln Asp Asn Gly Ile Ile Gln Gly Thr Leu Gln Ala |     |     |
| 565   | 570 | 575 |
| Pro Gln Ser Ser Ser Phe Ala Asn Met Ala Gln Arg Gln Arg Gln Val |     |     |
| 580   | 585 | 590 |
| Ala Asp Val Ile Leu Gln Asp Pro Ala Val Gln Ser Leu Thr Ser Phe |     |     |
| 595   | 600 | 605 |
| Val Gly Val Asp Gly Thr Asn Pro Ser Leu Asn Ser Ala Arg Leu Gln |     |     |
| 610   | 615 | 620 |
| Ile Asn Leu Lys Pro Leu Asp Glu Arg Asp Asp Arg Val Gln Lys Val |     |     |
| 625   | 630 | 635 |
| Ile Ala Arg Leu Gln Thr Ala Val Asp Lys Val Pro Gly Val Asp Leu |     |     |
| 645   | 650 | 655 |
| Phe Leu Gln Pro Thr Gln Asp Leu Thr Ile Asp Thr Gln Val Ser Arg |     |     |
| 660   | 665 | 670 |
| Thr Gln Tyr Gln Phe Thr Leu Gln Ala Thr Ser Leu Asp Ala Leu Ser |     |     |
| 675   | 680 | 685 |

Thr Trp Val Pro Gln Leu Met Glu Lys Leu Gln Gln Leu Pro Gln Leu  
 690 695 700  
 Ser Asp Val Ser Ser Asp Trp Gln Asp Lys Gly Leu Val Ala Tyr Val  
 705 710 715 720  
 Asn Val Asp Arg Asp Ser Ala Ser Arg Leu Gly Ile Ser Met Ala Asp  
 725 730 735  
 Val Asp Asn Ala Leu Tyr Asn Ala Phe Gly Gln Arg Leu Ile Ser Thr  
 740 745 750  
 Ile Tyr Thr Gln Ala Asn Gln Tyr Arg Val Val Leu Glu His Asn Thr  
 755 760 765  
 Glu Asn Thr Pro Gly Leu Ala Ala Leu Asp Thr Ile Arg Leu Thr Ser  
 770 775 780  
 Ser Asp Gly Gly Val Val Pro Leu Ser Ser Ile Ala Lys Ile Glu Gln  
 785 790 795 800  
 Arg Phe Ala Pro Leu Ser Ile Asn His Leu Asp Gln Phe Pro Val Thr  
 805 810 815  
 Thr Ile Ser Phe Asn Val Pro Asp Asn Tyr Ser Leu Gly Asp Ala Val  
 820 825 830  
 Gln Ala Ile Met Asp Thr Glu Lys Thr Leu Asn Leu Pro Val Asp Ile  
 835 840 845  
 Thr Thr Gln Phe Gln Gly Ser Thr Leu Ala Phe Gln Ser Ala Leu Gly  
 850 855 860  
 Ser Thr Val Trp Leu Ile Val Ala Ala Val Val Ala Met Tyr Ile Val  
 865 870 875 880  
 Leu Gly Ile Leu Tyr Glu Ser Phe Ile His Pro Ile Thr Ile Leu Ser  
 885 890 895  
 Thr Leu Pro Thr Ala Gly Val Gly Ala Leu Leu Ala Leu Ile Ala  
 900 905 910  
 Gly Ser Glu Leu Asp Val Ile Ala Ile Ile Gly Ile Ile Leu Leu Ile  
 915 920 925  
 Gly Ile Val Lys Lys Asn Ala Ile Met Met Ile Asp Phe Ala Leu Ala  
 930 935 940  
 Ala Glu Arg Glu Gln Gly Met Ser Pro Arg Glu Ala Ile Tyr Gln Ala  
 945 950 955 960  
 Cys Leu Leu Arg Phe Arg Pro Ile Leu Met Thr Thr Leu Ala Ala Leu  
 965 970 975  
 Leu Gly Ala Leu Pro Leu Met Leu Ser Thr Gly Val Gly Ala Glu Leu  
 980 985 990  
 Arg Arg Pro Leu Gly Ile Gly Met Val Gly Gly Leu Ile Val Ser Gln  
 995 1000 1005  
 Val Leu Thr Leu Phe Thr Thr Pro Val Ile Tyr Leu Leu Phe Asp Arg  
 1010 1015 1020  
 Leu Ala Leu Trp Thr Lys Ser Arg Phe Ala Arg His Glu Glu Glu Ala  
 1025 1030 1035 1040

&lt;210&gt; 283

&lt;211&gt; 1025

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 283

Met Lys Phe Phe Ala Leu Phe Ile Tyr Arg Pro Val Ala Thr Ile Leu  
 1 5 10 15  
 Leu Ser Val Ala Ile Thr Leu Cys Gly Ile Leu Gly Phe Arg Met Leu  
 20 25 30  
 Pro Val Ala Pro Leu Pro Gln Val Asp Phe Pro Val Ile Ile Val Ser  
 35 40 45  
 Ala Ser Leu Pro Gly Ala Ser Pro Glu Thr Met Ala Ser Ser Val Ala  
 50 55 60  
 Thr Pro Leu Glu Arg Ser Leu Gly Arg Ile Ala Gly Val Ser Glu Met

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Ser | Ser | Ser | Ser | Leu | Gly | Ser | Thr | Arg | Ile | Ile | Leu | Gln | Phe | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Asp | Arg | Asp | Ile | Asn | Gly | Ala | Ala | Arg | Asp | Val | Gln | Ala | Ala | Ile |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |
| Asn | Ala | Ala | Gln | Ser | Leu | Leu | Pro | Ser | Gly | Met | Pro | Ser | Arg | Pro | Thr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Arg | Lys | Ala | Asn | Pro | Ser | Asp | Ala | Pro | Ile | Met | Ile | Leu | Thr | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Ser | Asp | Thr | Tyr | Ser | Gln | Gly | Glu | Leu | Tyr | Asp | Phe | Ala | Ser | Thr |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gln | Leu | Ala | Pro | Thr | Ile | Ser | Gln | Ile | Asp | Gly | Val | Gly | Asp | Val | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Gly | Gly | Ser | Ser | Leu | Pro | Ala | Val | Arg | Val | Gly | Leu | Asn | Pro | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Leu | Phe | Asn | Gln | Gly | Val | Ser | Leu | Asp | Asp | Val | Arg | Thr | Ala | Val |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Asn | Ala | Asn | Val | Arg | Lys | Pro | Gln | Gly | Ala | Leu | Glu | Asp | Gly | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| His | Arg | Trp | Gln | Ile | Gln | Thr | Asn | Asp | Glu | Leu | Lys | Thr | Ala | Ala | Glu |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Tyr | Gln | Pro | Leu | Ile | Ile | His | Tyr | Asn | Asn | Gly | Gly | Ala | Val | Arg | Leu |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Gly | Asp | Val | Ala | Thr | Val | Thr | Asp | Ser | Val | Gln | Asp | Val | Arg | Asn | Ala |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Gly | Met | Thr | Asn | Ala | Lys | Pro | Ala | Ile | Leu | Leu | Met | Ile | Arg | Lys | Leu |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Pro | Glu | Ala | Asn | Ile | Ile | Gln | Thr | Val | Asp | Ser | Ile | Arg | Ala | Lys | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Pro | Glu | Leu | Gln | Glu | Thr | Ile | Pro | Ala | Ala | Ile | Asp | Leu | Gln | Ile | Ala |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Gln | Asp | Arg | Ser | Pro | Thr | Ile | Arg | Ala | Ser | Leu | Glu | Glu | Val | Glu | Gln |
|     |     |     | 325 |     |     |     | 330 |     |     |     |     |     |     | 335 |     |
| Thr | Leu | Ile | Ile | Ser | Val | Ala | Leu | Val | Ile | Leu | Val | Val | Phe | Leu | Phe |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Leu | Arg | Ser | Gly | Arg | Ala | Thr | Ile | Ile | Pro | Ala | Val | Ser | Val | Pro | Val |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Ser | Leu | Ile | Gly | Thr | Phe | Ala | Ala | Met | Tyr | Leu | Cys | Gly | Phe | Ser | Leu |
|     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |     |
| Asn | Asn | Leu | Ser | Leu | Met | Ala | Leu | Thr | Ile | Ala | Thr | Gly | Phe | Val | Val |
|     |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     | 400 |     |
| Asp | Asp | Ala | Ile | Val | Val | Leu | Glu | Asn | Ile | Ala | Arg | His | Leu | Glu | Ala |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Gly | Met | Lys | Pro | Leu | Gln | Ala | Ala | Leu | Gln | Gly | Thr | Arg | Glu | Val | Gly |
|     |     | 420 |     |     |     |     | 425 |     |     |     |     |     | 430 |     |     |
| Phe | Thr | Val | Leu | Ser | Met | Ser | Leu | Ser | Leu | Val | Ala | Val | Phe | Leu | Pro |
|     |     | 435 |     |     |     | 440 |     |     |     |     |     | 445 |     |     |     |
| Leu | Leu | Leu | Met | Gly | Gly | Leu | Pro | Gly | Arg | Leu | Leu | Arg | Glu | Phe | Ala |
|     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |     |
| Val | Thr | Leu | Ser | Val | Ala | Ile | Gly | Ile | Ser | Leu | Leu | Val | Ser | Leu | Thr |
|     | 465 |     |     |     | 470 |     |     |     |     | 475 |     |     |     | 480 |     |
| Leu | Thr | Pro | Met | Met | Cys | Gly | Trp | Met | Leu | Lys | Ala | Ser | Lys | Pro | Arg |
|     |     | 485 |     |     |     |     |     | 490 |     |     |     |     |     | 495 |     |
| Glu | Gln | Lys | Arg | Leu | Arg | Gly | Phe | Gly | Arg | Met | Leu | Val | Ala | Leu | Gln |
|     |     | 500 |     |     |     |     | 505 |     |     |     |     |     | 510 |     |     |
| Gln | Gly | Tyr | Gly | Lys | Ser | Leu | Lys | Trp | Val | Leu | Asn | His | Thr | Arg | Leu |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Val | Gly | Val | Val | Leu | Leu | Gly | Thr | Ile | Ala | Leu | Asn | Ile | Trp | Leu | Tyr |
|     | 530 |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |     |
| Ile | Ser | Ile | Pro | Lys | Thr | Phe | Phe | Pro | Glu | Gln | Asp | Thr | Gly | Val | Leu |
|     | 545 |     |     |     | 550 |     |     |     |     | 555 |     |     |     | 560 |     |

Met Gly Gly Ile Gln Ala Asp Gln Ser Ile Ser Phe Gln Ala Met Arg  
 565 570 575  
 Gly Lys Leu Gln Asp Phe Met Lys Ile Ile Arg Asp Asp Pro Ala Val  
 580 585 590  
 Asp Asn Val Thr Gly Phe Thr Gly Gly Ser Arg Val Asn Ser Gly Met  
 595 600 605  
 Met Phe Ile Thr Leu Lys Pro Arg Asp Glu Arg Ser Glu Thr Ala Gln  
 610 615 620  
 Gln Ile Ile Asp Arg Leu Arg Val Lys Leu Ala Lys Glu Pro Gly Ala  
 625 630 635 640  
 Asn Leu Phe Leu Met Ala Val Gln Asp Ile Arg Val Gly Gly Arg Gln  
 645 650 655  
 Ser Asn Ala Ser Tyr Gln Tyr Thr Leu Leu Ser Asp Asp Leu Ala Ala  
 660 665 670  
 Leu Arg Glu Trp Glu Pro Lys Ile Arg Lys Lys Leu Ala Thr Leu Pro  
 675 680 685  
 Glu Leu Ala Asp Val Asn Ser Asp Gln Gln Asp Asn Gly Ala Glu Met  
 690 695 700  
 Asn Leu Val Tyr Asp Arg Asp Thr Met Ala Arg Leu Gly Ile Asp Val  
 705 710 715 720  
 Gln Ala Ala Asn Ser Leu Leu Asn Asn Ala Phe Gly Gln Arg Gln Ile  
 725 730 735  
 Ser Thr Ile Tyr Gln Pro Met Asn Gln Tyr Lys Val Val Met Glu Val  
 740 745 750  
 Asp Pro Arg Tyr Thr Gln Asp Ile Ser Ala Leu Glu Lys Met Phe Val  
 755 760 765  
 Ile Asn Asn Glu Gly Lys Ala Ile Pro Leu Ser Tyr Phe Ala Lys Trp  
 770 775 780  
 Gln Pro Ala Asn Ala Pro Leu Ser Val Asn His Gln Gly Leu Ser Ala  
 785 790 795 800  
 Ala Ser Thr Ile Ser Phe Asn Leu Pro Thr Gly Lys Ser Leu Ser Asp  
 805 810 815  
 Ala Ser Ala Ala Ile Asp Arg Ala Met Thr Gln Leu Gly Val Pro Ser  
 820 825 830  
 Thr Val Arg Gly Ser Phe Ala Gly Thr Ala Gln Val Phe Gln Glu Thr  
 835 840 845  
 Met Asn Ser Gln Val Ile Leu Ile Ile Ala Ala Ile Ala Thr Val Tyr  
 850 855 860  
 Ile Val Leu Gly Ile Leu Tyr Glu Ser Tyr Val His Pro Leu Thr Ile  
 865 870 875 880  
 Leu Ser Thr Leu Pro Ser Ala Gly Val Gly Ala Leu Leu Ala Leu Glu  
 885 890 895  
 Leu Phe Asn Ala Pro Phe Ser Leu Ile Ala Leu Ile Gly Ile Met Leu  
 900 905 910  
 Leu Ile Gly Ile Val Lys Lys Asn Ala Ile Met Met Val Asp Phe Ala  
 915 920 925  
 Leu Glu Ala Gln Arg His Gly Asn Leu Thr Pro Gln Glu Ala Ile Phe  
 930 935 940  
 Gln Ala Cys Leu Leu Arg Phe Arg Pro Ile Met Met Thr Thr Leu Ala  
 945 950 955 960  
 Ala Leu Phe Gly Ala Leu Pro Leu Val Leu Ser Gly Gly Asp Gly Ser  
 965 970 975  
 Glu Leu Arg Gln Pro Leu Gly Ile Thr Ile Val Gly Gly Leu Val Met  
 980 985 990  
 Ser Gln Leu Leu Thr Leu Tyr Thr Thr Pro Val Val Tyr Leu Phe Phe  
 995 1000 1005  
 Asp Arg Leu Arg Leu Arg Phe Ser Arg Lys Pro Lys Gln Thr Val Thr  
 1010 1015 1020  
 Glu  
 1025

<210> 284  
 <211> 471  
 <212> PRT  
 <213> E. Coli

<400> 284

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Met Thr Asp Leu Pro Asp Ser Thr Arg Trp Gln Leu Trp Ile Val Ala
 1      5      10      15
Phe Gly Phe Phe Met Gln Ser Leu Asp Thr Thr Ile Val Asn Thr Ala
 20      25      30
Leu Pro Ser Met Ala Gln Ser Leu Gly Glu Ser Pro Leu His Met His
 35      40      45
Met Val Ile Val Ser Tyr Val Leu Thr Val Ala Val Met Leu Pro Ala
 50      55      60
Ser Gly Trp Leu Ala Asp Lys Val Gly Val Arg Asn Ile Phe Phe Thr
 65      70      75      80
Ala Ile Val Leu Phe Thr Leu Gly Ser Leu Phe Cys Ala Leu Ser Gly
 85      90      95
Thr Leu Asn Glu Leu Leu Leu Ala Arg Ala Leu Gln Gly Val Gly Gly
100     105     110
Ala Met Met Val Pro Val Gly Arg Leu Thr Val Met Lys Ile Val Pro
115     120     125
Arg Glu Gln Tyr Met Ala Ala Met Thr Phe Val Thr Leu Pro Gly Gln
130     135     140
Val Gly Pro Leu Leu Gly Pro Ala Leu Gly Gly Leu Leu Val Glu Tyr
145     150     155     160
Ala Ser Trp His Trp Ile Phe Leu Ile Asn Ile Pro Val Gly Ile Ile
165     170     175
Gly Ala Ile Ala Thr Leu Leu Leu Met Pro Asn Tyr Thr Met Gln Thr
180     185     190
Arg Arg Phe Asp Leu Ser Gly Phe Leu Leu Leu Ala Val Gly Met Ala
195     200     205
Val Leu Thr Leu Ala Leu Asp Gly Ser Lys Gly Thr Gly Leu Ser Pro
210     215     220
Leu Thr Ile Ala Gly Leu Val Ala Val Gly Val Val Ala Leu Val Leu
225     230     235     240
Tyr Leu Leu His Ala Arg Asn Asn Asn Arg Ala Leu Phe Ser Leu Lys
245     250     255
Leu Phe Arg Thr Arg Thr Phe Ser Leu Gly Leu Ala Gly Ser Phe Ala
260     265     270
Gly Arg Ile Gly Ser Gly Met Leu Pro Phe Met Thr Pro Val Phe Leu
275     280     285
Gln Ile Gly Leu Gly Phe Ser Pro Phe His Ala Gly Leu Met Met Ile
290     295     300
Pro Met Val Leu Gly Ser Met Gly Met Lys Arg Ile Val Val Gln Val
305     310     315     320
Val Asn Arg Phe Gly Tyr Arg Arg Val Leu Val Ala Thr Thr Leu Gly
325     330     335
Leu Ser Leu Val Thr Leu Leu Phe Met Thr Thr Ala Leu Leu Gly Trp
340     345     350
Tyr Tyr Val Leu Pro Phe Val Leu Phe Leu Gln Gly Met Val Asn Ser
355     360     365
Thr Arg Phe Ser Ser Met Asn Thr Leu Thr Leu Lys Asp Leu Pro Asp
370     375     380
Asn Leu Ala Ser Ser Gly Asn Ser Leu Leu Ser Met Ile Met Gln Leu
385     390     395     400
Ser Met Ser Ile Gly Val Thr Ile Ala Gly Leu Leu Leu Gly Leu Phe
405     410     415
Gly Ser Gln His Val Ser Val Asp Ser Gly Thr Thr Gln Thr Val Phe
420     425     430

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Met Tyr Thr Trp Leu Ser Met Ala Leu Ile Ile Ala Leu Pro Ala Phe  
 435 440 445  
 Ile Phe Ala Arg Val Pro Asn Asp Thr His Gln Asn Val Ala Ile Ser  
 450 455 460  
 Arg Arg Lys Arg Ser Ala Gln  
 465 470

<210> 285  
 <211> 344  
 <212> PRT  
 <213> E. Coli

<400> 285

Met Glu Ile Arg Ile Met Leu Phe Ile Leu Met Met Met Val Met Pro  
 1 5 10 15  
 Val Ser Tyr Ala Ala Cys Tyr Ser Glu Leu Ser Val Gln His Asn Leu  
 20 25 30  
 Val Val Gln Gly Asp Phe Ala Leu Thr Gln Thr Gln Met Ala Thr Tyr  
 35 40 45  
 Glu His Asn Phe Asn Asp Ser Ser Cys Val Ser Thr Asn Thr Ile Thr  
 50 55 60  
 Pro Met Ser Pro Ser Asp Ile Ile Val Gly Leu Tyr Asn Asp Thr Ile  
 65 70 75 80  
 Lys Leu Asn Leu His Phe Glu Trp Thr Asn Lys Asn Asn Ile Thr Leu  
 85 90 95  
 Ser Asn Asn Gln Thr Ser Phe Thr Ser Gly Tyr Ser Val Thr Val Thr  
 100 105 110  
 Pro Ala Ala Ser Asn Ala Lys Val Asn Val Ser Ala Gly Gly Gly Gly  
 115 120 125  
 Ser Val Met Ile Asn Gly Val Ala Thr Leu Ser Ser Ala Ser Ser Ser  
 130 135 140  
 Thr Arg Gly Ser Ala Ala Val Gln Phe Leu Leu Cys Leu Leu Gly Gly  
 145 150 155 160  
 Lys Ser Trp Asp Ala Cys Val Asn Ser Tyr Arg Asn Ala Leu Ala Gln  
 165 170 175  
 Asn Ala Gly Val Tyr Ser Phe Asn Leu Thr Leu Ser Tyr Asn Pro Ile  
 180 185 190  
 Thr Thr Thr Cys Lys Pro Asp Asp Leu Leu Ile Thr Leu Asp Ser Ile  
 195 200 205  
 Pro Val Ser Gln Leu Pro Ala Thr Gly Asn Lys Ala Thr Ile Asn Ser  
 210 215 220  
 Lys Gln Gly Asp Ile Ile Leu Arg Cys Lys Asn Leu Leu Gly Gln Gln  
 225 230 235 240  
 Asn Gln Thr Ser Arg Lys Met Gln Val Tyr Leu Ser Ser Ser Asp Leu  
 245 250 255  
 Leu Thr Asn Ser Asn Thr Ile Leu Lys Gly Ala Glu Asp Asn Gly Val  
 260 265 270  
 Gly Phe Ile Leu Glu Ser Asn Gly Ser Pro Val Thr Leu Leu Asn Ile  
 275 280 285  
 Thr Asn Ser Ser Lys Gly Tyr Thr Asn Leu Lys Glu Val Ala Ala Lys  
 290 295 300  
 Ser Lys Leu Thr Asp Thr Val Ser Ile Pro Ile Thr Ala Ser Tyr  
 305 310 315 320  
 Tyr Val Tyr Asp Thr Asn Lys Val Lys Ser Gly Ala Leu Glu Ala Thr  
 325 330 335  
 Ala Leu Ile Asn Val Lys Tyr Asp  
 340

<210> 286

<211> 826  
 <212> PRT  
 <213> E. Coli

<400> 286

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Met Leu Arg Met Thr Pro Leu Ala Ser Ala Ile Val Ala Leu Leu Leu
 1          5          10          15
Gly Ile Glu Ala Tyr Ala Ala Glu Glu Thr Phe Asp Thr His Phe Met
 20          25          30
Ile Gly Gly Met Lys Asp Gln Gln Val Ala Asn Ile Arg Leu Asp Asp
 35          40          45
Asn Gln Pro Leu Pro Gly Gln Tyr Asp Ile Asp Ile Tyr Val Asn Lys
 50          55          60
Gln Trp Arg Gly Lys Tyr Glu Ile Ile Val Lys Asp Asn Pro Gln Glu
 65          70          75          80
Thr Cys Leu Ser Arg Glu Val Ile Lys Arg Leu Gly Ile Asn Ser Asp
 85          90          95
Asn Phe Ala Ser Gly Lys Gln Cys Leu Thr Phe Glu Gln Leu Val Gln
100          105          110
Gly Gly Ser Tyr Thr Trp Asp Ile Gly Val Phe Arg Leu Asp Phe Ser
115          120          125
Val Pro Gln Ala Trp Val Glu Glu Leu Glu Ser Gly Tyr Val Pro Pro
130          135          140
Glu Asn Trp Glu Arg Gly Ile Asn Ala Phe Tyr Thr Ser Tyr Tyr Leu
145          150          155          160
Ser Gln Tyr Tyr Ser Asp Tyr Lys Ala Ser Gly Asn Asn Lys Ser Thr
165          170          175
Tyr Val Arg Phe Asn Ser Gly Leu Asn Leu Leu Gly Trp Gln Leu His
180          185          190
Ser Asp Ala Ser Phe Ser Lys Thr Asn Asn Asn Pro Gly Val Trp Lys
195          200          205
Ser Asn Thr Leu Tyr Leu Glu Arg Gly Phe Ala Gln Leu Leu Gly Thr
210          215          220
Leu Arg Val Gly Asp Met Tyr Thr Ser Ser Asp Ile Phe Asp Ser Val
225          230          235          240
Arg Phe Arg Gly Val Arg Leu Phe Arg Asp Met Gln Met Leu Pro Asn
245          250          255
Ser Lys Gln Asn Phe Thr Pro Arg Val Gln Gly Ile Ala Gln Ser Asn
260          265          270
Ala Leu Val Thr Ile Glu Gln Asn Gly Phe Val Val Tyr Gln Lys Glu
275          280          285
Val Pro Pro Gly Pro Phe Ala Ile Thr Asp Leu Gln Leu Ala Gly Gly
290          295          300
Gly Ala Asp Leu Asp Val Ser Val Lys Glu Ala Asp Gly Ser Val Thr
305          310          315          320
Thr Tyr Leu Val Pro Tyr Ala Ala Val Pro Asn Met Leu Gln Pro Gly
325          330          335
Val Ser Lys Tyr Asp Leu Ala Ala Gly Arg Ser His Ile Glu Gly Ala
340          345          350
Ser Lys Gln Ser Asp Phe Val Gln Ala Gly Tyr Gln Tyr Gly Phe Asn
355          360          365
Asn Leu Leu Thr Leu Tyr Gly Gly Ser Met Val Ala Asn Asn Tyr Tyr
370          375          380
Ala Phe Thr Leu Gly Ala Gly Trp Asn Thr Arg Ile Gly Ala Ile Ser
385          390          395          400
Val Asp Ala Thr Lys Ser His Ser Lys Gln Asp Asn Gly Asp Val Phe
405          410          415
Asp Gly Gln Ser Tyr Gln Ile Ala Tyr Asn Lys Phe Val Ser Gln Thr
420          425          430
Ser Thr Arg Phe Gly Leu Ala Ala Trp Arg Tyr Ser Ser Arg Asp Tyr
435          440          445

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Arg Thr Phe Asn Asp His Val Trp Ala Asn Asn Lys Asp Asn Tyr Arg  
 450 455 460  
 Arg Asp Glu Asn Asp Val Tyr Asp Ile Ala Asp Tyr Tyr Gln Asn Asp  
 465 470 475 480  
 Phe Gly Arg Lys Asn Ser Phe Ser Ala Asn Met Ser Gln Ser Leu Pro  
 485 490 495  
 Glu Gly Trp Gly Ser Val Ser Leu Ser Thr Leu Trp Arg Asp Tyr Trp  
 500 505 510  
 Gly Arg Ser Gly Ser Ser Lys Asp Tyr Gln Leu Ser Tyr Ser Asn Asn  
 515 520 525  
 Leu Arg Arg Ile Ser Tyr Thr Leu Ala Ala Ser Gln Ala Tyr Asp Glu  
 530 535 540  
 Asn His His Glu Glu Lys Arg Phe Asn Ile Phe Ile Ser Ile Pro Phe  
 545 550 555 560  
 Asp Trp Gly Asp Asp Val Ser Thr Pro Arg Arg Gln Ile Tyr Met Ser  
 565 570 575  
 Asn Ser Thr Thr Phe Asp Asp Gln Gly Phe Ala Ser Asn Asn Thr Gly  
 580 585 590  
 Leu Ser Gly Thr Val Gly Ser Arg Asp Gln Phe Asn Tyr Gly Val Asn  
 595 600 605  
 Leu Ser His Gln His Gln Gly Asn Glu Thr Thr Ala Gly Ala Asn Leu  
 610 615 620  
 Thr Trp Asn Ala Pro Val Ala Thr Val Asn Gly Ser Tyr Ser Gln Ser  
 625 630 635 640  
 Ser Thr Tyr Arg Gln Ala Gly Ala Ser Val Ser Gly Gly Ile Val Ala  
 645 650 655  
 Trp Ser Gly Gly Val Asn Leu Ala Asn Arg Leu Ser Glu Thr Phe Ala  
 660 665 670  
 Val Met Asn Ala Pro Gly Ile Lys Asp Ala Tyr Val Asn Gly Gln Lys  
 675 680 685  
 Tyr Arg Thr Thr Asn Arg Asn Gly Val Val Ile Tyr Asp Gly Met Thr  
 690 695 700  
 Pro Tyr Arg Glu Asn His Leu Met Leu Asp Val Ser Gln Ser Asp Ser  
 705 710 715 720  
 Glu Ala Glu Leu Arg Gly Asn Arg Lys Ile Ala Ala Pro Tyr Arg Gly  
 725 730 735  
 Ala Val Val Leu Val Asn Phe Asp Thr Asp Gln Arg Lys Pro Trp Phe  
 740 745 750  
 Ile Lys Ala Leu Arg Ala Asp Gly Gln Ser Leu Thr Phe Gly Tyr Glu  
 755 760 765  
 Val Asn Asp Ile His Gly His Asn Ile Gly Val Val Gly Gln Gly Ser  
 770 775 780  
 Gln Leu Phe Ile Arg Thr Asn Glu Val Pro Pro Ser Val Asn Val Ala  
 785 790 795 800  
 Ile Asp Lys Gln Gln Gly Leu Ser Cys Thr Ile Thr Phe Gly Lys Glu  
 805 810 815  
 Ile Asp Glu Ser Arg Asn Tyr Ile Cys Gln  
 820 825

&lt;210&gt; 287

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 287

Met Ala Ala Ile Pro Trp Arg Pro Phe Asn Leu Arg Gly Ile Lys Met  
 1 5 10 15  
 Lys Gly Leu Leu Ser Leu Leu Ile Phe Ser Met Val Leu Pro Ala His  
 20 25 30  
 Ala Gly Ile Val Ile Tyr Gly Thr Arg Ile Ile Tyr Pro Ala Glu Asn

```

      35      40      45
Lys Glu Val Met Val Gln Leu Met Asn Gln Gly Asn Arg Ser Ser Leu
  50      55      60
Leu Gln Ala Trp Ile Asp Asp Gly Asp Thr Ser Leu Pro Pro Glu Lys
  65      70      75      80
Ile Gln Val Pro Phe Met Leu Thr Pro Pro Val Ala Lys Ile Gly Ala
      85      90      95
Asn Ser Gly Gln Gln Val Lys Ile Lys Ile Met Pro Asn Lys Leu Pro
      100      105      110
Thr Asn Lys Glu Ser Ile Phe Tyr Leu Asn Val Leu Asp Ile Pro Pro
      115      120      125
Asn Ser Pro Glu Gln Glu Gly Lys Asn Ala Leu Lys Phe Ala Met Gln
      130      135      140
Asn Arg Ile Lys Leu Phe Tyr Arg Pro Ala Gly Ile Ala Pro Val Asn
      145      150      155      160
Lys Ala Thr Phe Lys Lys Leu Leu Val Asn Arg Ser Gly Asn Gly Leu
      165      170      175
Val Ile Lys Asn Asp Ser Ala Asn Trp Val Thr Ile Ser Asp Val Lys
      180      185      190
Ala Asn Asn Val Lys Val Asn Tyr Glu Thr Ile Met Ile Ala Pro Leu
      195      200      205
Glu Ser Gln Ser Val Asn Val Lys Ser Asn Asn Ala Asn Asn Trp His
      210      215      220
Leu Thr Ile Ile Asp Asp His Gly Asn Tyr Ile Ser Asp Lys Ile
      225      230      235

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<210> 288  
 <211> 180  
 <212> PRT  
 <213> E. Coli

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      <400> 288
Met Lys Arg Ser Ile Ile Ala Ala Ala Val Phe Ser Ser Phe Phe Met
  1      5      10      15
Ser Ala Gly Val Phe Ala Ala Asp Val Asp Thr Gly Thr Leu Thr Ile
      20      25      30
Lys Gly Asn Ile Ala Glu Ser Pro Cys Lys Phe Glu Ala Gly Gly Asp
      35      40      45
Ser Val Ser Ile Asn Met Pro Thr Val Pro Thr Ser Val Phe Glu Gly
      50      55      60
Lys Ala Lys Tyr Ser Thr Tyr Asp Asp Ala Val Gly Val Thr Ser Ser
      65      70      75      80
Met Leu Lys Ile Ser Cys Pro Lys Glu Val Ala Gly Val Lys Leu Ser
      85      90      95
Leu Ile Thr Asn Asp Lys Ile Thr Gly Asn Asp Lys Ala Ile Ala Ser
      100      105      110
Ser Asn Asp Thr Val Gly Tyr Tyr Leu Tyr Leu Gly Asp Asn Ser Asp
      115      120      125
Val Leu Asp Val Ser Ala Pro Phe Asn Ile Glu Ser Tyr Lys Thr Ala
      130      135      140
Glu Gly Gln Tyr Ala Ile Pro Phe Lys Ala Lys Tyr Leu Lys Leu Thr
      145      150      155      160
Asp Asn Ser Val Gln Ser Gly Asp Val Leu Ser Ser Leu Val Met Arg
      165      170      175
Val Ala Gln Asp
      180

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<210> 289

<211> 112  
 <212> PRT  
 <213> E. Coli

<400> 289  
 Met Ser Ser Glu Arg Asp Leu Val Asn Phe Leu Gly Asp Phe Ser Met  
 1 5 10 15  
 Asp Val Ala Lys Ala Val Ile Ala Gly Gly Val Ala Thr Ala Ile Gly  
 20 25 30  
 Ser Leu Ala Ser Phe Ala Cys Val Ser Phe Gly Phe Pro Val Ile Leu  
 35 40 45  
 Val Gly Gly Ala Ile Leu Leu Thr Gly Ile Val Cys Thr Val Val Leu  
 50 55 60  
 Asn Glu Ile Asp Ala Gln Cys His Leu Ser Glu Lys Leu Lys Tyr Ala  
 65 70 75 80  
 Ile Arg Asp Gly Leu Lys Arg Gln Gln Glu Leu Asp Lys Trp Lys Arg  
 85 90 95  
 Glu Asn Met Thr Pro Phe Met Tyr Val Leu Asn Thr Pro Pro Val Ile  
 100 105 110

<210> 290  
 <211> 193  
 <212> PRT  
 <213> E. Coli

<400> 290  
 Met Thr Asp Tyr Leu Leu Leu Phe Val Gly Thr Val Leu Val Asn Asn  
 1 5 10 15  
 Phe Val Leu Val Lys Phe Leu Gly Leu Cys Pro Phe Met Gly Val Ser  
 20 25 30  
 Lys Lys Leu Glu Thr Ala Met Gly Met Gly Leu Ala Thr Thr Phe Val  
 35 40 45  
 Met Thr Leu Ala Ser Ile Cys Ala Trp Leu Ile Asp Thr Trp Ile Leu  
 50 55 60  
 Ile Pro Leu Asn Leu Ile Tyr Leu Arg Thr Leu Ala Phe Ile Leu Val  
 65 70 75 80  
 Ile Ala Val Val Val Gln Phe Thr Glu Met Val Val Arg Lys Thr Ser  
 85 90 95  
 Pro Val Leu Tyr Arg Leu Leu Gly Ile Phe Leu Pro Leu Ile Thr Thr  
 100 105 110  
 Asn Cys Ala Val Leu Gly Val Ala Leu Leu Asn Ile Asn Leu Gly His  
 115 120 125  
 Asn Phe Leu Gln Ser Ala Leu Tyr Gly Phe Ser Ala Ala Val Gly Phe  
 130 135 140  
 Ser Leu Val Met Val Leu Phe Ala Ala Ile Arg Glu Arg Leu Ala Val  
 145 150 155 160  
 Ala Asp Val Pro Ala Pro Phe Arg Gly Asn Ala Ile Ala Leu Ile Thr  
 165 170 175  
 Ala Gly Leu Met Ser Leu Ala Phe Met Gly Phe Ser Gly Leu Val Lys  
 180 185 190  
 Leu

<210> 291  
 <211> 192  
 <212> PRT  
 <213> E. Coli

&lt;400&gt; 291

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Met Asn Ala Ile Trp Ile Ala Val Ala Ala Val Ser Leu Leu Gly Leu
 1           5           10           15
Ala Phe Gly Ala Ile Leu Gly Tyr Ala Ser Arg Arg Phe Ala Val Glu
          20           25           30
Asp Asp Pro Val Val Glu Lys Ile Asp Glu Ile Leu Pro Gln Ser Gln
          35           40           45
Cys Gly Gln Cys Gly Tyr Pro Gly Cys Arg Pro Tyr Ala Glu Ala Ile
 50           55           60
Ser Cys Asn Gly Glu Lys Ile Asn Arg Cys Ala Pro Gly Gly Glu Ala
 65           70           75           80
Val Met Leu Lys Ile Ala Glu Leu Leu Asn Val Glu Pro Gln Pro Leu
          85           90           95
Asp Gly Glu Ala Gln Glu Ile Thr Pro Ala Arg Met Val Ala Val Ile
          100          105          110
Asp Glu Asn Asn Cys Ile Gly Cys Thr Lys Cys Ile Gln Ala Cys Pro
          115          120          125
Val Asp Ala Ile Val Gly Ala Thr Arg Ala Met His Thr Val Met Ser
          130          135          140
Asp Leu Cys Thr Gly Cys Asn Leu Cys Val Asp Pro Cys Pro Thr His
 145          150          155          160
Cys Ile Ser Leu Gln Pro Val Ala Glu Thr Pro Asp Ser Trp Lys Trp
          165          170          175
Asp Leu Asn Thr Ile Pro Val Arg Ile Ile Pro Val Glu His His Ala
          180          185          190

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&lt;210&gt; 292

&lt;211&gt; 740

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 292

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Met Leu Lys Leu Phe Ser Ala Phe Arg Lys Asn Lys Ile Trp Asp Phe
 1           5           10           15
Asn Gly Gly Ile His Pro Pro Glu Met Lys Thr Gln Ser Asn Gly Thr
          20           25           30
Pro Leu Arg Gln Val Pro Leu Ala Gln Arg Phe Val Ile Pro Leu Lys
          35           40           45
Gln His Ile Gly Ala Glu Gly Glu Leu Cys Val Ser Val Gly Asp Lys
 50           55           60
Val Leu Arg Gly Gln Pro Leu Thr Arg Gly Arg Gly Lys Met Leu Pro
 65           70           75           80
Val His Ala Pro Thr Ser Gly Thr Val Thr Ala Ile Ala Pro His Ser
          85           90           95
Thr Ala His Pro Ser Ala Leu Ala Glu Leu Ser Val Ile Ile Asp Ala
          100          105          110
Asp Gly Glu Asp Cys Trp Ile Pro Arg Asp Gly Trp Ala Asp Tyr Arg
          115          120          125
Thr Arg Ser Arg Glu Glu Leu Ile Glu Arg Ile His Gln Phe Gly Val
          130          135          140
Ala Gly Leu Gly Gly Ala Gly Phe Pro Thr Gly Val Lys Leu Gln Gly
 145          150          155          160
Gly Gly Asp Lys Ile Glu Thr Leu Ile Ile Asn Ala Ala Glu Cys Glu
          165          170          175
Pro Tyr Ile Thr Ala Asp Asp Arg Leu Met Gln Asp Cys Ala Ala Gln
          180          185          190
Val Val Glu Gly Ile Arg Ile Leu Ala His Ile Leu Gln Pro Arg Glu
          195          200          205
Ile Leu Ile Gly Ile Glu Asp Asn Lys Pro Gln Ala Ile Ser Met Leu
          210          215          220

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Arg Ala Val Leu Ala Asp Ser Asn Asp Ile Ser Leu Arg Val Ile Pro
225                230                235                240
Thr Lys Tyr Pro Ser Gly Gly Ala Lys Gln Leu Thr Tyr Ile Leu Thr
                245                250                255
Gly Lys Gln Val Pro His Gly Gly Arg Ser Ser Asp Ile Gly Val Leu
                260                265                270
Met Gln Asn Val Gly Thr Ala Tyr Ala Val Lys Arg Ala Val Ile Asp
275                280                285
Gly Glu Pro Ile Thr Glu Arg Val Val Thr Leu Thr Gly Glu Ala Ile
290                295                300
Ala Arg Pro Gly Asn Val Trp Ala Arg Leu Gly Thr Pro Val Arg His
305                310                315                320
Leu Leu Asn Asp Ala Gly Phe Cys Pro Ser Ala Asp Gln Met Val Ile
                325                330                335
Met Gly Gly Pro Leu Met Gly Phe Thr Leu Pro Trp Leu Asp Val Pro
                340                345                350
Val Val Lys Ile Thr Asn Cys Leu Leu Ala Pro Ser Ala Asn Glu Leu
                355                360                365
Gly Glu Pro Gln Glu Glu Gln Ser Cys Ile Arg Cys Ser Ala Cys Ala
                370                375                380
Asp Ala Cys Pro Ala Asp Leu Leu Pro Gln Gln Leu Tyr Trp Phe Ser
385                390                395                400
Lys Gly Gln Gln His Asp Lys Ala Thr Thr His Asn Ile Ala Asp Cys
                405                410                415
Ile Glu Cys Gly Ala Cys Ala Trp Val Cys Pro Ser Asn Ile Pro Leu
                420                425                430
Val Gln Tyr Phe Arg Gln Glu Lys Ala Glu Ile Ala Ala Ile Arg Gln
                435                440                445
Glu Glu Lys Arg Ala Ala Glu Ala Lys Ala Arg Phe Glu Ala Arg Gln
                450                455                460
Ala Arg Leu Glu Arg Glu Lys Ala Ala Arg Leu Glu Arg His Lys Ser
465                470                475                480
Ala Ala Val Gln Pro Ala Ala Lys Asp Lys Asp Ala Ile Ala Ala Ala
                485                490                495
Leu Ala Arg Val Lys Glu Lys Gln Ala Gln Ala Thr Gln Pro Ile Val
                500                505                510
Ile Lys Ala Gly Glu Arg Pro Asp Asn Ser Ala Ile Ile Ala Ala Arg
                515                520                525
Glu Ala Arg Lys Ala Gln Ala Arg Ala Lys Gln Ala Glu Leu Gln Gln
                530                535                540
Thr Asn Asp Ala Ala Thr Val Ala Asp Pro Arg Lys Thr Ala Val Glu
545                550                555                560
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
                565                570                575
Asn Ala Glu Pro Glu Gln Gln Val Asp Pro Arg Lys Ala Ala Val Glu
                580                585                590
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
                595                600                605
Asn Ala Glu Pro Glu Glu Gln Val Asp Pro Arg Lys Ala Ala Val Glu
                610                615                620
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
                625                630                635                640
Asn Ala Glu Pro Glu Gln Gln Val Asp Pro Arg Lys Ala Ala Val Glu
                645                650                655
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Arg Glu Gln Gln Pro Ala
                660                665                670
Asn Ala Glu Pro Glu Glu Gln Val Asp Pro Arg Lys Ala Ala Val Glu
                675                680                685
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
                690                695                700
Asn Ala Val Pro Glu Glu Gln Val Asp Pro Arg Lys Ala Ala Val Ala

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<210> 293  
<211> 352  
<212> PRT  
<213> E. Coli

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Phe | Arg | Ile | Ala | Ser | Ser | Pro | Tyr | Thr | His | Asn | Gln | Arg | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Ser | Arg | Ile | Met | Leu | Leu | Val | Leu | Leu | Ala | Ala | Val | Pro | Gly | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ala | Gln | Leu | Trp | Phe | Phe | Gly | Trp | Gly | Thr | Leu | Val | Gln | Ile | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ala | Ser | Val | Ser | Ala | Leu | Leu | Ala | Glu | Ala | Leu | Val | Leu | Lys | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Lys | Gln | Ser | Val | Ala | Ala | Thr | Leu | Lys | Asp | Asn | Ser | Ala | Leu | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Gly | Leu | Leu | Leu | Ala | Val | Ser | Ile | Pro | Pro | Leu | Ala | Pro | Trp | Trp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Val | Val | Leu | Gly | Thr | Val | Phe | Ala | Val | Ile | Ile | Ala | Lys | Gln | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Gly | Gly | Leu | Gly | Gln | Asn | Pro | Phe | Asn | Pro | Ala | Met | Ile | Gly | Tyr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Val | Leu | Leu | Ile | Ser | Phe | Pro | Val | Gln | Met | Thr | Ser | Trp | Leu | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | His | Glu | Ile | Ala | Val | Asn | Ile | Pro | Gly | Phe | Ile | Asp | Ala | Ile | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Val | Ile | Phe | Ser | Gly | His | Thr | Ala | Ser | Gly | Gly | Asp | Met | Asn | Thr | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Leu | Gly | Ile | Asp | Gly | Ile | Ser | Gln | Ala | Thr | Pro | Leu | Asp | Thr | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Thr | Ser | Val | Arg | Ala | Gly | His | Ser | Val | Glu | Gln | Ile | Met | Gln | Tyr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Ile | Tyr | Ser | Gly | Ile | Leu | Ala | Gly | Ala | Gly | Trp | Gln | Trp | Val | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Ala | Trp | Leu | Ala | Gly | Gly | Val | Trp | Leu | Leu | Trp | Gln | Lys | Ala | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Arg | Trp | His | Ile | Pro | Leu | Ser | Phe | Leu | Val | Thr | Leu | Ala | Leu | Cys | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Met | Leu | Gly | Trp | Leu | Phe | Ser | Pro | Glu | Thr | Leu | Ala | Ala | Pro | Gln | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| His | Leu | Leu | Ser | Gly | Ala | Thr | Met | Leu | Gly | Ala | Phe | Phe | Ile | Leu | Thr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Pro | Val | Thr | Ala | Ser | Thr | Thr | Asn | Arg | Gly | Arg | Leu | Ile | Phe | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Leu | Ala | Gly | Leu | Leu | Val | Trp | Leu | Ile | Arg | Ser | Phe | Gly | Gly | Tyr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Pro | Asp | Gly | Val | Ala | Phe | Ala | Val | Leu | Leu | Ala | Asn | Ile | Thr | Val | Pro |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Ile | Asp | Tyr | Thr | Thr | Arg | Pro | Arg | Val | Tyr | Gly | His | Arg | Lys | Gly |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |

<210> 294



<211> 206  
 <212> PRT  
 <213> E. Coli

<400> 294

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Met Leu Lys Thr Ile Arg Lys His Gly Ile Thr Leu Ala Leu Phe Ala
 1          5          10          15
Ala Gly Ser Thr Gly Leu Thr Ala Ala Ile Asn Gln Met Thr Lys Thr
 20          25          30
Thr Ile Ala Glu Gln Ala Ser Leu Gln Gln Lys Ala Leu Phe Asp Gln
 35          40          45
Val Leu Pro Ala Glu Arg Tyr Asn Asn Ala Leu Ala Gln Ser Cys Tyr
 50          55          60
Leu Val Thr Ala Pro Glu Leu Gly Lys Gly Glu His Arg Val Tyr Ile
 65          70          75          80
Ala Lys Gln Asp Asp Lys Pro Val Ala Ala Val Leu Glu Ala Thr Ala
 85          90          95
Pro Asp Gly Tyr Ser Gly Ala Ile Gln Leu Leu Val Gly Ala Asp Phe
100          105          110
Asn Gly Thr Val Leu Gly Thr Arg Val Thr Glu His His Glu Thr Pro
115          120          125
Gly Leu Gly Asp Lys Ile Glu Leu Arg Leu Ser Asp Trp Ile Thr His
130          135          140
Phe Ala Gly Lys Lys Ile Ser Gly Ala Asp Asp Ala His Trp Ala Val
145          150          155          160
Lys Lys Asp Gly Gly Asp Phe Asp Gln Phe Thr Gly Ala Thr Ile Thr
165          170          175
Pro Arg Ala Val Asn Ala Val Lys Arg Ala Gly Leu Tyr Ala Gln
180          185          190
Thr Leu Pro Ala Gln Leu Ser Gln Leu Pro Ala Cys Gly Glu
195          200          205

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<210> 295  
 <211> 231  
 <212> PRT  
 <213> E. Coli

<400> 295

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Met Ser Glu Ile Lys Asp Val Ile Val Gln Gly Leu Trp Lys Asn Asn
 1          5          10          15
Ser Ala Leu Val Gln Leu Leu Gly Leu Cys Pro Leu Leu Ala Val Thr
 20          25          30
Ser Thr Ala Thr Asn Ala Leu Gly Leu Gly Leu Ala Thr Thr Leu Val
 35          40          45
Leu Thr Leu Thr Asn Leu Thr Ile Ser Thr Leu Arg His Trp Thr Pro
 50          55          60
Ala Glu Ile Arg Ile Pro Ile Tyr Val Met Ile Ile Ala Ser Val Val
 65          70          75          80
Ser Ala Val Gln Met Leu Ile Asn Ala Tyr Ala Phe Gly Leu Tyr Gln
 85          90          95
Ser Leu Gly Ile Phe Ile Pro Leu Ile Val Thr Asn Cys Ile Val Val
100          105          110
Gly Arg Ala Glu Ala Phe Ala Ala Lys Lys Gly Pro Ala Leu Ser Ala
115          120          125
Leu Asp Gly Phe Ser Ile Gly Met Gly Ala Thr Cys Ala Met Phe Val
130          135          140
Leu Gly Ser Leu Arg Glu Ile Ile Gly Asn Gly Thr Leu Phe Asp Gly
145          150          155          160
Ala Asp Ala Leu Leu Gly Ser Trp Ala Lys Val Leu Arg Val Glu Ile
165          170          175

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Phe His Thr Asp Ser Pro Phe Leu Leu Ala Met Leu Pro Pro Gly Ala  
 180 185 190  
 Phe Ile Gly Leu Gly Leu Met Leu Ala Gly Lys Tyr Leu Ile Asp Glu  
 195 200 205  
 Arg Met Lys Lys Arg Arg Ala Glu Ala Ala Ala Glu Arg Ala Leu Pro  
 210 215 220  
 Asn Gly Glu Thr Gly Asn Val  
 225 230

<210> 296  
 <211> 211  
 <212> PRT  
 <213> E. Coli

<400> 296  
 Met Asn Lys Ala Lys Arg Leu Glu Ile Leu Thr Arg Leu Arg Glu Asn  
 1 5 10 15  
 Asn Pro His Pro Thr Thr Glu Leu Asn Phe Ser Ser Pro Phe Glu Leu  
 20 25 30  
 Leu Ile Ala Val Leu Leu Ser Ala Gln Ala Thr Asp Val Ser Val Asn  
 35 40 45  
 Lys Ala Thr Ala Lys Leu Tyr Pro Val Ala Asn Thr Pro Ala Ala Met  
 50 55 60  
 Leu Glu Leu Gly Val Glu Gly Val Lys Thr Tyr Ile Lys Thr Ile Gly  
 65 70 75 80  
 Leu Tyr Asn Ser Lys Ala Glu Asn Ile Ile Lys Thr Cys Arg Ile Leu  
 85 90 95  
 Leu Glu Gln His Asn Gly Glu Val Pro Glu Asp Arg Ala Ala Leu Glu  
 100 105 110  
 Ala Leu Pro Gly Val Gly Arg Lys Thr Ala Asn Val Val Leu Asn Thr  
 115 120 125  
 Ala Phe Gly Trp Pro Thr Ile Ala Val Asp Thr His Ile Phe Arg Val  
 130 135 140  
 Cys Asn Arg Thr Gln Phe Ala Pro Gly Lys Asn Val Glu Gln Val Glu  
 145 150 155 160  
 Glu Lys Leu Leu Lys Val Val Pro Ala Glu Phe Lys Val Asp Cys His  
 165 170 175  
 His Trp Leu Ile Leu His Gly Arg Tyr Thr Cys Ile Ala Arg Lys Pro  
 180 185 190  
 Arg Cys Gly Ser Cys Ile Ile Glu Asp Leu Cys Glu Tyr Lys Glu Lys  
 195 200 205  
 Val Asp Ile  
 210

<210> 297  
 <211> 167  
 <212> PRT  
 <213> E. Coli

<400> 297  
 Met Lys Arg Leu His Lys Arg Phe Leu Leu Ala Thr Phe Cys Ala Leu  
 1 5 10 15  
 Phe Thr Ala Thr Leu Gln Ala Ala Asp Val Thr Ile Thr Val Asn Gly  
 20 25 30  
 Arg Val Val Ala Lys Pro Cys Thr Ile Gln Thr Lys Glu Ala Asn Val  
 35 40 45  
 Asn Leu Gly Asp Leu Tyr Thr Arg Asn Leu Gln Gln Pro Gly Ser Ala  
 50 55 60  
 Ser Gly Trp His Asn Ile Thr Leu Ser Leu Thr Asp Cys Pro Val Glu

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65              70              75              80
Thr Ser Ala Val Thr Ala Ile Val Thr Gly Ser Thr Asp Asn Thr Gly
              85              90              95
Tyr Tyr Lys Asn Glu Gly Thr Ala Glu Asn Ile Gln Ile Glu Leu Arg
              100              105              110
Asp Asp Gln Asp Ala Ala Leu Lys Asn Gly Asp Ser Lys Thr Val Ile
              115              120              125
Val Asp Glu Ile Thr Arg Asn Ala Gln Phe Pro Leu Lys Ala Arg Ala
              130              135              140
Ile Thr Val Asn Gly Asn Ala Ser Gln Gly Thr Ile Glu Ala Leu Ile
145              150              155              160
Asn Val Ile Tyr Thr Trp Gln
              165

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<210> 298  
 <211> 176  
 <212> PRT  
 <213> E. Coli

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<400> 298
Met Lys Tyr Asn Asn Ile Ile Phe Leu Gly Leu Cys Leu Gly Leu Thr
1              5              10              15
Thr Tyr Ser Ala Leu Ser Ala Asp Ser Val Ile Lys Ile Ser Gly Arg
              20              25              30
Val Leu Asp Tyr Gly Cys Thr Val Ser Ser Asp Ser Leu Asn Phe Thr
              35              40              45
Val Asp Leu Gln Lys Asn Ser Ala Arg Gln Phe Pro Thr Thr Gly Ser
50              55              60
Thr Ser Pro Ala Val Pro Phe Gln Ile Thr Leu Ser Glu Cys Ser Lys
65              70              75              80
Gly Thr Thr Gly Val Arg Val Ala Phe Asn Gly Ile Glu Asp Ala Glu
              85              90              95
Asn Asn Thr Leu Leu Lys Leu Asp Glu Gly Ser Asn Thr Ala Ser Gly
              100              105              110
Leu Gly Ile Glu Ile Leu Asp Ala Asn Met Arg Pro Val Lys Leu Asn
              115              120              125
Asp Leu His Ala Gly Met Gln Trp Ile Pro Leu Val Pro Glu Gln Asn
130              135              140
Asn Ile Leu Pro Tyr Ser Ala Arg Leu Lys Ser Thr Gln Lys Ser Val
145              150              155              160
Asn Pro Gly Leu Val Arg Ala Ser Ala Thr Phe Thr Leu Glu Phe Gln
              165              170              175

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<210> 299  
 <211> 382  
 <212> PRT  
 <213> E. Coli

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<400> 299
Met Ser Gly Tyr Thr Val Lys Pro Pro Thr Gly Asp Thr Asn Glu Gln
1              5              10              15
Thr Gln Phe Ile Asp Tyr Phe Asn Leu Phe Tyr Ser Lys Arg Gly Gln
              20              25              30
Glu Gln Ile Ser Ile Ser Gln Gln Leu Gly Asn Tyr Gly Thr Thr Phe
              35              40              45
Phe Ser Ala Ser Arg Gln Ser Tyr Trp Asn Thr Ser Arg Ser Asp Gln
50              55              60

```

Gln Ile Ser Phe Gly Leu Asn Val Pro Phe Gly Asp Ile Thr Thr Ser  
 65 70 75 80  
 Leu Asn Tyr Ser Tyr Ser Asn Asn Ile Trp Gln Asn Asp Arg Asp His  
 85 90 95  
 Leu Leu Ala Phe Thr Leu Asn Val Pro Phe Ser His Trp Met Arg Thr  
 100 105 110  
 Asp Ser Gln Ser Ala Phe Arg Asn Ser Asn Ala Ser Tyr Ser Met Ser  
 115 120 125  
 Asn Asp Leu Lys Gly Gly Met Thr Asn Leu Ser Gly Val Tyr Gly Thr  
 130 135 140  
 Leu Leu Pro Asp Asn Asn Leu Asn Tyr Ser Val Gln Val Gly Asn Thr  
 145 150 155 160  
 His Gly Gly Asn Thr Ser Ser Gly Thr Ser Gly Tyr Ser Ser Leu Asn  
 165 170 175  
 Tyr Arg Gly Ala Tyr Gly Asn Thr Asn Val Gly Tyr Ser Arg Ser Gly  
 180 185 190  
 Asp Ser Ser Gln Ile Tyr Tyr Gly Met Ser Gly Gly Ile Ile Ala His  
 195 200 205  
 Ala Asp Gly Ile Thr Phe Gly Gln Pro Leu Gly Asp Thr Met Val Leu  
 210 215 220  
 Val Lys Ala Pro Gly Ala Asp Asn Val Lys Ile Glu Asn Gln Thr Gly  
 225 230 235 240  
 Ile His Thr Asp Trp Arg Gly Tyr Ala Ile Leu Pro Phe Ala Thr Glu  
 245 250 255  
 Tyr Arg Glu Asn Arg Val Ala Leu Asn Ala Asn Ser Leu Ala Asp Asn  
 260 265 270  
 Val Glu Leu Asp Glu Thr Val Val Thr Val Ile Pro Thr His Gly Ala  
 275 280 285  
 Ile Ala Arg Ala Thr Phe Asn Ala Gln Ile Gly Gly Lys Val Leu Met  
 290 295 300  
 Thr Leu Lys Tyr Gly Asn Lys Ser Val Pro Phe Gly Ala Ile Val Thr  
 305 310 315 320  
 His Gly Glu Asn Lys Asn Gly Ser Ile Val Ala Glu Asn Gly Gln Val  
 325 330 335  
 Tyr Leu Thr Gly Leu Pro Gln Ser Gly Gln Leu Gln Val Ser Trp Gly  
 340 345 350  
 Lys Asp Lys Asn Ser Asn Cys Ile Val Glu Tyr Lys Leu Pro Glu Val  
 355 360 365  
 Ser Pro Gly Thr Leu Leu Asn Gln Gln Thr Ala Ile Cys Arg  
 370 375 380

<210> 300  
 <211> 138  
 <212> PRT  
 <213> E. Coli

<400> 300  
 Met Ile Ala Ile Ala Asp Ile Leu Gln Ala Gly Glu Lys Leu Thr Ala  
 1 5 10 15  
 Val Ala Pro Phe Leu Ala Gly Ile Gln Asn Glu Glu Gln Tyr Thr Gln  
 20 25 30  
 Ala Leu Glu Leu Val Asp His Leu Leu Asn Asp Pro Glu Asn Pro  
 35 40 45  
 Leu Leu Asp Leu Val Cys Ala Lys Ile Thr Ala Trp Glu Glu Ser Ala  
 50 55 60  
 Pro Glu Phe Ala Glu Phe Asn Ala Met Ala Gln Ala Met Pro Gly Gly  
 65 70 75 80  
 Ile Ala Val Ile Arg Thr Leu Met Asp Gln Tyr Gly Leu Thr Leu Ser  
 85 90 95  
 Asp Leu Pro Glu Ile Gly Ser Lys Ser Met Val Ser Arg Val Leu Ser

100 105 110  
 Gly Lys Arg Lys Leu Thr Leu Glu His Ala Lys Lys Leu Ala Thr Arg  
 115 120 125  
 Phe Gly Ile Ser Pro Ala Leu Phe Ile Asp  
 130 135

<210> 301  
 <211> 104  
 <212> PRT  
 <213> E. Coli

<400> 301  
 Met His Leu Ile Thr Gln Lys Ala Leu Lys Asp Ala Ala Glu Lys Tyr  
 1 5 10 15  
 Pro Gln His Lys Thr Glu Leu Val Ala Leu Gly Asn Thr Ile Ala Lys  
 20 25 30  
 Gly Tyr Phe Lys Lys Pro Glu Ser Leu Lys Ala Val Phe Pro Ser Leu  
 35 40 45  
 Asp Asn Phe Lys Tyr Leu Asp Lys His Tyr Val Phe Asn Val Gly Gly  
 50 55 60  
 Asn Glu Leu Arg Val Val Ala Met Val Phe Phe Glu Ser Gln Lys Cys  
 65 70 75 80  
 Tyr Ile Arg Glu Val Met Thr His Lys Glu Tyr Asp Phe Phe Thr Ala  
 85 90 95  
 Val His Arg Thr Lys Gly Lys Lys  
 100

<210> 302  
 <211> 2383  
 <212> PRT  
 <213> E. Coli

<400> 302  
 Met Leu Ser Val Phe Thr Phe Phe Arg Cys Ala Arg Lys Gly Ala Phe  
 1 5 10 15  
 Met Leu Ala Arg Ser Gly Lys Val Ser Met Ala Thr Lys Lys Arg Ser  
 20 25 30  
 Gly Glu Glu Ile Asn Asp Arg Gln Ile Leu Cys Gly Met Gly Ile Lys  
 35 40 45  
 Leu Arg Arg Leu Thr Ala Gly Ile Cys Leu Ile Thr Gln Leu Ala Phe  
 50 55 60  
 Pro Met Ala Ala Ala Ala Gln Gly Val Val Asn Ala Ala Thr Gln Gln  
 65 70 75 80  
 Pro Val Pro Ala Gln Ile Ala Ile Ala Asn Ala Asn Thr Val Pro Tyr  
 85 90 95  
 Thr Leu Gly Ala Leu Glu Ser Ala Gln Ser Val Ala Glu Arg Phe Gly  
 100 105 110  
 Ile Ser Val Ala Glu Leu Arg Lys Leu Asn Gln Phe Arg Thr Phe Ala  
 115 120 125  
 Arg Ser Phe Asp Asn Val Arg Gln Gly Asp Glu Leu Asp Val Pro Ala  
 130 135 140  
 Gln Val Ser Glu Lys Lys Leu Thr Pro Pro Pro Gly Asn Ser Ser Asp  
 145 150 155 160  
 Asn Leu Glu Gln Gln Ile Ala Ser Thr Ser Gln Gln Ile Gly Ser Leu  
 165 170 175  
 Leu Ala Glu Asp Met Asn Ser Glu Gln Ala Ala Asn Met Ala Arg Gly  
 180 185 190  
 Trp Ala Ser Ser Gln Ala Ser Gly Ala Met Thr Asp Trp Leu Ser Arg

|                                 |                                     |     |
|---------------------------------|-------------------------------------|-----|
| 195                             | 200                                 | 205 |
| Phe Gly Thr Ala Arg Ile Thr     | Leu Gly Val Asp Glu Asp Phe Ser Leu |     |
| 210                             | 215                                 | 220 |
| Lys Asn Ser Gln Phe Asp Phe     | Leu His Pro Trp Tyr Glu Thr Pro Asp |     |
| 225                             | 230                                 | 235 |
| Asn Leu Phe Phe Ser Gln His Thr | Leu His Arg Thr Asp Glu Arg Thr     |     |
| 245                             | 250                                 | 255 |
| Gln Ile Asn Asn Gly Leu Gly Trp | Arg His Phe Thr Pro Thr Trp Met     |     |
| 260                             | 265                                 | 270 |
| Ser Gly Ile Asn Phe Phe Phe     | Asp His Asp Leu Ser Arg Tyr His Ser |     |
| 275                             | 280                                 | 285 |
| Arg Ala Gly Ile Gly Ala Glu     | Tyr Trp Arg Asp Tyr Leu Lys Leu Ser |     |
| 290                             | 295                                 | 300 |
| Ser Asn Gly Tyr Leu Arg Leu Thr | Asn Trp Arg Ser Ala Pro Glu Leu     |     |
| 305                             | 310                                 | 315 |
| Asp Asn Asp Tyr Glu Ala Arg Pro | Ala Asn Gly Trp Asp Val Arg Ala     |     |
| 325                             | 330                                 | 335 |
| Glu Ser Trp Leu Pro Ala Trp Pro | His Leu Gly Gly Lys Leu Val Tyr     |     |
| 340                             | 345                                 | 350 |
| Glu Gln Tyr Tyr Gly Asp Glu Val | Ala Leu Phe Asp Lys Asp Asp Arg     |     |
| 355                             | 360                                 | 365 |
| Gln Ser Asn Pro His Ala Ile Thr | Ala Gly Leu Asn Tyr Thr Pro Phe     |     |
| 370                             | 375                                 | 380 |
| Pro Leu Met Thr Phe Ser Ala Glu | Gln Arg Gln Gly Lys Gln Gly Glu     |     |
| 385                             | 390                                 | 395 |
| Asn Asp Thr Arg Phe Ala Val Asp | Phe Thr Trp Gln Pro Gly Ser Ala     |     |
| 405                             | 410                                 | 415 |
| Met Gln Lys Gln Leu Asp Pro Asn | Glu Val Ala Ala Arg Arg Ser Leu     |     |
| 420                             | 425                                 | 430 |
| Ala Gly Ser Arg Tyr Asp Leu Val | Asp Arg Asn Asn Asn Ile Val Leu     |     |
| 435                             | 440                                 | 445 |
| Glu Tyr Arg Lys Lys Glu Leu Val | Arg Leu Thr Leu Thr Asp Pro Val     |     |
| 450                             | 455                                 | 460 |
| Thr Gly Lys Ser Gly Glu Val Lys | Ser Leu Val Ser Ser Leu Gln Thr     |     |
| 465                             | 470                                 | 475 |
| Lys Tyr Ala Leu Lys Gly Tyr Asn | Val Glu Ala Thr Ala Leu Glu Ala     |     |
| 485                             | 490                                 | 495 |
| Ala Gly Gly Lys Val Val Thr Thr | Gly Lys Asp Ile Leu Val Thr Leu     |     |
| 500                             | 505                                 | 510 |
| Pro Ala Tyr Arg Phe Thr Ser Thr | Pro Glu Thr Asp Asn Thr Trp Pro     |     |
| 515                             | 520                                 | 525 |
| Ile Glu Val Thr Ala Glu Asp Val | Lys Gly Asn Leu Ser Asn Arg Glu     |     |
| 530                             | 535                                 | 540 |
| Gln Ser Met Val Val Val Gln Ala | Pro Thr Leu Ser Gln Lys Asp Ser     |     |
| 545                             | 550                                 | 555 |
| Ser Val Ser Leu Ser Thr Gln Thr | Leu Asn Ala Asp Ser His Ser Thr     |     |
| 565                             | 570                                 | 575 |
| Ala Thr Leu Thr Phe Ile Ala His | Asp Ala Ala Gly Asn Pro Val Val     |     |
| 580                             | 585                                 | 590 |
| Gly Leu Val Leu Ser Thr Arg His | Glu Gly Val Gln Asp Ile Thr Leu     |     |
| 595                             | 600                                 | 605 |
| Ser Asp Trp Lys Asp Asn Gly Asp | Gly Ser Tyr Thr Gln Ile Leu Thr     |     |
| 610                             | 615                                 | 620 |
| Thr Gly Ala Met Ser Gly Thr Leu | Thr Leu Met Pro Gln Leu Asn Gly     |     |
| 625                             | 630                                 | 635 |
| Val Asp Ala Ala Lys Ala Pro Ala | Val Val Asn Ile Ile Ser Val Ser     |     |
| 645                             | 650                                 | 655 |
| Ser Ser Arg Thr His Ser Ser Ile | Lys Ile Asp Lys Asp Arg Tyr Leu     |     |
| 660                             | 665                                 | 670 |
| Ser Gly Asn Pro Ile Glu Val Thr | Val Glu Leu Arg Asp Glu Asn Asp     |     |
| 675                             | 680                                 | 685 |

Lys Pro Val Lys Glu Gln Lys Gln Gln Leu Asn Asn Ala Val Ser Ile  
 690 695 700  
 Asp Asn Val Lys Pro Gly Val Thr Thr Asp Trp Lys Glu Thr Ala Asp  
 705 710 715 720  
 Gly Val Tyr Lys Ala Thr Tyr Thr Ala Tyr Thr Lys Gly Ser Gly Leu  
 725 730 735  
 Thr Ala Lys Leu Leu Met Gln Asn Trp Asn Glu Asp Leu His Thr Ala  
 740 745 750  
 Gly Phe Ile Ile Asp Ala Asn Pro Gln Ser Ala Lys Ile Ala Thr Leu  
 755 760 765  
 Ser Ala Ser Asn Asn Gly Val Leu Ala Asn Glu Asn Ala Ala Asn Thr  
 770 775 780  
 Val Ser Val Asn Val Ala Asp Glu Gly Ser Asn Pro Ile Asn Asp His  
 785 790 795 800  
 Thr Val Thr Phe Ala Val Leu Ser Gly Ser Ala Thr Ser Phe Asn Asn  
 805 810 815  
 Gln Asn Thr Ala Lys Thr Asp Val Asn Gly Leu Ala Thr Phe Asp Leu  
 820 825 830  
 Lys Ser Ser Lys Gln Glu Asp Asn Thr Val Glu Val Thr Leu Glu Asn  
 835 840 845  
 Gly Val Lys Gln Thr Leu Ile Val Ser Phe Val Gly Asp Ser Ser Thr  
 850 855 860  
 Ala Gln Val Asp Leu Gln Lys Ser Lys Asn Glu Val Val Ala Asp Gly  
 865 870 875 880  
 Asn Asp Ser Val Thr Met Thr Ala Thr Val Arg Asp Ala Lys Gly Asn  
 885 890 895  
 Leu Leu Asn Asp Val Met Val Thr Phe Asn Val Asn Ser Ala Glu Ala  
 900 905 910  
 Lys Leu Ser Gln Thr Glu Val Asn Ser His Asp Gly Ile Ala Thr Ala  
 915 920 925  
 Thr Leu Thr Ser Leu Lys Asn Gly Asp Tyr Arg Val Thr Ala Ser Val  
 930 935 940  
 Ser Ser Gly Ser Gln Ala Asn Gln Gln Val Asn Phe Ile Gly Asp Gln  
 945 950 955 960  
 Ser Thr Ala Ala Leu Thr Leu Ser Val Pro Ser Gly Asp Ile Thr Val  
 965 970 975  
 Thr Asn Thr Ala Pro Gln Tyr Met Thr Ala Thr Leu Gln Asp Lys Asn  
 980 985 990  
 Gly Asn Pro Leu Lys Asp Lys Glu Ile Thr Phe Ser Val Pro Asn Asp  
 995 1000 1005  
 Val Ala Ser Lys Phe Ser Ile Ser Asn Gly Gly Lys Gly Met Thr Asp  
 1010 1015 1020  
 Ser Asn Gly Val Ala Ile Ala Ser Leu Thr Gly Thr Leu Ala Gly Thr  
 1025 1030 1035 1040  
 His Met Ile Met Ala Arg Leu Ala Asn Ser Asn Val Ser Asp Ala Gln  
 1045 1050 1055  
 Pro Met Thr Phe Val Ala Asp Lys Asp Arg Ala Val Val Val Leu Gln  
 1060 1065 1070  
 Thr Ser Lys Ala Glu Ile Ile Gly Asn Gly Val Asp Glu Thr Thr Leu  
 1075 1080 1085  
 Thr Ala Thr Val Lys Asp Pro Ser Asn His Pro Val Ala Gly Ile Thr  
 1090 1095 1100  
 Val Asn Phe Thr Met Pro Gln Asp Val Ala Ala Asn Phe Thr Leu Glu  
 1105 1110 1115 1120  
 Asn Asn Gly Ile Ala Ile Thr Gln Ala Asn Gly Glu Ala His Val Thr  
 1125 1130 1135  
 Leu Lys Gly Lys Lys Ala Gly Thr His Thr Val Thr Ala Thr Leu Gly  
 1140 1145 1150  
 Asn Asn Asn Thr Ser Asp Ser Gln Pro Val Thr Phe Val Ala Asp Lys  
 1155 1160 1165  
 Ala Ser Ala Gln Val Val Leu Gln Ile Ser Lys Asp Glu Ile Thr Gly

|   |      |      |
|---|------|------|
| 1170  | 1175 | 1180 |
| Asn Gly Val Asp Ser Ala Thr Leu Thr Ala Thr Val Lys Asp Gln Phe |      |      |
| 1185  | 1190 | 1195 |
| Asp Asn Glu Val Asn Asn Leu Pro Val Thr Phe Ser Ser Ala Ser Ser |      | 1200 |
|   | 1205 | 1210 |
| Gly Leu Thr Leu Thr Pro Gly Val Ser Asn Thr Asn Glu Ser Gly Ile |      | 1215 |
|   | 1220 | 1225 |
| Ala Gln Ala Thr Leu Ala Gly Val Ala Phe Gly Glu Lys Thr Val Thr |      | 1230 |
|   | 1235 | 1240 |
| Ala Ser Leu Ala Asn Asn Gly Ala Ser Asp Asn Lys Thr Val His Phe |      | 1245 |
|   | 1250 | 1255 |
| Ile Gly Asp Thr Ala Ala Lys Ile Ile Glu Leu Ala Pro Val Pro     |      | 1260 |
|   | 1265 | 1270 |
| Asp Ser Ile Ile Ala Gly Thr Pro Gln Asn Ser Ser Gly Ser Val Ile |      | 1275 |
|   | 1285 | 1290 |
| Thr Ala Thr Val Val Asp Asn Asn Gly Phe Pro Val Lys Gly Val Thr |      | 1295 |
|   | 1300 | 1305 |
| Val Asn Phe Thr Ser Asn Ala Ala Thr Ala Glu Met Thr Asn Gly Gly |      | 1310 |
|   | 1315 | 1320 |
| Gln Ala Val Thr Asn Glu Gln Gly Lys Ala Thr Val Thr Tyr Thr Asn |      | 1325 |
|   | 1330 | 1335 |
| Thr Arg Ser Ser Ile Glu Ser Gly Ala Arg Pro Asp Thr Val Glu Ala |      | 1340 |
|   | 1345 | 1350 |
| Ser Leu Glu Asn Gly Ser Ser Thr Leu Ser Thr Ser Ile Asn Val Asn |      | 1355 |
|   | 1365 | 1370 |
| Ala Asp Ala Ser Thr Ala His Leu Thr Leu Leu Gln Ala Leu Phe Asp |      | 1375 |
|   | 1380 | 1385 |
| Thr Val Ser Ala Gly Glu Thr Thr Ser Leu Tyr Ile Glu Val Lys Asp |      | 1390 |
|   | 1395 | 1400 |
| Asn Tyr Gly Asn Gly Val Pro Gln Gln Glu Val Thr Leu Ser Val Ser |      | 1405 |
|   | 1410 | 1415 |
| Pro Ser Glu Gly Val Thr Pro Ser Asn Asn Ala Ile Tyr Thr Thr Asn |      | 1420 |
|   | 1425 | 1430 |
| His Asp Gly Asn Phe Tyr Ala Ser Phe Thr Ala Thr Lys Ala Gly Val |      | 1435 |
|   | 1445 | 1450 |
| Tyr Gln Leu Thr Ala Thr Leu Glu Asn Gly Asp Ser Met Gln Gln Thr |      | 1455 |
|   | 1460 | 1465 |
| Val Thr Tyr Val Pro Asn Val Ala Asn Ala Glu Ile Thr Leu Ala Ala |      | 1470 |
|   | 1475 | 1480 |
| Ser Lys Asp Pro Val Ile Ala Asp Asn Asn Asp Leu Thr Thr Leu Thr |      | 1485 |
|   | 1490 | 1495 |
| Ala Thr Val Ala Asp Thr Glu Gly Asn Ala Ile Ala Asn Thr Glu Val |      | 1500 |
|   | 1505 | 1510 |
| Thr Phe Thr Leu Pro Glu Asp Val Lys Ala Asn Phe Thr Leu Ser Asp |      | 1515 |
|   | 1525 | 1530 |
| Gly Gly Lys Val Ile Thr Asp Ala Glu Gly Lys Ala Lys Val Thr Leu |      | 1535 |
|   | 1540 | 1545 |
| Lys Gly Thr Lys Ala Gly Ala His Thr Val Thr Ala Ser Met Thr Gly |      | 1550 |
|   | 1555 | 1560 |
| Gly Lys Ser Glu Gln Leu Val Val Asn Phe Ile Ala Asp Thr Leu Thr |      | 1565 |
|   | 1570 | 1575 |
| Ala Gln Val Asn Leu Asn Val Thr Glu Asp Asn Phe Ile Ala Asn Asn |      | 1580 |
|   | 1585 | 1590 |
| Val Gly Met Thr Arg Leu Gln Ala Thr Val Thr Asp Gly Asn Gly Asn |      | 1595 |
|   | 1605 | 1610 |
| Pro Leu Ala Asn Glu Ala Val Thr Phe Thr Leu Pro Ala Asp Val Ser |      | 1615 |
|   | 1620 | 1625 |
| Ala Ser Phe Thr Leu Gly Gln Gly Gly Ser Ala Ile Thr Asp Ile Asn |      | 1630 |
|   | 1635 | 1640 |
| Gly Lys Ala Glu Val Thr Leu Ser Gly Thr Lys Ser Gly Thr Tyr Pro |      | 1645 |
|   | 1650 | 1655 |
|   |      | 1660 |



Val Thr Val Ser Val Asn Asn Tyr Gly Val Ser Asp Thr Lys Gln Val  
 1665 1670 1675 1680  
 Thr Leu Ile Ala Asp Ala Gly Thr Ala Lys Leu Ala Ser Leu Thr Ser  
 1685 1690 1695  
 Val Tyr Ser Phe Val Val Ser Thr Thr Glu Gly Ala Thr Met Thr Ala  
 1700 1705 1710  
 Ser Val Thr Asp Ala Asn Gly Asn Pro Val Glu Gly Ile Lys Val Asn  
 1715 1720 1725  
 Phe Arg Gly Thr Ser Val Thr Leu Ser Ser Thr Ser Val Glu Thr Asp  
 1730 1735 1740  
 Asp Arg Gly Phe Ala Glu Ile Leu Val Thr Ser Thr Glu Val Gly Leu  
 1745 1750 1755 1760  
 Lys Thr Val Ser Ala Ser Leu Ala Asp Lys Pro Thr Glu Val Ile Ser  
 1765 1770 1775  
 Arg Leu Leu Asn Ala Ser Ala Asp Val Asn Ser Ala Thr Ile Thr Ser  
 1780 1785 1790  
 Leu Glu Ile Pro Glu Gly Gln Val Met Val Ala Gln Asp Val Ala Val  
 1795 1800 1805  
 Lys Ala His Val Asn Asp Gln Phe Gly Asn Pro Val Ala His Gln Pro  
 1810 1815 1820  
 Val Thr Phe Ser Ala Glu Pro Ser Ser Gln Met Ile Ile Ser Gln Asn  
 1825 1830 1835 1840  
 Thr Val Ser Thr Asn Thr Gln Gly Val Ala Glu Val Thr Met Thr Pro  
 1845 1850 1855  
 Glu Arg Asn Gly Ser Tyr Met Val Lys Ala Ser Leu Pro Asn Gly Ala  
 1860 1865 1870  
 Ser Leu Glu Lys Gln Leu Glu Ala Ile Asp Glu Lys Leu Thr Leu Thr  
 1875 1880 1885  
 Ala Ser Ser Pro Leu Ile Gly Val Tyr Ala Pro Thr Gly Ala Thr Leu  
 1890 1895 1900  
 Thr Ala Thr Leu Thr Ser Ala Asn Gly Thr Pro Val Glu Gly Gln Val  
 1905 1910 1915 1920  
 Ile Asn Phe Ser Val Thr Pro Glu Gly Ala Thr Leu Ser Gly Gly Lys  
 1925 1930 1935  
 Val Arg Thr Asn Ser Ser Gly Gln Ala Pro Val Val Leu Thr Ser Asn  
 1940 1945 1950  
 Lys Val Gly Thr Tyr Thr Val Thr Ala Ser Phe His Asn Gly Val Thr  
 1955 1960 1965  
 Ile Gln Thr Gln Thr Thr Val Lys Val Thr Gly Asn Ser Ser Thr Ala  
 1970 1975 1980  
 His Val Ala Ser Phe Ile Ala Asp Pro Ser Thr Ile Ala Ala Thr Asn  
 1985 1990 1995 2000  
 Thr Asp Leu Ser Thr Leu Lys Ala Thr Val Glu Asp Gly Ser Gly Asn  
 2005 2010 2015  
 Leu Ile Glu Gly Leu Thr Val Tyr Phe Ala Leu Lys Ser Gly Ser Ala  
 2020 2025 2030  
 Thr Leu Thr Ser Leu Thr Ala Val Thr Asp Gln Asn Gly Ile Ala Thr  
 2035 2040 2045  
 Thr Ser Val Lys Gly Ala Met Thr Gly Ser Val Thr Val Ser Ala Val  
 2050 2055 2060  
 Thr Thr Ala Gly Gly Met Gln Thr Val Asp Ile Thr Leu Val Ala Gly  
 2065 2070 2075 2080  
 Pro Ala Asp Thr Ser Gln Ser Val Leu Lys Ser Asn Arg Ser Ser Leu  
 2085 2090 2095  
 Lys Gly Asp Tyr Thr Asp Ser Ala Glu Leu Arg Leu Val Leu His Asp  
 2100 2105 2110  
 Ile Ser Gly Asn Pro Ile Lys Val Ser Glu Gly Met Glu Phe Val Gln  
 2115 2120 2125  
 Ser Gly Thr Asn Val Pro Tyr Ile Lys Ile Ser Ala Ile Asp Tyr Ser  
 2130 2135 2140  
 Leu Asn Ile Asn Gly Asp Tyr Lys Ala Thr Val Thr Gly Gly Gly Glu

2145                      2150                      2155                      2160  
 Gly Ile Ala Thr Leu Ile Pro Val Leu Asn Gly Val His Gln Ala Gly  
                                  2165                      2170                      2175  
 Leu Ser Thr Thr Ile Gln Phe Thr Arg Ala Glu Asp Lys Ile Met Ser  
                                  2180                      2185                      2190  
 Gly Thr Val Ser Val Asn Gly Thr Asp Leu Pro Thr Thr Thr Phe Pro  
                                  2195                      2200                      2205  
 Ser Gln Gly Phe Thr Gly Ala Tyr Tyr Gln Leu Asn Asn Asp Asn Phe  
                                  2210                      2215                      2220  
 Ala Pro Gly Lys Thr Ala Ala Asp Tyr Glu Phe Ser Ser Ser Ala Ser  
                                  2225                      2230                      2235                      2240  
 Trp Val Asp Val Asp Ala Thr Gly Lys Val Thr Phe Lys Asn Val Gly  
                                  2245                      2250                      2255  
 Ser Asn Ser Glu Arg Ile Thr Ala Thr Pro Lys Ser Gly Gly Pro Ser  
                                  2260                      2265                      2270  
 Tyr Val Tyr Glu Ile Arg Val Lys Ser Trp Trp Val Asn Ala Gly Glu  
                                  2275                      2280                      2285  
 Ala Phe Met Ile Tyr Ser Leu Ala Glu Asn Phe Cys Ser Ser Asn Gly  
                                  2290                      2295                      2300  
 Tyr Thr Leu Pro Arg Ala Asn Tyr Leu Asn His Cys Ser Ser Arg Gly  
                                  2305                      2310                      2315                      2320  
 Ile Gly Ser Leu Tyr Ser Glu Trp Gly Asp Met Gly His Tyr Thr Thr  
                                  2325                      2330                      2335  
 Asp Ala Gly Phe Gln Ser Asn Met Tyr Trp Ser Ser Ser Pro Ala Asn  
                                  2340                      2345                      2350  
 Ser Ser Glu Gln Tyr Val Val Ser Leu Ala Thr Gly Asp Gln Ser Val  
                                  2355                      2360                      2365  
 Phe Glu Lys Leu Gly Phe Ala Tyr Ala Thr Cys Tyr Lys Asn Leu  
                                  2370                      2375                      2380

<210> 303  
 <211> 61  
 <212> PRT  
 <213> E. Coli

<400> 303  
 Met Ser Lys Gly Ala Leu Tyr Glu Phe Asn Asn Pro Asp Gln Leu Lys  
   1                                  5                                  10                                  15  
 Ile Pro Leu Pro His Lys His Ile Ala Ser Thr Phe Asn Asp Ile Met  
                                   20                                  25                                  30  
 Ser Lys Asp Val Gly Tyr Ala Tyr Val Ser Leu Leu Tyr Ala Cys Pro  
                                   35                                  40                                  45  
 Leu Lys Thr His Ser Leu Arg Leu Asn Pro Phe Ser Lys  
   50                                  55                                  60

<210> 304  
 <211> 398  
 <212> PRT  
 <213> E. Coli

<400> 304  
 Met Gln Val Ala Glu Gln Arg Ile Gln Leu Ala Glu Ala Gln Ala Lys  
   1                                  5                                  10                                  15  
 Ala Val Ala Thr Gln Asp Gly Pro Gln Ile Asp Phe Ser Ala Asp Met  
                                   20                                  25                                  30  
 Glu Arg Gln Lys Met Ser Ala Glu Gly Leu Met Gly Pro Phe Ala Leu  
                                   35                                  40                                  45  
 Asn Asp Pro Ala Ala Gly Thr Thr Gly Pro Trp Tyr Thr Asn Gly Thr  
   50                                  55                                  60

Phe Gly Leu Thr Ala Gly Trp His Leu Asp Ile Trp Gly Lys Asn Arg  
 65 70 75 80  
 Ala Glu Val Thr Ala Arg Leu Gly Thr Val Lys Ala Arg Ala Ala Glu  
 85 90 95  
 Arg Glu Gln Thr Arg Gln Leu Leu Ala Gly Ser Val Ala Arg Leu Tyr  
 100 105 110  
 Trp Glu Trp Gln Thr Gln Ala Ala Leu Asn Thr Val Leu Gln Gln Ile  
 115 120 125  
 Glu Lys Glu Gln Asn Thr Ile Ile Ala Thr Asp Arg Gln Leu Tyr Gln  
 130 135 140  
 Asn Gly Ile Thr Ser Ser Val Glu Gly Val Glu Thr Asp Ile Asn Ala  
 145 150 155 160  
 Ser Lys Thr Arg Gln Gln Leu Asn Asp Val Ala Gly Lys Met Lys Ile  
 165 170 175  
 Ile Glu Ala Arg Leu Ser Ala Leu Thr Asn Asn Gln Thr Lys Ser Leu  
 180 185 190  
 Lys Leu Lys Pro Val Ala Leu Pro Lys Val Ala Ser Gln Leu Pro Asp  
 195 200 205  
 Glu Leu Gly Tyr Ser Leu Leu Ala Arg Arg Ala Asp Leu Gln Ala Ala  
 210 215 220  
 His Trp Tyr Val Glu Ser Ser Leu Ser Thr Ile Asp Ala Ala Lys Ala  
 225 230 235 240  
 Ala Phe Tyr Pro Asp Ile Asn Leu Met Ala Phe Leu Gln Gln Asp Ala  
 245 250 255  
 Leu His Leu Ser Asp Leu Phe Arg His Ser Ala Gln Gln Met Gly Val  
 260 265 270  
 Thr Ala Gly Leu Thr Leu Pro Ile Phe Asp Ser Gly Arg Leu Asn Ala  
 275 280 285  
 Asn Leu Asp Ile Ala Lys Ala Glu Ser Asn Leu Ser Ile Ala Ser Tyr  
 290 295 300  
 Asn Lys Ala Val Val Glu Ala Val Asn Asp Val Ala Arg Ala Ala Ser  
 305 310 315 320  
 Gln Val Gln Thr Leu Ala Glu Lys Asn Gln His Gln Ala Gln Ile Glu  
 325 330 335  
 Arg Asp Ala Leu Arg Val Val Gly Leu Ala Gln Ala Arg Phe Asn Ala  
 340 345 350  
 Gly Ile Ile Ala Gly Ser Arg Val Ser Glu Ala Arg Ile Pro Ala Leu  
 355 360 365  
 Arg Glu Arg Ala Asn Gly Leu Leu Leu Gln Gly Gln Trp Leu Asp Ala  
 370 375 380  
 Ser Ile Gln Leu Thr Gly Ala Leu Gly Gly Gly Tyr Lys Arg  
 385 390 395

<210> 305  
 <211> 96  
 <212> PRT  
 <213> E. Coli

<400> 305  
 Met Tyr Cys His Ala Lys Leu Lys Asn Ile Ser Gln His Thr Val Ile  
 1 5 10 15  
 Ser Ala His Leu Phe Leu Pro Asp Tyr Ser Pro Met Asn Arg Asp Ser  
 20 25 30  
 Phe Tyr Pro Ala Ile Ala Cys Phe Pro Leu Leu Leu Met Leu Ala Gly  
 35 40 45  
 Cys Ala Pro Met His Glu Thr Arg Gln Ala Leu Ser Gln Gln Thr Pro  
 50 55 60  
 Ala Ala Gln Val Asp Thr Ala Leu Pro Thr Ala Leu Lys Met Val Gly  
 65 70 75 80  
 Gln Thr Ala Asn Gly Gly Trp Ser Ile Thr Ile Ile Asn Ser Leu Pro

85

90

95

<210> 306  
 <211> 315  
 <212> PRT  
 <213> E. Coli

<400> 306

```

Met Arg Val Leu Leu Ala Pro Met Glu Gly Val Leu Asp Ser Leu Val
 1      5      10      15
Arg Glu Leu Leu Thr Glu Val Asn Asp Tyr Asp Leu Cys Ile Thr Glu
 20      25      30
Phe Val Arg Val Val Asp Gln Leu Pro Val Lys Val Phe His Arg
 35      40      45
Ile Cys Pro Glu Leu Gln Asn Ala Ser Arg Thr Pro Ser Gly Thr Leu
 50      55      60
Val Arg Val Gln Leu Leu Gly Gln Phe Pro Gln Trp Leu Ala Glu Asn
 65      70      75      80
Ala Ala Arg Ala Val Glu Leu Gly Ser Trp Gly Val Asp Leu Asn Cys
 85      90      95
Gly Cys Pro Ser Lys Thr Val Asn Gly Ser Gly Gly Gly Ala Thr Leu
100      105      110
Leu Lys Asp Pro Glu Leu Ile Tyr Gln Gly Ala Lys Ala Met Arg Glu
115      120      125
Ala Val Pro Ala His Leu Pro Val Ser Val Lys Val Arg Leu Gly Trp
130      135      140
Asp Ser Gly Glu Lys Lys Phe Glu Ile Ala Asp Ala Val Gln Gln Ala
145      150      155      160
Gly Ala Thr Glu Leu Val Val His Gly Arg Thr Lys Glu Gln Gly Tyr
165      170      175
Arg Ala Glu His Ile Asp Trp Gln Ala Ile Gly Asp Ile Arg Gln Arg
180      185      190
Leu Asn Ile Pro Val Ile Ala Asn Gly Glu Ile Trp Asp Trp Gln Ser
195      200      205
Ala Gln Gln Cys Met Ala Ile Ser Gly Cys Asp Ala Val Met Ile Gly
210      215      220
Arg Gly Ala Leu Asn Ile Pro Asn Leu Ser Arg Val Val Lys Tyr Asn
225      230      235      240
Glu Pro Arg Met Pro Trp Pro Glu Val Val Ala Leu Leu Gln Lys Tyr
245      250      255
Thr Arg Leu Glu Lys Gln Gly Asp Thr Gly Leu Tyr His Val Ala Arg
260      265      270
Ile Lys Gln Trp Leu Ser Tyr Leu Arg Lys Glu Tyr Asp Glu Ala Thr
275      280      285
Glu Leu Phe Gln His Val Arg Val Leu Asn Asn Ser Pro Asp Ile Ala
290      295      300
Arg Ala Ile Gln Ala Ile Asp Ile Glu Lys Leu
305      310      315

```

<210> 307  
 <211> 296  
 <212> PRT  
 <213> E. Coli

<400> 307

```

Met Thr Ile Ser Thr Thr Ser Thr Pro His Asp Ala Val Phe Lys Ser
 1      5      10      15
Phe Leu Arg His Pro Asp Thr Ala Arg Asp Phe Ile Asp Ile His Leu
 20      25      30

```

```

Pro Ala Pro Leu Arg Lys Leu Cys Asp Leu Thr Thr Leu Lys Leu Glu
   35           40           45
Pro Asn Ser Phe Ile Asp Glu Asp Leu Arg Gln Tyr Tyr Ser Asp Leu
   50           55           60
Leu Trp Ser Val Lys Thr Gln Glu Gly Val Gly Tyr Ile Tyr Val Val
   65           70           75           80
Ile Glu His Gln Ser Lys Pro Glu Glu Leu Met Ala Phe Arg Met Met
   85           90           95
Arg Tyr Ser Ile Ala Ala Met Gln Asn His Leu Asp Ala Gly Tyr Lys
  100          105          110
Glu Leu Pro Leu Val Leu Pro Met Leu Phe Tyr His Gly Cys Arg Ser
  115          120          125
Pro Tyr Pro Tyr Ser Leu Cys Trp Leu Asp Glu Phe Ala Glu Pro Ala
  130          135          140
Ile Ala Arg Lys Ile Tyr Ser Ser Ala Phe Pro Leu Val Asp Ile Thr
  145          150          155          160
Val Val Pro Asp Asp Glu Ile Met Gln His Arg Lys Met Ala Leu Leu
  165          170          175
Glu Leu Ile Gln Lys His Ile Arg Gln Arg Asp Leu Leu Gly Leu Val
  180          185          190
Asp Gln Ile Val Ser Leu Leu Val Thr Gly Asn Thr Asn Asp Arg Gln
  195          200          205
Leu Lys Ala Leu Phe Asn Tyr Val Leu Gln Thr Gly Asp Ala Gln Arg
  210          215          220
Phe Arg Ala Phe Ile Gly Glu Ile Ala Glu Arg Ala Pro Gln Glu Lys
  225          230          235          240
Glu Lys Leu Met Thr Ile Ala Asp Arg Leu Arg Glu Glu Gly Ala Met
  245          250          255
Gln Gly Lys His Glu Glu Ala Leu Arg Ile Ala Gln Glu Met Leu Asp
  260          265          270
Arg Gly Leu Asp Arg Glu Leu Val Met Met Val Thr Arg Leu Ser Pro
  275          280          285
Asp Asp Leu Ile Ala Gln Ser His
  290          295

```

<210> 308  
 <211> 555  
 <212> PRT  
 <213> E. Coli

<400> 308

```

<400> 3
Met Ala Gln Phe Val Tyr Thr Met His Arg Val Gly Lys Val Val Pro
   1           5           10          15
Pro Lys Arg His Ile Leu Lys Asn Ile Ser Leu Ser Phe Phe Pro Gly
  20          25          30
Ala Lys Ile Gly Val Leu Gly Leu Asn Gly Ala Gly Lys Ser Thr Leu
  35          40          45
Leu Arg Ile Met Ala Gly Ile Asp Lys Asp Ile Glu Gly Glu Ala Arg
  50          55          60
Pro Gln Pro Asp Ile Lys Ile Gly Tyr Leu Pro Gln Glu Pro Gln Leu
  65          70          75          80
Asn Pro Glu His Thr Val Arg Glu Ser Ile Glu Glu Ala Val Ser Glu
  85          90          95
Val Val Asn Ala Leu Lys Arg Leu Asp Glu Val Tyr Ala Leu Tyr Ala
 100          105          110
Asp Pro Asp Ala Asp Phe Asp Lys Leu Ala Ala Glu Gln Gly Arg Leu
 115          120          125
Glu Glu Ile Ile Gln Ala His Asp Gly His Asn Leu Asn Val Gln Leu
 130          135          140

```

Glu Arg Ala Ala Asp Ala Leu Arg Leu Pro Asp Trp Asp Ala Lys Ile  
 145 150 155 160  
 Ala Asn Leu Ser Gly Gly Glu Arg Arg Arg Val Ala Leu Cys Arg Leu  
 165 170 175  
 Leu Leu Glu Lys Pro Asp Met Leu Leu Leu Asp Glu Pro Thr Asn His  
 180 185 190  
 Leu Asp Ala Glu Ser Val Ala Trp Leu Glu Arg Phe Leu His Asp Phe  
 195 200 205  
 Glu Gly Thr Val Val Ala Ile Thr His Asp Arg Tyr Phe Leu Asp Asn  
 210 215 220  
 Val Ala Gly Trp Ile Leu Glu Leu Asp Arg Gly Glu Gly Ile Pro Trp  
 225 230 235 240  
 Glu Gly Asn Tyr Ser Ser Trp Leu Glu Gln Lys Asp Gln Arg Leu Ala  
 245 250 255  
 Gln Glu Ala Ser Gln Glu Ala Ala Arg Arg Lys Ser Ile Glu Lys Glu  
 260 265 270  
 Leu Glu Trp Val Arg Gln Gly Thr Lys Gly Arg Gln Ser Lys Gly Lys  
 275 280 285  
 Ala Arg Leu Ala Arg Phe Glu Glu Leu Asn Ser Thr Glu Tyr Gln Lys  
 290 295 300  
 Arg Asn Glu Thr Asn Glu Leu Phe Ile Pro Pro Gly Pro Arg Leu Gly  
 305 310 315 320  
 Asp Lys Val Leu Glu Val Ser Asn Leu Arg Lys Ser Tyr Gly Asp Arg  
 325 330 335  
 Leu Leu Ile Asp Asp Leu Ser Phe Ser Ile Pro Lys Gly Ala Ile Val  
 340 345 350  
 Gly Ile Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Phe Arg Met  
 355 360 365  
 Ile Ser Gly Gln Glu Gln Pro Asp Ser Gly Thr Ile Thr Leu Gly Glu  
 370 375 380  
 Thr Val Lys Leu Ala Ser Val Asp Gln Phe Arg Asp Ser Met Asp Asn  
 385 390 395 400  
 Ser Lys Thr Val Trp Glu Glu Val Ser Gly Gly Leu Asp Ile Met Lys  
 405 410 415  
 Ile Gly Asn Thr Glu Met Pro Ser Arg Ala Tyr Val Gly Arg Phe Asn  
 420 425 430  
 Phe Lys Gly Val Asp Gln Gly Lys Arg Val Gly Glu Leu Ser Gly Gly  
 435 440 445  
 Glu Arg Gly Arg Leu His Leu Ala Lys Leu Leu Gln Val Gly Gly Asn  
 450 455 460  
 Met Leu Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp Ile Glu Thr Leu  
 465 470 475 480  
 Arg Ala Leu Glu Asn Ala Leu Leu Glu Phe Pro Gly Cys Ala Met Val  
 485 490 495  
 Ile Ser His Asp Arg Trp Phe Leu Asp Arg Ile Ala Thr His Ile Leu  
 500 505 510  
 Asp Tyr Gln Asp Glu Gly Lys Val Glu Phe Phe Glu Gly Asn Phe Thr  
 515 520 525  
 Glu Tyr Glu Glu Tyr Lys Lys Arg Thr Leu Gly Ala Asp Ala Leu Glu  
 530 535 540  
 Pro Lys Arg Ile Lys Tyr Lys Arg Ile Ala Lys  
 545 550

<210> 309  
 <211> 173  
 <212> PRT  
 <213> E. Coli

<400> 309

```

Met Ser Lys Pro Lys Tyr Pro Phe Glu Lys Arg Leu Glu Val Val Asn
 1           5           10           15
His Tyr Phe Thr Thr Asp Asp Gly Tyr Arg Ile Ile Ser Ala Arg Phe
           20           25           30
Gly Val Pro Arg Thr Gln Val Arg Thr Trp Val Ala Leu Tyr Glu Lys
           35           40           45
His Gly Glu Lys Gly Leu Ile Pro Lys Pro Lys Gly Val Ser Ala Asp
 50           55           60
Pro Glu Leu Arg Ile Lys Val Val Lys Ala Val Ile Glu Gln His Met
65           70           75           80
Ser Leu Asn Gln Ala Ala Ala His Phe Met Leu Ala Gly Ser Gly Ser
           85           90           95
Val Ala Arg Trp Leu Lys Val Tyr Glu Glu Arg Gly Glu Ala Gly Leu
           100          105          110
Arg Ala Leu Lys Ile Gly Thr Lys Arg Asn Ile Ala Ile Ser Val Asp
           115          120          125
Pro Glu Lys Ala Ala Ser Ala Leu Glu Leu Ser Lys Asp Arg Arg Ile
130          135          140
Glu Asp Leu Glu Arg Gln Val Arg Phe Leu Glu Thr Arg Leu Met Tyr
145          150          155          160
Leu Lys Lys Leu Lys Ala Leu Ala His Pro Thr Lys Lys
           165          170

```

<210> 310  
 <211> 283  
 <212> PRT  
 <213> E. Coli

```

<400> 310
Met Lys Val Leu Asn Glu Leu Arg Gln Phe Tyr Pro Leu Asp Glu Leu
 1           5           10           15
Leu Arg Ala Ala Glu Ile Pro Arg Ser Thr Phe Tyr Tyr His Leu Lys
           20           25           30
Ala Leu Ser Lys Pro Asp Lys Tyr Ala Asp Val Lys Lys Arg Ile Ser
           35           40           45
Glu Ile Tyr His Glu Asn Arg Gly Arg Tyr Gly Tyr Arg Arg Val Thr
 50           55           60
Leu Ser Leu His Arg Glu Gly Lys Gln Ile Asn His Lys Ala Val Gln
65           70           75           80
Arg Leu Met Gly Thr Leu Ser Leu Lys Ala Ala Ile Lys Val Lys Arg
           85           90           95
Tyr Arg Ser Tyr Arg Gly Glu Val Gly Gln Thr Ala Pro Asn Val Leu
           100          105          110
Gln Arg Asp Phe Lys Ala Thr Arg Pro Asn Glu Lys Trp Val Thr Asp
           115          120          125
Val Thr Glu Phe Ala Val Asn Gly Arg Lys Leu Tyr Leu Ser Pro Val
           130          135          140
Ile Asp Leu Phe Asn Asn Glu Val Ile Ser Tyr Ser Leu Ser Glu Arg
145          150          155          160
Pro Val Met Asn Met Val Glu Asn Met Leu Asp Gln Ala Phe Lys Lys
           165          170          175
Leu Asn Pro His Glu His Pro Val Leu His Ser Asp Gln Gly Trp Gln
           180          185          190
Tyr Arg Met Arg Arg Tyr Gln Asn Ile Leu Lys Glu His Gly Ile Lys
           195          200          205
Gln Ser Met Ser Arg Lys Gly Asn Cys Leu Asp Asn Ala Val Val Glu
           210          215          220
Cys Phe Phe Gly Thr Leu Lys Ser Glu Cys Phe Tyr Leu Asp Glu Phe
225          230          235          240
Ser Asn Ile Ser Glu Leu Lys Asp Ala Val Thr Glu Tyr Ile Glu Tyr

```

Tyr Asn Ser Arg Arg Ile Ser Leu Lys Leu Lys Gly Leu Thr Pro Ile  
 245 250 255  
 260 265 270  
 Glu Tyr Arg Asn Gln Thr Tyr Met Pro Arg Val  
 275 280

<210> 311  
 <211> 38  
 <212> PRT  
 <213> E. Coli

<400> 311  
 Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile  
 1 5 10 15  
 Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys  
 20 25 30  
 His Lys Gln Arg Gln Gly  
 35

<210> 312  
 <211> 443  
 <212> PRT  
 <213> E. Coli

<400> 312  
 Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu  
 1 5 10 15  
 Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val  
 20 25 30  
 Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val  
 35 40 45  
 Leu Ala Lys Leu Leu Glu Gln Gln Arg Gly Thr Ile Ile Glu Met Phe  
 50 55 60  
 Asn Met Phe Ser Gly Gly Ala Leu Ser Arg Ala Ser Ile Phe Ala Leu  
 65 70 75 80  
 Gly Ile Met Pro Tyr Ile Ser Ala Ser Ile Ile Gln Leu Leu Thr  
 85 90 95  
 Val Val His Pro Thr Leu Ala Glu Ile Lys Lys Glu Gly Glu Ser Gly  
 100 105 110  
 Arg Arg Lys Ile Ser Gln Tyr Thr Arg Tyr Gly Thr Leu Val Leu Ala  
 115 120 125  
 Ile Phe Gln Ser Ile Gly Ile Ala Thr Gly Leu Pro Asn Met Pro Gly  
 130 135 140  
 Met Gln Gly Leu Val Ile Asn Pro Gly Phe Ala Phe Tyr Phe Thr Ala  
 145 150 155 160  
 Val Val Ser Leu Val Thr Gly Thr Met Phe Leu Met Trp Leu Gly Glu  
 165 170 175  
 Gln Ile Thr Glu Arg Gly Ile Gly Asn Gly Ile Ser Ile Ile Phe  
 180 185 190  
 Ala Gly Ile Val Ala Gly Leu Pro Pro Ala Ile Ala His Thr Ile Glu  
 195 200 205  
 Gln Ala Arg Gln Gly Asp Leu His Phe Leu Val Leu Leu Val Ala  
 210 215 220  
 Val Leu Val Phe Ala Val Thr Phe Phe Val Val Phe Val Glu Arg Gly  
 225 230 235 240  
 Gln Arg Arg Ile Val Val Asn Tyr Ala Lys Arg Gln Gln Gly Arg Arg  
 245 250 255  
 Val Tyr Ala Ala Gln Ser Thr His Leu Pro Leu Lys Val Asn Met Ala  
 260 265 270  
 Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala



```

      275      280      285
Thr Ile Ala Ser Trp Phe Gly Gly Gly Thr Gly Trp Asn Trp Leu Thr
290      295      300
Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu
305      310      315      320
Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val
325      330      335
Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe
340      345      350
Val Pro Gly Ile Arg Pro Gly Glu Gln Thr Ala Lys Tyr Ile Asp Lys
355      360      365
Val Met Thr Arg Leu Thr Leu Val Gly Ala Leu Tyr Ile Thr Phe Ile
370      375      380
Cys Leu Ile Pro Glu Phe Met Arg Asp Ala Met Lys Val Pro Phe Tyr
385      390      395      400
Phe Gly Gly Thr Ser Leu Leu Ile Val Val Val Val Ile Met Asp Phe
405      410      415
Met Ala Gln Val Gln Thr Leu Met Met Ser Ser Gln Tyr Glu Ser Ala
420      425      430
Leu Lys Lys Ala Asn Leu Lys Gly Tyr Gly Arg
435      440

```

<210> 313  
 <211> 144  
 <212> PRT  
 <213> E. Coli

```

      <400> 313
Met Arg Leu Asn Thr Leu Ser Pro Ala Glu Gly Ser Lys Lys Ala Gly
1      5      10      15
Lys Arg Leu Gly Arg Gly Ile Gly Ser Gly Leu Gly Lys Thr Gly Gly
20      25      30
Arg Gly His Lys Gly Gln Lys Ser Arg Ser Gly Gly Gly Val Arg Arg
35      40      45
Gly Phe Glu Gly Gly Gln Met Pro Leu Tyr Arg Arg Leu Pro Lys Phe
50      55      60
Gly Phe Thr Ser Arg Lys Ala Ala Ile Thr Ala Glu Ile Arg Leu Ser
65      70      75      80
Asp Leu Ala Lys Val Glu Gly Gly Val Val Asp Leu Asn Thr Leu Lys
85      90      95
Ala Ala Asn Ile Ile Gly Ile Gln Ile Glu Phe Ala Lys Val Ile Leu
100      105      110
Ala Gly Glu Val Thr Thr Pro Val Thr Val Arg Gly Leu Arg Val Thr
115      120      125
Lys Gly Ala Arg Ala Ala Ile Glu Ala Ala Gly Gly Lys Ile Glu Glu
130      135      140

```

<210> 314  
 <211> 59  
 <212> PRT  
 <213> E. Coli

```

      <400> 314
Met Ala Lys Thr Ile Lys Ile Thr Gln Thr Arg Ser Ala Ile Gly Arg
1      5      10      15
Leu Pro Lys His Lys Ala Thr Leu Leu Gly Leu Gly Leu Arg Arg Ile
20      25      30
Gly His Thr Val Glu Arg Glu Asp Thr Pro Ala Ile Arg Gly Met Ile

```

35 40 45  
 Asn Ala Val Ser Phe Met Val Lys Val Glu Glu  
 50 55

<210> 315  
 <211> 167  
 <212> PRT  
 <213> E. Coli

<400> 315  
 Met Ala His Ile Glu Lys Gln Ala Gly Glu Leu Gln Glu Lys Leu Ile  
 1 5 10 15  
 Ala Val Asn Arg Val Ser Lys Thr Val Lys Gly Gly Arg Ile Phe Ser  
 20 25 30  
 Phe Thr Ala Leu Thr Val Val Gly Asp Gly Asn Gly Arg Val Gly Phe  
 35 40 45  
 Gly Tyr Gly Lys Ala Arg Glu Val Pro Ala Ala Ile Gln Lys Ala Met  
 50 55 60  
 Glu Lys Ala Arg Arg Asn Met Ile Asn Val Ala Leu Asn Asn Gly Thr  
 65 70 75 80  
 Leu Gln His Pro Val Lys Gly Val His Thr Gly Ser Arg Val Phe Met  
 85 90 95  
 Gln Pro Ala Ser Glu Gly Thr Gly Ile Ile Ala Gly Gly Ala Met Arg  
 100 105 110  
 Ala Val Leu Glu Val Ala Gly Val His Asn Val Leu Ala Lys Ala Tyr  
 115 120 125  
 Gly Ser Thr Asn Pro Ile Asn Val Val Arg Ala Thr Ile Asp Gly Leu  
 130 135 140  
 Glu Asn Met Asn Ser Pro Glu Met Val Ala Ala Lys Arg Gly Lys Ser  
 145 150 155 160  
 Val Glu Glu Ile Leu Gly Lys  
 165

<210> 316  
 <211> 117  
 <212> PRT  
 <213> E. Coli

<400> 316  
 Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg  
 1 5 10 15  
 Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro  
 20 25 30  
 Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu  
 35 40 45  
 Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr  
 50 55 60  
 Thr Gly Asn Lys Asp Ala Ala Ala Val Gly Lys Ala Val Ala Glu  
 65 70 75 80  
 Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly  
 85 90 95  
 Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu  
 100 105 110  
 Ala Gly Leu Gln Phe  
 115

<210> 317  
 <211> 177

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 317

```

Met Ser Arg Val Ala Lys Ala Pro Val Val Val Pro Ala Gly Val Asp
1      5      10      15
Val Lys Ile Asn Gly Gln Val Ile Thr Ile Lys Gly Lys Asn Gly Glu
20      25      30
Leu Thr Arg Thr Leu Asn Asp Ala Val Glu Val Lys His Ala Asp Asn
35      40      45
Thr Leu Thr Phe Gly Pro Arg Asp Gly Tyr Ala Asp Gly Trp Ala Gln
50      55      60
Ala Gly Thr Ala Arg Ala Leu Leu Asn Ser Met Val Ile Gly Val Thr
65      70      75      80
Glu Gly Phe Thr Lys Lys Leu Gln Leu Val Gly Val Gly Tyr Arg Ala
85      90      95
Ala Val Lys Gly Asn Val Ile Asn Leu Ser Leu Gly Phe Ser His Pro
100     105     110
Val Asp His Gln Leu Pro Ala Gly Ile Thr Ala Glu Cys Pro Thr Gln
115     120     125
Thr Glu Ile Val Leu Lys Gly Ala Asp Lys Gln Val Ile Gly Gln Val
130     135     140
Ala Ala Asp Leu Arg Ala Tyr Arg Arg Pro Glu Pro Tyr Lys Gly Lys
145     150     155     160
Gly Val Arg Tyr Ala Asp Glu Val Val Arg Thr Lys Glu Ala Lys Lys
165     170     175
Lys

```

&lt;210&gt; 318

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 318

```

Met Ser Met Gln Asp Pro Ile Ala Asp Met Leu Thr Arg Ile Arg Asn
1      5      10      15
Gly Gln Ala Ala Asn Lys Ala Ala Val Thr Met Pro Ser Ser Lys Leu
20      25      30
Lys Val Ala Ile Ala Asn Val Leu Lys Glu Glu Gly Phe Ile Glu Asp
35      40      45
Phe Lys Val Glu Gly Asp Thr Lys Pro Glu Leu Glu Leu Thr Leu Lys
50      55      60
Tyr Phe Gln Gly Lys Ala Val Val Glu Ser Ile Gln Arg Val Ser Arg
65      70      75      80
Pro Gly Leu Arg Ile Tyr Lys Arg Lys Asp Glu Leu Pro Lys Val Met
85      90      95
Ala Gly Leu Gly Ile Ala Val Val Ser Thr Ser Lys Gly Val Met Thr
100     105     110
Asp Arg Ala Ala Arg Gln Ala Gly Leu Gly Gly Glu Ile Ile Cys Tyr
115     120     125
Val Ala
130

```

&lt;210&gt; 319

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 319

```

Met Ala Lys Gln Ser Met Lys Ala Arg Glu Val Lys Arg Val Ala Leu
1      5      10      15
Ala Asp Lys Tyr Phe Ala Lys Arg Ala Glu Leu Lys Ala Ile Ile Ser
20      25      30
Asp Val Asn Ala Ser Asp Glu Asp Arg Trp Asn Ala Val Leu Lys Leu
35      40      45
Gln Thr Leu Pro Arg Asp Ser Ser Pro Ser Arg Gln Arg Asn Arg Cys
50      55      60
Arg Gln Thr Gly Arg Pro His Gly Phe Leu Arg Lys Phe Gly Leu Ser
65      70      75      80
Arg Ile Lys Val Arg Glu Ala Ala Met Arg Gly Glu Ile Pro Gly Leu
85      90      95
Lys Lys Ala Ser Trp
100

```

&lt;210&gt; 320

&lt;211&gt; 179

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 320

```

Met Ala Lys Leu His Asp Tyr Tyr Lys Asp Glu Val Val Lys Lys Leu
1      5      10      15
Met Thr Glu Phe Asn Tyr Asn Ser Val Met Gln Val Pro Arg Val Glu
20      25      30
Lys Ile Thr Leu Asn Met Gly Val Gly Glu Ala Ile Ala Asp Lys Lys
35      40      45
Leu Leu Asp Asn Ala Ala Ala Asp Leu Ala Ala Ile Ser Gly Gln Lys
50      55      60
Pro Leu Ile Thr Lys Ala Arg Lys Ser Val Ala Gly Phe Lys Ile Arg
65      70      75      80
Gln Gly Tyr Pro Ile Gly Cys Lys Val Thr Leu Arg Gly Glu Arg Met
85      90      95
Trp Glu Phe Phe Glu Arg Leu Ile Thr Ile Ala Val Pro Arg Ile Arg
100      105      110
Asp Phe Arg Gly Leu Ser Ala Lys Ser Phe Asp Gly Arg Gly Asn Tyr
115      120      125
Ser Met Gly Val Arg Glu Gln Ile Ile Phe Pro Glu Ile Asp Tyr Asp
130      135      140
Lys Val Asp Arg Val Arg Gly Leu Asp Ile Thr Ile Thr Thr Thr Ala
145      150      155      160
Lys Ser Asp Glu Glu Gly Arg Ala Leu Leu Ala Ala Phe Asp Phe Pro
165      170      175
Phe Arg Lys

```

&lt;210&gt; 321Z

&lt;211&gt; 104

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 321

```

Met Ala Ala Lys Ile Arg Arg Asp Asp Glu Val Ile Val Leu Thr Gly
1      5      10      15
Lys Asp Lys Gly Lys Arg Gly Lys Val Lys Asn Val Leu Ser Ser Gly
20      25      30

```

Lys Val Ile Val Glu Gly Ile Asn Leu Val Lys Lys His Gln Lys Pro  
 35 40 45  
 Val Pro Ala Leu Asn Gln Pro Gly Gly Ile Val Glu Lys Glu Ala Ala  
 50 55 60  
 Ile Gln Val Ser Asn Val Ala Ile Phe Asn Ala Ala Thr Gly Lys Ala  
 65 70 75 80  
 Asp Arg Val Gly Phe Arg Phe Glu Asp Gly Lys Lys Val Arg Phe Phe  
 85 90 95  
 Lys Ser Asn Ser Glu Thr Ile Lys  
 100

<210> 322  
 <211> 123  
 <212> PRT  
 <213> E. Coli

<400> 322  
 Met Ile Gln Glu Gln Thr Met Leu Asn Val Ala Asp Asn Ser Gly Ala  
 1 5 10 15  
 Arg Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr  
 20 25 30  
 Ala Gly Val Gly Asp Ile Ile Lys Ile Thr Ile Lys Glu Ala Ile Pro  
 35 40 45  
 Arg Gly Lys Val Lys Lys Gly Asp Val Leu Lys Ala Val Val Val Arg  
 50 55 60  
 Thr Lys Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp  
 65 70 75 80  
 Gly Asn Ala Cys Val Leu Leu Asn Asn Asn Ser Glu Gln Pro Ile Gly  
 85 90 95  
 Thr Arg Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Ser Glu Lys Phe  
 100 105 110  
 Met Lys Ile Ile Ser Leu Ala Pro Glu Val Leu  
 115 120

<210> 323  
 <211> 188  
 <212> PRT  
 <213> E. Coli

<400> 323  
 Met Phe Lys Gly Gln Lys Thr Leu Ala Ala Leu Ala Val Ser Leu Leu  
 1 5 10 15  
 Phe Thr Ala Pro Val Tyr Ala Ala Asp Glu Gly Ser Gly Glu Ile His  
 20 25 30  
 Phe Lys Gly Glu Val Ile Glu Ala Pro Cys Glu Ile His Pro Glu Asp  
 35 40 45  
 Ile Asp Lys Asn Ile Asp Leu Gly Gln Val Thr Thr Thr His Ile Asn  
 50 55 60  
 Arg Glu His His Ser Asn Lys Val Ala Val Asp Ile Arg Leu Ile Asn  
 65 70 75 80  
 Cys Asp Leu Pro Ala Ser Asp Asn Gly Ser Gly Met Pro Val Ser Lys  
 85 90 95  
 Val Gly Val Thr Phe Asp Ser Thr Ala Lys Thr Thr Gly Ala Thr Pro  
 100 105 110  
 Leu Leu Ser Asn Thr Ser Ala Gly Glu Ala Thr Gly Val Gly Val Arg  
 115 120 125  
 Leu Met Asp Lys Asn Asp Gly Asn Ile Val Leu Gly Ser Ala Ala Pro  
 130 135 140  
 Asp Leu Asp Leu Asp Ala Ser Ser Ser Glu Gln Thr Leu Asn Phe Phe

145                      150                      155                      160  
 Ala Trp Met Glu Gln Ile Asp Asn Ala Val Asp Val Thr Ala Gly Glu  
                                  165                      170                      175  
 Val Thr Ala Asn Ala Thr Tyr Val Leu Asp Tyr Lys  
                                  180                      185

<210> 324  
 <211> 427  
 <212> PRT  
 <213> E. Coli

<400> 324  
 Met Ala Asp Thr Lys Ala Lys Leu Thr Leu Asn Gly Asp Thr Ala Val  
   1                                  5                                  10                                  15  
 Glu Leu Asp Val Leu Lys Gly Thr Leu Gly Gln Asp Val Ile Asp Ile  
                                   20                                  25                                  30  
 Arg Thr Leu Gly Ser Lys Gly Val Phe Thr Phe Asp Pro Gly Phe Thr  
                                   35                                  40                                  45  
 Ser Thr Ala Ser Cys Glu Ser Lys Ile Thr Phe Ile Asp Gly Asp Glu  
                                   50                                  55                                  60  
 Gly Ile Leu Leu His Arg Gly Phe Pro Ile Asp Gln Leu Ala Thr Asp  
   65                                  70                                  75                                  80  
 Ser Asn Tyr Leu Glu Val Cys Tyr Ile Leu Leu Asn Gly Glu Lys Pro  
                                   85                                  90                                  95  
 Thr Gln Glu Gln Tyr Asp Glu Phe Lys Thr Thr Val Thr Arg His Thr  
                                   100                                  105                                  110  
 Met Ile His Glu Gln Ile Thr Arg Leu Phe His Ala Phe Arg Arg Asp  
                                   115                                  120                                  125  
 Ser His Pro Met Ala Val Met Cys Gly Ile Thr Gly Ala Leu Ala Ala  
   130                                  135                                  140  
 Phe Tyr His Asp Ser Leu Asp Val Asn Asn Pro Arg His Arg Glu Ile  
   145                                  150                                  155                                  160  
 Ala Ala Phe Arg Leu Ser Lys Met Pro Thr Met Ala Ala Met Cys  
                                   165                                  170                                  175  
 Tyr Lys Tyr Ser Ile Gly Gln Pro Phe Val Tyr Pro Arg Asn Asp Leu  
                                   180                                  185                                  190  
 Ser Tyr Ala Gly Asn Phe Leu Asn Met Met Phe Ser Thr Pro Cys Glu  
                                   195                                  200                                  205  
 Pro Tyr Glu Val Asn Pro Ile Leu Glu Arg Ala Met Asp Arg Ile Leu  
   210                                  215                                  220  
 Ile Leu His Ala Asp His Glu Gln Asn Ala Ser Thr Ser Thr Val Arg  
   225                                  230                                  235                                  240  
 Thr Ala Gly Ser Ser Gly Ala Asn Pro Phe Ala Cys Ile Ala Ala Gly  
                                   245                                  250                                  255  
 Ile Ala Ser Leu Trp Gly Pro Ala His Gly Gly Ala Asn Glu Ala Ala  
                                   260                                  265                                  270  
 Leu Lys Met Leu Glu Glu Ile Ser Ser Val Lys His Ile Pro Glu Phe  
                                   275                                  280                                  285  
 Val Arg Arg Ala Lys Asp Lys Asn Asp Ser Phe Arg Leu Met Gly Phe  
   290                                  295                                  300  
 Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Thr Val Met Arg  
   305                                  310                                  315                                  320  
 Glu Thr Cys His Glu Val Leu Lys Glu Leu Gly Thr Lys Asp Asp Leu  
                                   325                                  330                                  335  
 Leu Glu Val Ala Met Glu Leu Glu Asn Ile Ala Leu Asn Asp Pro Tyr  
                                   340                                  345                                  350  
 Phe Ile Glu Lys Lys Leu Tyr Pro Asn Val Asp Phe Tyr Ser Gly Ile  
                                   355                                  360                                  365  
 Ile Leu Lys Ala Met Gly Ile Pro Ser Ser Met Phe Thr Val Ile Phe  
   370                                  375                                  380

Ala Met Ala Arg Thr Val Gly Trp Ile Ala His Trp Ser Glu Met His  
 385 390 395 400  
 Ser Asp Gly Met Lys Ile Ala Arg Pro Arg Gln Leu Tyr Thr Gly Tyr  
 405 410 415  
 Glu Lys Arg Asp Phe Lys Ser Asp Ile Lys Arg  
 420 425

<210> 325  
 <211> 477  
 <212> PRT  
 <213> E. Coli

<400> 325  
 Met Lys Val Thr Leu Pro Glu Phe Glu Arg Ala Gly Val Met Val Val  
 1 5 10 15  
 Gly Asp Val Met Leu Asp Arg Tyr Trp Tyr Gly Pro Thr Ser Arg Ile  
 20 25 30  
 Ser Pro Glu Ala Pro Val Pro Val Val Lys Val Asn Thr Ile Glu Glu  
 35 40 45  
 Arg Pro Gly Gly Ala Ala Asn Val Ala Met Asn Ile Ala Ser Leu Gly  
 50 55 60  
 Ala Asn Ala Arg Leu Val Gly Leu Thr Gly Ile Asp Asp Ala Ala Arg  
 65 70 75 80  
 Ala Leu Ser Lys Ser Leu Ala Asp Val Asn Val Lys Cys Asp Phe Val  
 85 90 95  
 Ser Val Pro Thr His Pro Thr Ile Thr Lys Leu Arg Val Leu Ser Arg  
 100 105 110  
 Asn Gln Gln Leu Ile Arg Leu Asp Phe Glu Glu Gly Phe Glu Gly Val  
 115 120 125  
 Asp Pro Gln Pro Leu His Glu Arg Ile Asn Gln Ala Leu Ser Ser Ile  
 130 135 140  
 Gly Ala Leu Val Leu Ser Asp Tyr Ala Lys Gly Ala Leu Ala Ser Val  
 145 150 155 160  
 Gln Gln Met Ile Gln Leu Ala Arg Lys Ala Gly Val Pro Val Leu Ile  
 165 170 175  
 Asp Pro Lys Gly Thr Asp Phe Glu Arg Tyr Arg Gly Ala Thr Leu Leu  
 180 185 190  
 Thr Pro Asn Leu Ser Glu Phe Glu Ala Val Val Gly Lys Cys Lys Thr  
 195 200 205  
 Glu Glu Glu Ile Val Glu Arg Gly Met Lys Leu Ile Ala Asp Tyr Glu  
 210 215 220  
 Leu Ser Ala Leu Leu Val Thr Arg Ser Glu Gln Gly Met Ser Leu Leu  
 225 230 235 240  
 Gln Pro Gly Lys Ala Pro Leu His Met Pro Thr Gln Ala Gln Glu Val  
 245 250 255  
 Tyr Asp Val Thr Gly Ala Gly Asp Thr Val Ile Gly Val Leu Ala Ala  
 260 265 270  
 Thr Leu Ala Ala Gly Asn Ser Leu Glu Glu Ala Cys Phe Phe Ala Asn  
 275 280 285  
 Ala Ala Ala Gly Val Val Val Gly Lys Leu Gly Thr Ser Thr Val Ser  
 290 295 300  
 Pro Ile Glu Leu Glu Asn Ala Val Arg Gly Arg Ala Asp Thr Gly Phe  
 305 310 315 320  
 Gly Val Met Thr Glu Glu Glu Leu Lys Leu Ala Val Ala Ala Arg  
 325 330 335  
 Lys Arg Gly Glu Lys Val Val Met Thr Asn Gly Val Phe Asp Ile Leu  
 340 345 350  
 His Ala Gly His Val Ser Tyr Leu Ala Asn Ala Arg Lys Leu Gly Asp  
 355 360 365  
 Arg Leu Ile Val Ala Val Asn Ser Asp Ala Ser Thr Lys Arg Leu Lys

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      370              375              380
Gly Asp Ser Arg Pro Val Asn Pro Leu Glu Gln Arg Met Ile Val Leu
385              390              395              400
Gly Ala Leu Glu Ala Val Asp Trp Val Val Ser Phe Glu Glu Asp Thr
      405              410              415
Pro Gln Arg Leu Ile Ala Gly Ile Leu Pro Asp Leu Leu Val Lys Gly
      420              425              430
Gly Asp Tyr Lys Pro Glu Glu Ile Ala Gly Ser Lys Glu Val Trp Ala
      435              440              445
Asn Gly Gly Glu Val Leu Val Leu Asn Phe Glu Asp Gly Cys Ser Thr
      450              455              460
Thr Asn Ile Ile Lys Lys Ile Gln Gln Asp Lys Lys Gly
465              470              475

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<210> 326
<211> 946
<212> PRT
<213> E. Coli

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      <400> 326
Met Lys Pro Leu Ser Ser Pro Leu Gln Gln Tyr Trp Gln Thr Val Val
1              5              10              15
Glu Arg Leu Pro Glu Pro Leu Ala Glu Glu Ser Leu Ser Ala Gln Ala
      20              25              30
Lys Ser Val Leu Thr Phe Ser Asp Phe Val Gln Asp Ser Val Ile Ala
      35              40              45
His Pro Glu Trp Leu Thr Glu Leu Glu Ser Gln Pro Pro Gln Ala Asp
      50              55              60
Glu Trp Gln His Tyr Ala Ala Trp Leu Gln Glu Ala Leu Cys Asn Val
65              70              75              80
Ser Asp Glu Ala Gly Leu Met Arg Glu Leu Arg Leu Phe Arg Arg Arg
      85              90              95
Ile Met Val Arg Ile Ala Trp Ala Gln Thr Leu Ala Leu Val Thr Glu
      100              105              110
Glu Ser Ile Leu Gln Gln Leu Ser Tyr Leu Ala Glu Thr Leu Ile Val
      115              120              125
Ala Ala Arg Asp Trp Leu Tyr Asp Ala Cys Cys Arg Glu Trp Gly Thr
      130              135              140
Pro Cys Asn Ala Gln Gly Glu Ala Gln Pro Leu Leu Ile Leu Gly Met
145              150              155              160
Gly Lys Leu Gly Gly Gly Glu Leu Asn Phe Ser Ser Asp Ile Asp Leu
      165              170              175
Ile Phe Ala Trp Pro Glu His Gly Cys Thr Gln Gly Gly Arg Arg Glu
      180              185              190
Leu Asp Asn Ala Gln Phe Phe Thr Arg Met Gly Gln Arg Leu Ile Lys
      195              200              205
Val Leu Asp Gln Pro Thr Gln Asp Gly Phe Val Tyr Arg Val Asp Met
      210              215              220
Arg Leu Arg Pro Phe Gly Glu Ser Gly Pro Leu Val Leu Ser Phe Ala
225              230              235              240
Ala Leu Glu Asp Tyr Tyr Gln Glu Gln Gly Arg Asp Trp Glu Arg Tyr
      245              250              255
Ala Met Val Lys Ala Arg Ile Met Gly Asp Ser Glu Gly Val Tyr Ala
      260              265              270
Asn Glu Leu Arg Ala Met Leu Arg Pro Phe Val Phe Arg Arg Tyr Ile
      275              280              285
Asp Phe Ser Val Ile Gln Ser Leu Arg Asn Met Lys Gly Met Ile Ala
      290              295              300
Arg Glu Val Arg Arg Arg Gly Leu Thr Asp Asn Ile Lys Leu Gly Ala
305              310              315              320

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Gly Gly Ile Arg Glu Ile Glu Phe Ile Val Gln Val Phe Gln Leu Ile  
 325 330 335  
 Arg Gly Gly Arg Glu Pro Ser Leu Gln Ser Arg Ser Leu Leu Pro Thr  
 340 345 350  
 Leu Ser Ala Ile Ala Glu Leu His Leu Leu Ser Glu Asn Asp Ala Glu  
 355 360 365  
 Gln Leu Arg Val Ala Tyr Leu Phe Leu Arg Arg Leu Glu Asn Leu Leu  
 370 375 380  
 Gln Ser Ile Asn Asp Glu Gln Thr Gln Thr Leu Pro Ser Asp Glu Leu  
 385 390 395 400  
 Asn Arg Ala Arg Leu Ala Trp Ala Met Asp Phe Ala Asp Trp Pro Gln  
 405 410 415  
 Leu Thr Gly Ala Leu Thr Ala His Met Thr Asn Val Arg Arg Val Phe  
 420 425 430  
 Asn Glu Leu Ile Gly Asp Asp Glu Ser Glu Thr Gln Glu Glu Ser Leu  
 435 440 445  
 Ser Glu Gln Trp Arg Glu Leu Trp Gln Asp Ala Leu Gln Glu Asp Asp  
 450 455 460  
 Thr Thr Pro Val Leu Ala His Leu Ser Glu Asp Asp Arg Lys Gln Val  
 465 470 475 480  
 Leu Thr Leu Ile Ala Asp Phe Arg Lys Glu Leu Asp Lys Arg Thr Ile  
 485 490 495  
 Gly Pro Arg Gly Arg Gln Val Leu Asp His Leu Met Pro His Leu Leu  
 500 505 510  
 Ser Asp Val Cys Ala Arg Glu Asp Ala Ala Val Thr Leu Ser Arg Ile  
 515 520 525  
 Thr Ala Leu Leu Val Gly Ile Val Thr Arg Thr Thr Tyr Leu Glu Leu  
 530 535 540  
 Leu Ser Glu Phe Pro Ala Ala Leu Lys His Leu Ile Ser Leu Cys Ala  
 545 550 555 560  
 Ala Ser Pro Met Ile Ala Ser Gln Leu Ala Arg Tyr Pro Leu Leu Leu  
 565 570 575  
 Asp Glu Leu Leu Asp Pro Asn Thr Leu Tyr Gln Pro Thr Ala Thr Asp  
 580 585 590  
 Ala Tyr Arg Asp Glu Leu Arg Gln Tyr Leu Leu Arg Val Pro Glu Asp  
 595 600 605  
 Asp Glu Glu Gln Gln Leu Glu Ala Leu Arg Gln Phe Lys Gln Ala Gln  
 610 615 620  
 Leu Leu Arg Ile Ala Ala Ala Asp Ile Ala Gly Thr Leu Pro Val Met  
 625 630 635 640  
 Lys Val Ser Asp His Leu Thr Trp Leu Ala Glu Ala Met Ile Asp Ala  
 645 650 655  
 Val Val Gln Gln Ala Trp Val Gln Met Val Ala Arg Tyr Gly Lys Pro  
 660 665 670  
 Asn His Leu Asn Glu Arg Glu Gly Arg Gly Phe Ala Val Val Gly Tyr  
 675 680 685  
 Gly Lys Leu Gly Gly Trp Glu Leu Gly Tyr Ser Ser Asp Leu Asp Leu  
 690 695 700  
 Ile Phe Leu His Asp Cys Pro Met Asp Ala Met Thr Asp Gly Glu Arg  
 705 710 715 720  
 Glu Ile Asp Gly Arg Gln Phe Tyr Leu Arg Leu Ala Gln Arg Ile Met  
 725 730 735  
 His Leu Phe Ser Thr Arg Thr Ser Ser Gly Ile Leu Tyr Glu Val Asp  
 740 745 750  
 Ala Arg Leu Arg Pro Ser Gly Ala Ala Gly Met Leu Val Thr Ser Ala  
 755 760 765  
 Glu Ala Phe Ala Asp Tyr Gln Lys Asn Glu Ala Trp Thr Trp Glu His  
 770 775 780  
 Gln Ala Leu Val Arg Ala Arg Val Val Tyr Gly Asp Pro Gln Leu Thr  
 785 790 795 800  
 Ala His Phe Asp Ala Val Arg Arg Glu Ile Met Thr Leu Pro Arg Glu

805 810 815  
 Gly Lys Thr Leu Gln Thr Glu Val Arg Glu Met Arg Glu Lys Met Arg  
 820 825 830  
 Ala His Leu Gly Asn Lys His Arg Asp Arg Phe Asp Ile Lys Ala Asp  
 835 840 845  
 Glu Gly Gly Ile Thr Asp Ile Glu Phe Ile Thr Gln Tyr Leu Val Leu  
 850 855 860  
 Arg Tyr Ala His Glu Lys Pro Lys Leu Thr Arg Trp Ser Asp Asn Val  
 865 870 875 880  
 Arg Ile Leu Glu Leu Leu Ala Gln Asn Asp Ile Met Glu Glu Gln Glu  
 885 890 895  
 Ala Met Ala Leu Thr Arg Ala Tyr Thr Thr Leu Arg Asp Glu Leu His  
 900 905 910  
 His Leu Ala Leu Gln Glu Leu Pro Gly His Val Ser Glu Asp Cys Phe  
 915 920 925  
 Thr Ala Glu Arg Glu Leu Val Arg Ala Ser Trp Gln Lys Trp Leu Val  
 930 935 940  
 Glu Glu  
 945

<210> 327  
 <211> 433  
 <212> PRT  
 <213> E. Coli

<400> 327  
 Met Ala Gln Glu Ile Glu Leu Lys Phe Ile Val Asn His Ser Ala Val  
 1 5 10 15  
 Glu Ala Leu Arg Asp His Leu Asn Thr Leu Gly Gly Glu His His Asp  
 20 25 30  
 Pro Val Gln Leu Leu Asn Ile Tyr Tyr Glu Thr Pro Asp Asn Trp Leu  
 35 40 45  
 Arg Gly His Asp Met Gly Leu Arg Ile Arg Gly Glu Asn Gly Arg Tyr  
 50 55 60  
 Glu Met Thr Met Lys Val Ala Gly Arg Val Thr Gly Gly Leu His Gln  
 65 70 75 80  
 Arg Pro Glu Tyr Asn Val Ala Leu Ser Glu Pro Thr Leu Asp Leu Ala  
 85 90 95  
 Gln Leu Pro Thr Glu Val Trp Pro Asn Gly Glu Leu Pro Ala Asp Leu  
 100 105 110  
 Ala Ser Arg Val Gln Pro Leu Phe Ser Thr Asp Phe Tyr Arg Glu Lys  
 115 120 125  
 Trp Leu Val Ala Val Asp Gly Ser Gln Ile Glu Ile Ala Leu Asp Gln  
 130 135 140  
 Gly Glu Val Lys Ala Gly Glu Phe Ala Glu Pro Ile Cys Glu Leu Glu  
 145 150 155 160  
 Leu Glu Leu Leu Ser Gly Asp Thr Arg Ala Val Leu Lys Leu Ala Asn  
 165 170 175  
 Gln Leu Val Ser Gln Thr Gly Leu Arg Gln Gly Ser Leu Ser Lys Ala  
 180 185 190  
 Ala Arg Gly Tyr His Leu Ala Gln Gly Asn Pro Ala Arg Glu Ile Lys  
 195 200 205  
 Pro Thr Thr Ile Leu His Val Ala Ala Lys Ala Asp Val Glu Gln Gly  
 210 215 220  
 Leu Glu Ala Ala Leu Glu Leu Ala Leu Ala Gln Trp Gln Tyr His Glu  
 225 230 235 240  
 Glu Leu Trp Val Arg Gly Asn Asp Ala Ala Lys Glu Gln Val Leu Ala  
 245 250 255  
 Ala Ile Ser Leu Val Arg His Thr Leu Met Leu Phe Gly Gly Ile Val

260 265 270  
 Pro Arg Lys Ala Ser Thr His Leu Arg Asp Leu Leu Thr Gln Cys Glu  
 275 280 285  
 Ala Thr Ile Ala Ser Ala Val Ser Ala Val Thr Ala Val Tyr Ser Thr  
 290 295 300  
 Glu Thr Ala Met Ala Lys Leu Ala Leu Thr Glu Trp Leu Val Ser Lys  
 305 310 315 320  
 Ala Trp Gln Pro Phe Leu Asp Ala Lys Ala Gln Gly Lys Ile Ser Asp  
 325 330 335  
 Ser Phe Lys Arg Phe Ala Asp Ile His Leu Ser Arg His Ala Ala Glu  
 340 345 350  
 Leu Lys Ser Val Phe Cys Gln Pro Leu Gly Asp Arg Tyr Arg Asp Gln  
 355 360 365  
 Leu Pro Arg Leu Thr Arg Asp Ile Asp Ser Ile Leu Leu Ala Gly  
 370 375 380  
 Tyr Tyr Asp Pro Val Val Ala Gln Ala Trp Leu Glu Asn Trp Gln Gly  
 385 390 395 400  
 Leu His His Ala Ile Ala Thr Gly Gln Arg Ile Glu Ile Glu His Phe  
 405 410 415  
 Arg Asn Glu Ala Asn Asn Gln Glu Pro Phe Trp Leu His Ser Gly Lys  
 420 425 430  
 Arg

<210> 328  
 <211> 70  
 <212> PRT  
 <213> E. Coli

<400> 328  
 Met Ser Gly Lys Met Thr Gly Ile Val Lys Trp Phe Asn Ala Asp Lys  
 1 5 10 15  
 Gly Phe Gly Phe Ile Thr Pro Asp Asp Gly Ser Lys Asp Val Phe Val  
 20 25 30  
 His Phe Ser Ala Ile Gln Asn Asp Gly Tyr Lys Ser Leu Asp Glu Gly  
 35 40 45  
 Gln Lys Val Ser Phe Thr Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala  
 50 55 60  
 Gly Asn Val Thr Ser Leu  
 65 70

<210> 329  
 <211> 523  
 <212> PRT  
 <213> E. Coli

<400> 329  
 Met Arg Asp Ile Val Asp Pro Val Phe Ser Ile Gly Ile Ser Ser Leu  
 1 5 10 15  
 Trp Asp Glu Leu Arg His Met Pro Ala Gly Gly Val Trp Trp Phe Asn  
 20 25 30  
 Val Asp Arg His Glu Asp Ala Ile Ser Leu Ala Asn Gln Thr Ile Ala  
 35 40 45  
 Ser Gln Ala Glu Thr Ala His Val Ala Val Ile Ser Met Asp Ser Asp  
 50 55 60  
 Pro Ala Lys Ile Phe Gln Leu Asp Asp Ser Gln Gly Pro Glu Lys Ile  
 65 70 75 80

Lys Leu Phe Ser Met Leu Asn His Glu Lys Gly Leu Tyr Tyr Leu Thr  
 85 90 95  
 Arg Asp Leu Gln Cys Ser Ile Asp Pro His Asn Tyr Leu Phe Ile Leu  
 100 105 110  
 Val Cys Ala Asn Asn Ala Trp Gln Asn Ile Pro Ala Glu Arg Leu Arg  
 115 120 125  
 Ser Trp Leu Asp Lys Met Asn Lys Trp Ser Arg Leu Asn His Cys Ser  
 130 135 140  
 Leu Leu Val Ile Asn Pro Gly Asn Asn Asn Asp Lys Gln Phe Ser Leu  
 145 150 155 160  
 Leu Leu Glu Glu Tyr Arg Ser Leu Phe Gly Leu Ala Ser Leu Arg Phe  
 165 170 175  
 Gln Gly Asp Gln His Leu Leu Asp Ile Ala Phe Trp Cys Asn Glu Lys  
 180 185 190  
 Gly Val Ser Ala Arg Gln Gln Leu Ser Val Gln Gln Gln Asn Gly Ile  
 195 200 205  
 Trp Thr Leu Val Gln Ser Glu Glu Ala Glu Ile Gln Pro Arg Ser Asp  
 210 215 220  
 Glu Lys Arg Ile Leu Ser Asn Val Ala Val Leu Glu Gly Ala Pro Pro  
 225 230 235 240  
 Leu Ser Glu His Trp Gln Leu Phe Asn Asn Asn Glu Val Leu Phe Asn  
 245 250 255  
 Glu Ala Arg Thr Ala Gln Ala Ala Thr Val Val Phe Ser Leu Gln Gln  
 260 265 270  
 Asn Ala Gln Ile Glu Pro Leu Ala Arg Ser Ile His Thr Leu Arg Arg  
 275 280 285  
 Gln Arg Gly Ser Ala Met Lys Ile Leu Val Arg Glu Asn Thr Ala Ser  
 290 295 300  
 Leu Arg Ala Thr Asp Glu Arg Leu Leu Leu Ala Cys Gly Ala Asn Met  
 305 310 315 320  
 Val Ile Pro Trp Asn Ala Pro Leu Ser Arg Cys Leu Thr Met Ile Glu  
 325 330 335  
 Ser Val Gln Gly Gln Lys Phe Ser Arg Tyr Val Pro Glu Asp Ile Thr  
 340 345 350  
 Thr Leu Leu Ser Met Thr Gln Pro Leu Lys Leu Arg Gly Phe Gln Lys  
 355 360 365  
 Trp Asp Val Phe Cys Asn Ala Val Asn Asn Met Met Asn Asn Pro Leu  
 370 375 380  
 Leu Pro Ala His Gly Lys Gly Val Leu Val Ala Leu Arg Pro Val Pro  
 385 390 395 400  
 Gly Ile Arg Val Glu Gln Ala Leu Thr Leu Cys Arg Pro Asn Arg Thr  
 405 410 415  
 Gly Asp Ile Met Thr Ile Gly Gly Asn Arg Leu Val Leu Phe Leu Ser  
 420 425 430  
 Phe Cys Arg Ile Asn Asp Leu Asp Thr Ala Leu Asn His Ile Phe Pro  
 435 440 445  
 Leu Pro Thr Gly Asp Ile Phe Ser Asn Arg Met Val Trp Phe Glu Asp  
 450 455 460  
 Asp Gln Ile Ser Ala Glu Leu Val Gln Met Arg Leu Leu Ala Pro Glu  
 465 470 475 480  
 Gln Trp Gly Met Pro Leu Pro Leu Thr Gln Ser Ser Lys Pro Val Ile  
 485 490 495  
 Asn Ala Glu His Asp Gly Arg His Trp Arg Arg Ile Pro Glu Pro Met  
 500 505 510  
 Arg Leu Leu Asp Asp Ala Val Glu Arg Ser Ser  
 515 520

&lt;210&gt; 330

&lt;211&gt; 62

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 330

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Met Thr Ile Ser Asp Ile Ile Glu Ile Ile Val Val Cys Ala Leu Ile
 1          5          10          15
Phe Phe Pro Leu Gly Tyr Leu Ala Arg His Ser Leu Arg Arg Ile Arg
      20          25          30
Asp Thr Leu Arg Leu Phe Phe Ala Lys Pro Arg Tyr Val Lys Pro Ala
      35          40          45
Gly Thr Leu Arg Arg Thr Glu Lys Ala Arg Ala Thr Lys Lys
      50          55          60

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&lt;210&gt; 331

&lt;211&gt; 559

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 331

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Met Thr Gln Phe Thr Gln Asn Thr Ala Met Pro Ser Ser Leu Trp Gln
 1          5          10          15
Tyr Trp Arg Gly Leu Ser Gly Trp Asn Phe Tyr Phe Leu Val Lys Phe
      20          25          30
Gly Leu Leu Trp Ala Gly Tyr Leu Asn Phe His Pro Leu Leu Asn Leu
      35          40          45
Val Phe Ala Ala Phe Leu Leu Met Pro Leu Pro Arg Tyr Ser Leu His
      50          55          60
Arg Leu Arg His Trp Ile Ala Leu Pro Ile Gly Phe Ala Leu Phe Trp
      65          70          75          80
His Asp Thr Trp Leu Pro Gly Pro Glu Ser Ile Met Ser Gln Gly Ser
      85          90          95
Gln Val Ala Gly Phe Ser Thr Asp Tyr Leu Ile Asp Leu Val Thr Arg
      100          105          110
Phe Ile Asn Trp Gln Met Ile Gly Ala Ile Phe Val Leu Leu Val Ala
      115          120          125
Trp Leu Phe Leu Ser Gln Trp Ile Arg Ile Thr Val Phe Val Val Ala
      130          135          140
Ile Leu Leu Trp Leu Asn Val Leu Thr Leu Ala Gly Pro Ser Phe Ser
      145          150          155          160
Leu Trp Pro Ala Gly Gln Pro Thr Thr Val Thr Thr Thr Gly Gly
      165          170          175          180
Asn Ala Ala Ala Thr Val Ala Ala Thr Gly Gly Ala Pro Val Val Gly
      180          185          190
Asp Met Pro Ala Gln Thr Ala Pro Pro Thr Thr Ala Asn Leu Asn Ala
      195          200          205
Trp Leu Asn Asn Phe Tyr Asn Ala Glu Ala Lys Arg Lys Ser Thr Phe
      210          215          220
Pro Ser Ser Leu Pro Ala Asp Ala Gln Pro Phe Glu Leu Leu Val Ile
      225          230          235          240
Asn Ile Cys Ser Leu Ser Trp Ser Asp Ile Glu Ala Ala Gly Leu Met
      245          250          255
Ser His Pro Leu Trp Ser His Phe Asp Ile Glu Phe Lys Asn Phe Asn
      260          265          270
Ser Ala Thr Ser Tyr Ser Gly Pro Ala Ala Ile Arg Leu Leu Arg Ala
      275          280          285
Ser Cys Gly Gln Thr Ser His Thr Asn Leu Tyr Gln Pro Ala Asn Asn
      290          295          300
Asp Cys Tyr Leu Phe Asp Asn Leu Ser Lys Leu Gly Phe Thr Gln His
      305          310          315          320
Leu Met Met Gly His Asn Gly Gln Phe Gly Gly Phe Leu Lys Glu Val
      325          330          335

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Arg Glu Asn Gly Gly Met Gln Ser Glu Leu Met Asp Gln Thr Asn Leu  
 340 345 350  
 Pro Val Ile Leu Leu Gly Phe Asp Gly Ser Pro Val Tyr Asp Asp Thr  
 355 360 365  
 Ala Val Leu Asn Arg Trp Leu Asp Val Thr Glu Lys Asp Lys Asn Ser  
 370 375 380  
 Arg Ser Ala Thr Phe Tyr Asn Thr Leu Pro Leu His Asp Gly Asn His  
 385 390 395 400  
 Tyr Pro Gly Val Ser Lys Thr Ala Asp Tyr Lys Ala Arg Ala Gln Lys  
 405 410 415  
 Phe Phe Asp Glu Leu Asp Ala Phe Phe Thr Glu Leu Glu Lys Ser Gly  
 420 425 430  
 Arg Lys Val Met Val Val Val Val Pro Glu His Gly Gly Ala Leu Lys  
 435 440 445  
 Gly Asp Arg Met Gln Val Ser Gly Leu Arg Asp Ile Pro Ser Pro Ser  
 450 455 460  
 Ile Thr Asp Val Pro Val Gly Val Lys Phe Phe Gly Met Lys Ala Pro  
 465 470 475 480  
 His Gln Gly Ala Pro Ile Val Ile Glu Gln Pro Ser Ser Phe Leu Ala  
 485 490 495  
 Ile Ser Asp Leu Val Val Arg Val Leu Asp Gly Lys Ile Phe Thr Glu  
 500 505 510  
 Asp Asn Val Asp Trp Lys Lys Leu Thr Ser Gly Leu Pro Gln Thr Ala  
 515 520 525  
 Pro Val Ser Glu Asn Ser Asn Ala Val Val Ile Gln Tyr Gln Asp Lys  
 530 535 540  
 Pro Tyr Val Arg Leu Asn Gly Gly Asp Trp Val Pro Tyr Pro Gln  
 545 550 555

<210> 332  
 <211> 127  
 <212> PRT  
 <213> E. Coli

<400> 332  
 Met Glu Gly Ser Arg Met Lys Tyr Arg Ile Ala Leu Ala Val Ser Leu  
 1 5 10 15  
 Phe Ala Leu Ser Ala Gly Ser Tyr Ala Thr Thr Leu Cys Gln Glu Lys  
 20 25 30  
 Glu Gln Asn Ile Leu Lys Glu Ile Ser Tyr Ala Glu Lys His Gln Asn  
 35 40 45  
 Gln Asn Arg Ile Asp Gly Leu Asn Lys Ala Leu Ser Glu Val Arg Ala  
 50 55 60  
 Asn Cys Ser Asp Ser Gln Leu Arg Ala Asp His Gln Lys Lys Ile Ala  
 65 70 75 80  
 Lys Gln Lys Asp Glu Val Ala Glu Arg Gln Gln Asp Leu Ala Glu Ala  
 85 90 95  
 Lys Gln Lys Gly Asp Ala Asp Lys Ile Ala Lys Arg Glu Arg Lys Leu  
 100 105 110  
 Ala Glu Ala Gln Glu Glu Leu Lys Lys Leu Glu Ala Arg Asp Tyr  
 115 120 125

<210> 333  
 <211> 101  
 <212> PRT  
 <213> E. Coli

<400> 333  
 Met Ser Lys Glu His Thr Thr Glu His Leu Arg Ala Glu Leu Lys Ser

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1           5           10           15
Leu Ser Asp Thr Leu Glu Glu Val Leu Ser Ser Ser Gly Glu Lys Ser
20
Lys Glu Glu Leu Ser Lys Ile Arg Ser Lys Ala Glu Gln Ala Leu Lys
35
Gln Ser Arg Tyr Arg Leu Gly Glu Thr Gly Asp Ala Ile Ala Lys Gln
50
Thr Arg Val Ala Ala Ala Arg Ala Asp Glu Tyr Val Arg Glu Asn Pro
65
Trp Thr Gly Val Gly Ile Gly Ala Ala Ile Gly Val Val Leu Gly Val
85
Leu Leu Ser Arg Arg
100

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<210> 334
<211> 134
<212> PRT
<213> E. Coli

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<400> 334
Met Ala Asp Thr His His Ala Gln Gly Pro Gly Lys Ser Val Leu Gly
1           5           10           15
Ile Gly Gln Arg Ile Val Ser Ile Met Val Glu Met Val Glu Thr Arg
20
Leu Arg Leu Ala Val Val Glu Leu Glu Glu Glu Lys Ala Asn Leu Phe
35
Gln Leu Leu Leu Met Leu Gly Leu Thr Met Leu Phe Ala Ala Phe Gly
50
Leu Met Ser Leu Met Val Leu Ile Ile Trp Ala Val Asp Pro Gln Tyr
65
Arg Leu Asn Ala Met Ile Ala Thr Thr Val Val Leu Leu Leu Ala
85
Leu Ile Gly Gly Ile Trp Thr Leu Arg Lys Ser Arg Lys Ser Thr Leu
100
Leu Arg His Thr Arg His Glu Leu Ala Asn Asp Arg Gln Leu Leu Glu
115
Glu Glu Ser Arg Glu Gln
130

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<210> 335
<211> 99
<212> PRT
<213> E. Coli

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<400> 335
Met Ser Ser Lys Val Glu Arg Glu Arg Arg Lys Ala Gln Leu Leu Ser
1           5           10           15
Gln Ile Gln Gln Gln Arg Leu Asp Leu Ser Ala Ser Arg Arg Glu Trp
20
Leu Glu Thr Thr Gly Ala Tyr Asp Arg Arg Trp Asn Met Leu Leu Ser
35
Leu Arg Ser Trp Ala Leu Val Gly Ser Ser Val Met Ala Ile Trp Thr
50
Ile Arg His Pro Asn Met Leu Val Arg Trp Ala Arg Arg Gly Phe Gly
65
Val Trp Ser Ala Trp Arg Leu Val Lys Thr Thr Leu Lys Gln Gln Gln
85
Leu Arg Gly
90

```

<210> 336  
 <211> 160  
 <212> PRT  
 <213> E. Coli

<400> 336  
 Met Ile Leu Ser Ile Asp Ser Asn Asp Ala Asn Thr Ala Pro Leu His  
 1 5 10 15  
 Lys Lys Thr Ile Ser Ser Leu Ser Gly Ala Val Glu Ser Met Met Lys  
 20 25 30  
 Lys Leu Glu Asp Val Gly Val Leu Val Ala Arg Ile Leu Met Pro Ile  
 35 40 45  
 Leu Phe Ile Thr Ala Gly Trp Gly Lys Ile Thr Gly Tyr Ala Gly Thr  
 50 55 60  
 Gln Gln Tyr Met Glu Ala Met Gly Val Pro Gly Phe Met Leu Pro Leu  
 65 70 75 80  
 Val Ile Leu Leu Glu Phe Gly Gly Gly Leu Ala Ile Leu Phe Gly Phe  
 85 90 95  
 Leu Thr Arg Thr Thr Ala Leu Phe Thr Ala Gly Phe Thr Leu Leu Thr  
 100 105 110  
 Ala Phe Leu Phe His Ser Asn Phe Ala Glu Gly Val Asn Ser Leu Met  
 115 120 125  
 Phe Met Lys Asn Leu Thr Ile Ser Gly Gly Phe Leu Leu Leu Ala Ile  
 130 135 140  
 Thr Gly Pro Gly Ala Tyr Ser Ile Asp Arg Leu Leu Asn Lys Lys Trp  
 145 150 155 160

<210> 337  
 <211> 296  
 <212> PRT  
 <213> E. Coli

<400> 337  
 Met Ile Lys Lys Thr Thr Glu Ile Asp Ala Ile Leu Leu Asn Leu Asn  
 1 5 10 15  
 Lys Ala Ile Asp Ala His Tyr Gln Trp Leu Val Ser Met Phe His Ser  
 20 25 30  
 Val Val Ala Arg Asp Ala Ser Lys Pro Glu Ile Thr Asp Asn His Ser  
 35 40 45  
 Tyr Gly Leu Cys Gln Phe Gly Arg Trp Ile Asp His Leu Gly Pro Leu  
 50 55 60  
 Asp Asn Asp Glu Leu Pro Tyr Val Arg Leu Met Asp Ser Ala His Gln  
 65 70 75 80  
 His Met His Asn Cys Gly Arg Glu Leu Met Leu Ala Ile Val Glu Asn  
 85 90 95  
 His Trp Gln Asp Ala His Phe Asp Ala Phe Gln Glu Gly Leu Leu Ser  
 100 105 110  
 Phe Thr Ala Ala Leu Thr Asp Tyr Lys Ile Tyr Leu Leu Thr Ile Arg  
 115 120 125  
 Ser Asn Met Asp Val Leu Thr Gly Leu Pro Gly Arg Arg Val Leu Asp  
 130 135 140  
 Glu Ser Phe Asp His Gln Leu Arg Asn Ala Glu Pro Leu Asn Leu Tyr  
 145 150 155 160  
 Leu Met Leu Leu Asp Ile Asp Arg Phe Lys Leu Val Asn Asp Thr Tyr  
 165 170 175



Gly His Leu Ile Gly Asp Val Val Leu Arg Thr Leu Ala Thr Tyr Leu  
 180 185 190  
 Ala Ser Trp Thr Arg Asp Tyr Glu Thr Val Tyr Arg Tyr Gly Gly Glu  
 195 200 205  
 Glu Phe Ile Ile Ile Val Lys Ala Ala Asn Asp Glu Glu Ala Cys Arg  
 210 215 220  
 Ala Gly Val Arg Ile Cys Gln Leu Val Asp Asn His Ala Ile Thr His  
 225 230 235 240  
 Ser Glu Gly His Ile Asn Ile Thr Val Thr Ala Gly Val Ser Arg Ala  
 245 250 255  
 Phe Pro Glu Glu Pro Leu Asp Val Val Ile Gly Arg Ala Asp Arg Ala  
 260 265 270  
 Met Tyr Glu Gly Lys Gln Thr Gly Arg Asn Arg Cys Met Phe Ile Asp  
 275 280 285  
 Glu Gln Asn Val Ile Asn Arg Val  
 290 295

<210> 338  
 <211> 203  
 <212> PRT  
 <213> E. Coli

<400> 338  
 Met Arg Leu Arg Val Val Pro Gly Phe Ile Ser Pro Pro Pro Gly Phe  
 1 5 10 15  
 Gly Gly Leu Gly Tyr Thr Pro Thr Ala Arg Ala Cys Val Asn Ile Ser  
 20 25 30  
 Ile Pro Leu Gln Leu Arg Val Ile Asp Met Leu Asp Val Phe Thr Pro  
 35 40 45  
 Leu Leu Lys Leu Phe Ala Asn Glu Pro Leu Glu Arg Leu Met Tyr Thr  
 50 55 60  
 Ile Ile Ile Phe Gly Leu Thr Leu Trp Leu Ile Pro Lys Glu Phe Thr  
 65 70 75 80  
 Val Ala Phe Asn Ala Tyr Thr Glu Ile Pro Trp Leu Phe Gln Ile Ile  
 85 90 95  
 Val Phe Ala Phe Ser Phe Val Val Ala Ile Ser Phe Ser Arg Leu Arg  
 100 105 110  
 Ala His Ile Gln Lys His Tyr Ser Leu Leu Pro Glu Gln Arg Val Leu  
 115 120 125  
 Leu Arg Leu Ser Glu Lys Glu Ile Ala Val Phe Lys Asp Phe Leu Lys  
 130 135 140  
 Thr Gly Asn Leu Ile Ile Thr Ser Pro Cys Arg Asn Pro Val Met Lys  
 145 150 155 160  
 Lys Leu Glu Arg Lys Gly Ile Ile Gln His Gln Ser Asp Ser Ala Asn  
 165 170 175  
 Cys Ser Tyr Tyr Leu Val Thr Glu Lys Tyr Ser His Phe Met Lys Leu  
 180 185 190  
 Phe Trp Asn Ser Arg Ser Arg Arg Phe Asn Arg  
 195 200

<210> 339  
 <211> 58  
 <212> PRT  
 <213> E. Coli

<400> 339  
 Met Leu Leu Gln Pro Ser Ala Arg Thr Ser Phe Gly Phe Lys Cys Phe

1                    5                    10                    15  
 Ala Phe Gly Ile Arg His Gly Ser Glu Arg Ser Ile Leu Val Gly Glu  
                   20                    25                    30  
 His Ala Ala His Gln Gly Phe Val Val Ala Glu Val Asp Phe Leu His  
                   35                    40                    45  
 Phe Ala Asn Leu Thr Ser Cys Cys Tyr Val  
                   50                    55

<210> 340  
 <211> 1426  
 <212> PRT  
 <213> E. Coli

<400> 340  
 Met Ser Gly Lys Pro Ala Ala Arg Gln Gly Asp Met Thr Gln Tyr Gly  
 1                    5                    10                    15  
 Gly Pro Ile Val Gln Gly Ser Ala Gly Val Arg Ile Gly Ala Pro Thr  
                   20                    25                    30  
 Gly Val Ala Cys Ser Val Cys Pro Gly Gly Met Thr Ser Gly Asn Pro  
                   35                    40                    45  
 Val Asn Pro Leu Leu Gly Ala Lys Val Leu Pro Gly Glu Thr Asp Leu  
                   50                    55                    60  
 Ala Leu Pro Gly Pro Leu Pro Phe Ile Leu Ser Arg Thr Tyr Ser Ser  
 65                    70                    75                    80  
 Tyr Arg Thr Lys Thr Pro Ala Pro Val Gly Val Phe Gly Pro Gly Trp  
                   85                    90                    95  
 Lys Ala Pro Ser Asp Ile Arg Leu Gln Leu Arg Asp Asp Gly Leu Ile  
                   100                    105                    110  
 Leu Asn Asp Asn Gly Gly Arg Ser Ile His Phe Glu Pro Leu Leu Pro  
                   115                    120                    125  
 Gly Glu Ala Val Tyr Ser Arg Ser Glu Ser Met Trp Leu Val Arg Gly  
 130                    135                    140  
 Gly Lys Ala Ala Gln Pro Asp Gly His Thr Leu Ala Arg Leu Trp Gly  
 145                    150                    155                    160  
 Ala Leu Pro Pro Asp Ile Arg Leu Ser Pro His Leu Tyr Leu Ala Thr  
                   165                    170                    175  
 Asn Ser Ala Gln Gly Pro Trp Trp Ile Leu Gly Trp Ser Glu Arg Val  
                   180                    185                    190  
 Pro Gly Ala Glu Asp Val Leu Pro Ala Pro Leu Pro Pro Tyr Arg Val  
                   195                    200                    205  
 Leu Thr Gly Met Ala Asp Arg Phe Gly Arg Thr Leu Thr Tyr Arg Arg  
                   210                    215                    220  
 Glu Ala Ala Gly Asp Leu Ala Gly Glu Ile Thr Gly Val Thr Asp Gly  
 225                    230                    235                    240  
 Ala Gly Arg Glu Phe Arg Leu Val Leu Thr Thr Gln Ala Gln Arg Ala  
                   245                    250                    255  
 Glu Glu Ala Arg Thr Ser Ser Leu Ser Ser Ser Asp Ser Ser Arg Pro  
                   260                    265                    270  
 Leu Ser Ala Ser Ala Phe Pro Asp Thr Leu Pro Gly Thr Glu Tyr Gly  
                   275                    280                    285  
 Pro Asp Arg Gly Ile Arg Leu Ser Ala Val Trp Leu Met His Asp Pro  
                   290                    295                    300  
 Ala Tyr Pro Glu Ser Leu Pro Ala Ala Pro Leu Val Arg Tyr Thr Tyr  
 305                    310                    315                    320  
 Thr Glu Ala Gly Glu Leu Leu Ala Val Tyr Asp Arg Ser Asn Thr Gln  
                   325                    330                    335  
 Val Arg Ala Phe Thr Tyr Asp Ala Gln His Pro Gly Arg Met Val Ala  
                   340                    345                    350  
 His Arg Tyr Ala Gly Arg Pro Glu Met Arg Tyr Arg Tyr Asp Asp Thr  
                   355                    360                    365

Gly Arg Val Val Glu Gln Leu Asn Pro Ala Gly Leu Ser Tyr Arg Tyr  
 370 375 380  
 Leu Tyr Glu Gln Asp Arg Ile Thr Val Thr Asp Ser Leu Asn Arg Arg  
 385 390 395 400  
 Glu Val Leu His Thr Glu Gly Gly Ala Gly Leu Lys Arg Val Val Lys  
 405 410 415  
 Lys Glu Leu Ala Asp Gly Ser Val Thr Arg Ser Gly Tyr Asp Ala Ala  
 420 425 430  
 Gly Arg Leu Thr Ala Gln Thr Asp Ala Ala Gly Arg Arg Thr Glu Tyr  
 435 440 445  
 Gly Leu Asn Val Val Ser Gly Asp Ile Thr Asp Ile Thr Thr Pro Asp  
 450 455 460  
 Gly Arg Glu Thr Lys Phe Tyr Tyr Asn Asp Gly Asn Gln Leu Thr Ala  
 465 470 475 480  
 Val Val Ser Pro Asp Gly Leu Glu Ser Arg Arg Glu Tyr Asp Glu Pro  
 485 490 495  
 Gly Arg Leu Val Ser Glu Thr Ser Arg Ser Gly Glu Thr Val Arg Tyr  
 500 505 510  
 Arg Tyr Asp Asp Ala His Ser Glu Leu Pro Ala Thr Thr Thr Asp Ala  
 515 520 525  
 Thr Gly Ser Thr Arg Gln Met Thr Trp Ser Arg Tyr Gly Gln Leu Leu  
 530 535 540  
 Ala Phe Thr Asp Cys Ser Gly Tyr Gln Thr Arg Tyr Glu Tyr Asp Arg  
 545 550 555 560  
 Phe Gly Gln Met Thr Ala Val His Arg Glu Glu Gly Ile Ser Leu Tyr  
 565 570 575  
 Arg Arg Tyr Asp Asn Arg Gly Arg Leu Thr Ser Val Lys Asp Ala Gln  
 580 585 590  
 Gly Arg Glu Thr Arg Tyr Glu Tyr Asn Ala Ala Gly Asp Leu Thr Ala  
 595 600 605  
 Val Ile Thr Pro Asp Gly Asn Arg Ser Glu Thr Gln Tyr Asp Ala Trp  
 610 615 620  
 Gly Lys Ala Val Ser Thr Thr Gln Gly Gly Leu Thr Arg Ser Met Glu  
 625 630 635 640  
 Tyr Asp Ala Ala Gly Arg Val Ile Ser Leu Thr Asn Glu Asn Gly Ser  
 645 650 655  
 His Ser Val Phe Ser Tyr Asp Ala Leu Asp Arg Leu Val Gln Gln Gly  
 660 665 670  
 Gly Phe Asp Gly Arg Thr Gln Arg Tyr His Tyr Asp Leu Thr Gly Lys  
 675 680 685  
 Leu Thr Gln Ser Glu Asp Glu Gly Leu Val Ile Leu Trp Tyr Tyr Asp  
 690 695 700  
 Glu Ser Asp Arg Ile Thr His Arg Thr Val Asn Gly Glu Pro Ala Glu  
 705 710 715 720  
 Gln Trp Gln Tyr Asp Gly His Gly Trp Leu Thr Asp Ile Ser His Leu  
 725 730 735  
 Ser Glu Gly His Arg Val Ala Val His Tyr Gly Tyr Asp Asp Lys Gly  
 740 745 750  
 Arg Leu Thr Gly Glu Cys Gln Thr Val Glu Asn Pro Glu Thr Gly Glu  
 755 760 765  
 Leu Leu Trp Gln His Glu Thr Lys His Ala Tyr Asn Glu Gln Gly Leu  
 770 775 780  
 Ala Asn Arg Val Thr Pro Asp Ser Leu Pro Pro Val Glu Trp Leu Thr  
 785 790 795 800  
 Tyr Gly Ser Gly Tyr Leu Ala Gly Met Lys Leu Gly Gly Thr Pro Leu  
 805 810 815  
 Val Glu Tyr Thr Arg Asp Arg Leu His Arg Glu Thr Val Arg Ser Phe  
 820 825 830  
 Gly Ser Met Ala Gly Ser Asn Ala Ala Tyr Glu Leu Thr Ser Thr Tyr  
 835 840 845  
 Thr Pro Ala Gly Gln Leu Gln Ser Gln His Leu Asn Ser Leu Val Tyr

|                         |                     |                     |
|-------------------------|---------------------|---------------------|
| 850                     | 855                 | 860                 |
| Asp Arg Asp Tyr Gly Trp | Ser Asp Asn Gly Asp | Leu Val Arg Ile Ser |
| 865                     | 870                 | 875                 |
| Gly Pro Arg Gln Thr Arg | Glu Tyr Gly Tyr Ser | Ala Thr Gly Arg Leu |
| 885                     | 890                 | 895                 |
| Glu Ser Val Arg Thr Leu | Ala Pro Asp Leu Asp | Ile Arg Ile Pro Tyr |
| 900                     | 905                 | 910                 |
| Ala Thr Asp Pro Ala Gly | Asn Arg Leu Pro Asp | Pro Glu Leu His Pro |
| 915                     | 920                 | 925                 |
| Asp Ser Thr Leu Thr Val | Trp Pro Asp Asn Arg | Ile Ala Glu Asp Ala |
| 930                     | 935                 | 940                 |
| His Tyr Val Tyr Arg His | Asp Glu Tyr Gly Arg | Leu Thr Glu Lys Thr |
| 945                     | 950                 | 955                 |
| Asp Arg Ile Pro Ala Gly | Val Ile Arg Thr Asp | Asp Glu Arg Thr His |
| 965                     | 970                 | 975                 |
| His Tyr His Tyr Asp Ser | Gln His Arg Leu Val | Phe Tyr Thr Arg Ile |
| 980                     | 985                 | 990                 |
| Gln His Gly Glu Pro Leu | Val Glu Ser Arg Tyr | Leu Tyr Asp Pro Leu |
| 995                     | 1000                | 1005                |
| Gly Arg Arg Met Ala Lys | Arg Val Trp Arg Arg | Glu Arg Asp Leu Thr |
| 1010                    | 1015                | 1020                |
| Gly Trp Met Ser Leu Ser | Arg Lys Pro Glu Val | Thr Trp Tyr Gly Trp |
| 1025                    | 1030                | 1035                |
| Asp Gly Asp Arg Leu Thr | Thr Val Gln Thr Asp | Thr Thr Arg Ile Gln |
| 1045                    | 1050                | 1055                |
| Thr Val Tyr Glu Pro Gly | Ser Phe Thr Pro Leu | Ile Arg Val Glu Thr |
| 1060                    | 1065                | 1070                |
| Glu Asn Gly Glu Arg Glu | Lys Ala Gln Arg Arg | Ser Leu Ala Glu Thr |
| 1075                    | 1080                | 1085                |
| Leu Gln Gln Glu Gly Ser | Glu Asn Gly His Gly | Val Phe Pro Ala     |
| 1090                    | 1095                | 1100                |
| Glu Leu Val Arg Leu Leu | Asp Arg Leu Glu Glu | Glu Ile Arg Ala Asp |
| 1105                    | 1110                | 1115                |
| Arg Val Ser Ser Glu Ser | Arg Ala Trp Leu Ala | Gln Cys Gly Leu Thr |
| 1125                    | 1130                | 1135                |
| Val Glu Gln Leu Ala Arg | Gln Val Glu Pro Glu | Tyr Thr Pro Ala Arg |
| 1140                    | 1145                | 1150                |
| Lys Ala His Leu Tyr His | Cys Asp His Arg Gly | Leu Pro Leu Ala Leu |
| 1155                    | 1160                | 1165                |
| Ile Ser Glu Asp Gly Asn | Thr Ala Trp Ser Ala | Glu Tyr Asp Glu Trp |
| 1170                    | 1175                | 1180                |
| Gly Asn Gln Leu Asn Glu | Glu Asn Pro His His | Val Tyr Gln Pro Tyr |
| 1185                    | 1190                | 1195                |
| Arg Leu Pro Gly Gln Gln | His Asp Glu Glu Ser | Gly Leu Tyr Tyr Asn |
| 1205                    | 1210                | 1215                |
| Arg His Arg Tyr Tyr Asp | Pro Leu Gln Gly Arg | Tyr Ile Thr Gln Asp |
| 1220                    | 1225                | 1230                |
| Pro Met Gly Leu Lys Gly | Gly Trp Asn Leu Tyr | Gln Tyr Pro Leu Asn |
| 1235                    | 1240                | 1245                |
| Pro Leu Gln Gln Ile Asp | Pro Met Gly Leu Leu | Gln Thr Trp Asp Asp |
| 1250                    | 1255                | 1260                |
| Ala Arg Ser Gly Ala Cys | Thr Gly Gly Val Cys | Gly Val Leu Ser Arg |
| 1265                    | 1270                | 1275                |
| Ile Ile Gly Pro Ser Lys | Phe Asp Ser Thr Ala | Asp Ala Ala Leu Asp |
| 1285                    | 1290                | 1295                |
| Ala Leu Lys Glu Thr Gln | Asn Arg Ser Leu Cys | Asn Asp Met Glu Tyr |
| 1300                    | 1305                | 1310                |
| Ser Gly Ile Val Cys Lys | Asp Thr Asn Gly Lys | Tyr Phe Ala Ser Lys |
| 1315                    | 1320                | 1325                |
| Ala Glu Thr Asp Asn Leu | Arg Lys Glu Ser Tyr | Pro Leu Lys Arg Lys |
| 1330                    | 1335                | 1340                |

Cys Pro Thr Gly Thr Asp Arg Val Ala Ala Tyr His Thr His Gly Ala  
 1345 1350 1355 1360  
 Asp Ser His Gly Asp Tyr Val Asp Glu Phe Phe Ser Ser Ser Asp Lys  
 1365 1370 1375  
 Asn Leu Val Arg Ser Lys Asp Asn Asn Leu Glu Ala Phe Tyr Leu Ala  
 1380 1385 1390  
 Thr Pro Asp Gly Arg Phe Glu Ala Leu Asn Asn Lys Gly Glu Tyr Ile  
 1395 1400 1405  
 Phe Ile Arg Asn Ser Val Pro Gly Leu Ser Ser Val Cys Ile Pro Tyr  
 1410 1415 1420  
 His Asp  
 1425

<210> 341  
 <211> 122  
 <212> PRT  
 <213> E. Coli

<400> 341  
 Met Lys Tyr Ser Ser Ile Phe Ser Met Leu Ser Phe Phe Ile Leu Phe  
 1 5 10 15  
 Ala Cys Asn Glu Thr Ala Val Tyr Gly Ser Asp Glu Asn Ile Ile Phe  
 20 25 30  
 Met Arg Tyr Val Glu Lys Leu His Leu Asp Lys Tyr Ser Val Lys Asn  
 35 40 45  
 Thr Val Lys Thr Glu Thr Met Ala Ile Gln Leu Ala Glu Ile Tyr Val  
 50 55 60  
 Arg Tyr Arg Tyr Gly Glu Arg Ile Ala Glu Glu Glu Lys Pro Tyr Leu  
 65 70 75 80  
 Ile Thr Glu Leu Pro Asp Ser Trp Val Val Glu Gly Ala Lys Leu Pro  
 85 90 95  
 Tyr Glu Val Ala Gly Gly Val Phe Ile Ile Glu Ile Asn Lys Lys Asn  
 100 105 110  
 Gly Cys Val Leu Asn Phe Leu His Ser Lys  
 115 120

<210> 342  
 <211> 236  
 <212> PRT  
 <213> E. Coli

<400> 342  
 Met Leu Ala Leu Met Asp Ala Asp Gly Asn Ile Ala Trp Ser Gly Glu  
 1 5 10 15  
 Tyr Asp Glu Trp Gly Asn Gln Leu Asn Glu Glu Asn Pro His His Leu  
 20 25 30  
 His Gln Pro Tyr Arg Leu Pro Gly Gln Gln Tyr Asp Lys Glu Ser Gly  
 35 40 45  
 Leu Tyr Tyr Asn Arg Asn Arg Tyr Tyr Asp Pro Leu Gln Gly Arg Tyr  
 50 55 60  
 Ile Thr Gln Asp Pro Ile Gly Leu Glu Gly Gly Trp Ser Leu Tyr Ala  
 65 70 75 80  
 Tyr Pro Leu Asn Pro Val Asn Gly Ile Asp Pro Leu Gly Leu Ser Pro  
 85 90 95  
 Ala Asp Val Ala Leu Ile Arg Arg Lys Asp Gln Leu Asn His Gln Arg  
 100 105 110  
 Ala Trp Asp Ile Leu Ser Asp Thr Tyr Glu Asp Met Lys Arg Leu Asn  
 115 120 125  
 Leu Gly Gly Thr Asp Gln Phe Phe His Cys Met Ala Phe Cys Arg Val

```

      130              135              140
Ser Lys Leu Asn Asp Ala Gly Val Ser Arg Ser Ala Lys Gly Leu Gly
145              150              155              160
Tyr Glu Lys Glu Ile Arg Asp Tyr Gly Leu Asn Leu Phe Gly Met Tyr
      165              170              175
Gly Arg Lys Val Lys Leu Ser His Ser Glu Met Ile Glu Asp Asn Lys
      180              185              190
Lys Asp Leu Ala Val Asn Asp His Gly Leu Thr Cys Pro Ser Thr Thr
      195              200              205
Asp Cys Ser Asp Arg Cys Ser Asp Tyr Ile Asn Pro Glu His Lys Lys
210              215              220
Thr Ile Lys Ala Leu Gln Asp Ala Gly Tyr Leu Lys
225              230              235

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<210> 343  
 <211> 86  
 <212> PRT  
 <213> E. Coli

```

      <400> 343
Met Leu Ala Ile Ser Ser Asn Leu Ser Lys Met Ile Ile Phe Ile Phe
1              5              10              15
Ala Ile Ile Ile Ile Val Val Leu Cys Val Ile Thr Tyr Leu Tyr Leu
      20              25              30
Tyr Lys Asp Glu Ser Leu Val Ser Lys His Tyr Ile Asn Tyr Met Ala
      35              40              45
Ile Pro Glu Asn Asp Gly Val Phe Thr Trp Leu Pro Asp Phe Phe Pro
      50              55              60
His Val Ala Val Asp Ile Ser Ile Tyr Thr Asn Val Glu Asp Asp Tyr
65              70              75              80
Phe Phe Leu Ile Phe Pro
      85

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<210> 344  
 <211> 63  
 <212> PRT  
 <213> E. Coli

```

      <400> 344
Met Arg Ala Arg Glu Gln Val Ala Lys Ile Val Ser Lys Asn Asp Pro
1              5              10              15
Asp Thr Lys Lys Val Trp Cys Lys Tyr Gly Lys Ile Pro Gly Gln Gly
      20              25              30
Asp Gly Val Asn Leu Phe Phe Val Gly Glu Ile Asn Val Thr His Tyr
      35              40              45
Phe Ile Thr Asn Ile Gly Ala Gly Leu Pro Asp Ala Cys Ala Glu
50              55              60

```

<210> 345  
 <211> 167  
 <212> PRT  
 <213> E. Coli

```

      <400> 345
Met Pro Gly Asn Ser Pro His Tyr Gly Arg Trp Pro Gln His Asp Phe
1              5              10              15

```

Thr Ser Leu Lys Lys Leu Arg Pro Gln Ser Val Thr Ser Arg Ile Gln  
 20 25 30  
 Pro Gly Ser Asp Val Ile Val Cys Ala Glu Met Asp Glu Gln Trp Gly  
 35 40 45  
 Tyr Val Gly Ala Lys Ser Arg Gln Arg Trp Leu Phe Tyr Ala Tyr Asp  
 50 55 60  
 Ser Leu Arg Lys Thr Val Val Ala His Val Phe Gly Glu Arg Thr Met  
 65 70 75 80  
 Ala Thr Leu Gly Arg Leu Met Ser Leu Leu Ser Pro Phe Asp Val Val  
 85 90 95  
 Ile Trp Met Thr Asp Gly Trp Pro Leu Tyr Glu Ser Arg Leu Lys Gly  
 100 105 110  
 Lys Leu His Val Ile Ser Lys Arg Tyr Thr Gln Arg Ile Glu Arg His  
 115 120 125  
 Asn Leu Asn Leu Arg Gln His Leu Ala Arg Leu Gly Arg Lys Ser Leu  
 130 135 140  
 Ser Phe Ser Lys Ser Val Glu Leu His Asp Lys Val Ile Gly His Tyr  
 145 150 155 160  
 Leu Asn Ile Lys His Tyr Gln  
 165

<210> 346  
 <211> 91  
 <212> PRT  
 <213> E. Coli

<400> 346  
 Met Ala Ser Val Ser Ile Ser Cys Pro Ser Cys Ser Ala Thr Asp Gly  
 1 5 10 15  
 Val Val Arg Asn Gly Lys Ser Thr Ala Gly His Gln Arg Tyr Leu Cys  
 20 25 30  
 Ser His Cys Arg Lys Thr Trp Gln Leu Gln Phe Thr Tyr Thr Ala Ser  
 35 40 45  
 Gln Pro Gly Thr His Gln Lys Ile Ile Asp Met Ala Met Asn Gly Val  
 50 55 60  
 Gly Cys Arg Ala Thr Ala Arg Ile Met Gly Val Gly Leu Asn Thr Ile  
 65 70 75 80  
 Leu Arg His Leu Lys Asn Ser Gly Arg Ser Arg  
 85 90

<210> 347  
 <211> 138  
 <212> PRT  
 <213> E. Coli

<400> 347  
 Met Met Thr Lys Thr Gln Ile Asn Lys Leu Ile Lys Met Met Asn Asp  
 1 5 10 15  
 Leu Asp Tyr Pro Phe Glu Ala Pro Leu Lys Glu Ser Phe Ile Glu Ser  
 20 25 30  
 Ile Ile Gln Ile Glu Phe Asn Ser Asn Ser Thr Asn Cys Leu Glu Lys  
 35 40 45  
 Leu Cys Asn Glu Val Ser Ile Leu Phe Lys Asn Gln Pro Asp Tyr Leu  
 50 55 60  
 Thr Phe Leu Arg Ala Met Asp Gly Phe Glu Val Asn Gly Leu Arg Leu  
 65 70 75 80  
 Phe Ser Leu Ser Ile Pro Glu Pro Ser Val Lys Asn Leu Phe Ala Val  
 85 90 95

Asn Glu Phe Tyr Arg Asn Asn Asp Asp Phe Ile Asn Pro Asp Leu Gln  
 100 105 110  
 Glu Arg Leu Val Ile Gly Asp Tyr Ser Ile Ser Ile Phe Thr Tyr Asp  
 115 120 125  
 Ile Lys Gly Asp Ala Ala Asn Leu Leu Ile  
 130 135

<210> 348  
 <211> 392  
 <212> PRT  
 <213> E. Coli

<400> 348  
 Met Ser Asn Ile Val Tyr Leu Thr Val Thr Gly Glu Gln Gln Gly Ser  
 1 5 10 15  
 Ile Ser Ala Gly Cys Gly Thr Ser Glu Ser Thr Gly Asn Arg Trp Gln  
 20 25 30  
 Ser Gly His Glu Asp Glu Ile Phe Thr Phe Ser Leu Leu Asn Asn Ile  
 35 40 45  
 Asn Asn Thr Gly Leu Gly Ser Gln Phe His Gly Ile Thr Phe Cys Lys  
 50 55 60  
 Leu Ile Asp Lys Ser Thr Pro Leu Phe Ile Asn Ser Ile Asn Asn Asn  
 65 70 75 80  
 Glu Gln Leu Phe Met Gly Phe Asp Phe Tyr Arg Ile Asn Arg Phe Gly  
 85 90 95  
 Arg Leu Glu Lys Tyr Tyr Tyr Ile Gln Leu Arg Gly Ala Phe Leu Ser  
 100 105 110  
 Ala Ile His His Gln Ile Ile Glu Asn Gln Leu Asp Thr Glu Thr Ile  
 115 120 125  
 Thr Ile Ser Tyr Glu Phe Ile Leu Cys Gln His Leu Ile Ala Asn Thr  
 130 135 140  
 Glu Phe Ser Tyr Leu Ala Leu Pro Glu Asn Tyr Asn Arg Leu Phe Leu  
 145 150 155 160  
 Pro Asn Ser Lys Asn Gln Thr Asn Asn Arg Phe Lys Thr Leu Asn Ser  
 165 170 175  
 Lys Ala Ile Gly Arg Leu Leu Ala Ala Gly Gly Val Tyr Asn Gly Asn  
 180 185 190  
 Ile Glu Gly Phe Arg Asp Thr Ala Glu Lys Leu Gly Gly Asp Ala Ile  
 195 200 205  
 Lys Gly Tyr Asp Gln Ile Leu Asn Glu Lys Thr Ala Gly Ile Ala Ile  
 210 215 220  
 Ala Thr Ala Ser Ile Leu Leu Thr Lys Arg Ser Asn Val Asp Thr Tyr  
 225 230 235 240  
 Thr Glu Ile Asn Ser Tyr Leu Gly Lys Leu Arg Gly Gln Gln Lys Leu  
 245 250 255  
 Leu Asp Gly Ile Asp Ile Ile Glu Ile Ile Tyr Ile Lys Arg Pro Ser  
 260 265 270  
 Lys Asp Leu Ala Asn Leu Arg Lys Glu Phe Asn Lys Thr Val Arg Lys  
 275 280 285  
 Asn Phe Leu Ile Lys Leu Ala Lys Thr Ser Glu Ala Ser Gly Arg Phe  
 290 295 300  
 Asn Ala Glu Asp Leu Leu Arg Met Arg Lys Gly Asn Val Pro Leu Asn  
 305 310 315 320  
 Tyr Asn Val His His Lys Leu Ser Leu Asp Asp Gly Gly Thr Asn Asp  
 325 330 335  
 Phe Glu Asn Leu Val Leu Ile Glu Asn Glu Pro Tyr His Lys Val Phe  
 340 345 350  
 Thr Asn Met Gln Ser Arg Ile Ala Lys Gly Ile Leu Val Gly Glu Ser  
 355 360 365  
 Lys Ile Thr Pro Trp Ala Ile Pro Ser Gly Ser Ile Tyr Pro Pro Met



370 375 380  
 Lys Asn Ile Met Asp His Thr Lys  
 385 390

<210> 349  
 <211> 221  
 <212> PRT  
 <213> E. Coli

<400> 349  
 Met Val Leu Ala Leu Asn Tyr Asn Met His Gly Val Asn Ile Arg Ser  
 1 5 10 15  
 Glu Asn Ala Ala Lys Pro His Thr Met Pro Ser Arg Tyr Leu Cys Glu  
 20 25 30  
 Tyr Ile Arg Ser Ile Glu Lys Asn Gly His Ala Leu Asp Phe Gly Cys  
 35 40 45  
 Gly Lys Leu Arg Tyr Ser Asp Glu Leu Ile Ser Lys Phe Asp Glu Val  
 50 55 60  
 Thr Phe Leu Asp Ser Lys Arg Gln Leu Glu Arg Glu Gln Ile Ile Arg  
 65 70 75 80  
 Gly Ile Lys Thr Lys Ile Ile Asp Tyr Val Pro Arg Tyr Tyr Lys Asn  
 85 90 95  
 Ala Asn Thr Val Ala Phe Glu Asp Val Asp Lys Ile Ile Gly Gly Tyr  
 100 105 110  
 Asp Phe Ile Leu Cys Ser Asn Val Leu Ser Ala Val Pro Cys Arg Asp  
 115 120 125  
 Thr Ile Asp Lys Ile Val Leu Ser Ile Lys Arg Leu Leu Lys Ser Gly  
 130 135 140  
 Gly Glu Thr Leu Ile Val Asn Gln Tyr Lys Ser Ser Tyr Phe Lys Lys  
 145 150 155 160  
 Tyr Glu Thr Gly Arg Lys His Leu Tyr Gly Tyr Ile Tyr Lys Asn Ser  
 165 170 175  
 Lys Ser Val Ser Tyr Tyr Gly Leu Leu Asp Glu Leu Ala Val Gln Glu  
 180 185 190  
 Ile Cys Ser Ser His Gly Leu Glu Ile Leu Lys Ser Trp Ser Lys Ala  
 195 200 205  
 Gly Ser Ser Tyr Val Thr Val Gly Ser Cys Asn Ala Ile  
 210 215 220

<210> 350  
 <211> 234  
 <212> PRT  
 <213> E. Coli

<400> 350  
 Met Asn Asn Met Phe Glu Pro Pro Lys Asn Tyr Asn Glu Met Leu Pro  
 1 5 10 15  
 Lys Leu His Lys Ala Thr Phe Leu Asn Thr Leu Ile Tyr Cys Ile Leu  
 20 25 30  
 Leu Val Ile Tyr Glu Tyr Ile Pro Leu Ile Thr Leu Pro Thr Lys Tyr  
 35 40 45  
 Val Pro Pro Ile Lys Asp His Glu Ser Phe Ile Asn Trp Ala Leu Ser  
 50 55 60  
 Phe Gly Ile Leu Pro Cys Ala Phe Ala Ile Phe Ala Tyr Leu Ile Ser  
 65 70 75 80  
 Gly Ala Leu Asp Leu His Asn Asn Ala Ala Lys Leu Leu Arg Val Arg  
 85 90 95  
 Tyr Leu Trp Asp Lys His Leu Ile Ile Lys Pro Leu Ser Arg Arg Ala

```

      100      105      110
Gly Val Asn Arg Lys Leu Asn Lys Asp Glu Ala His Asn Val Met Ser
      115      120      125
Asn Leu Tyr Tyr Pro Glu Val Arg Lys Ile Glu Asp Lys His Tyr Ile
      130      135      140
Glu Leu Phe Trp Asn Lys Val Tyr Tyr Phe Trp Ile Phe Phe Glu Phe
      145      150      155      160
Ser Ile Ile Ala Leu Ile Ser Phe Leu Ile Ile Phe Phe Cys Lys Gln
      165      170      175
Met Asp Ile Phe His Val Glu Gly Ser Leu Leu Ser Leu Phe Phe Phe
      180      185      190
Val Ile Leu Ser Phe Ser Val Ser Gly Ile Ile Phe Ala Leu Thr Val
      195      200      205
Lys Pro Arg Thr Glu Ser Gln Val Gly Lys Ile Pro Asp Asp Lys Ile
      210      215      220
Lys Glu Phe Phe Thr Lys Asn Asn Ile Asn
      225      230

```

<210> 351  
 <211> 94  
 <212> PRT  
 <213> E. Coli

```

      <400> 351
Met Phe Thr Ile Asn Ala Glu Val Arg Lys Glu Gln Gly Lys Gly Ala
      1      5      10      15
Ser Arg Arg Leu Arg Ala Ala Asn Lys Phe Pro Ala Ile Ile Tyr Gly
      20      25      30
Gly Lys Glu Ala Pro Leu Ala Ile Glu Leu Asp His Asp Lys Val Met
      35      40      45
Asn Met Gln Ala Lys Ala Glu Phe Tyr Ser Glu Val Leu Thr Ile Val
      50      55      60
Val Asp Gly Lys Glu Ile Lys Val Lys Ala Gln Asp Val Gln Arg His
      65      70      75      80
Pro Tyr Lys Pro Lys Leu Gln His Ile Asp Phe Val Arg Ala
      85      90

```

<210> 352  
 <211> 658  
 <212> PRT  
 <213> E. Coli

```

      <400> 352
Met Val Leu Phe Tyr Arg Ala His Trp Arg Asp Tyr Lys Asn Asp Gln
      1      5      10      15
Val Arg Ile Met Met Asn Leu Thr Thr Leu Thr His Arg Asp Ala Leu
      20      25      30
Cys Leu Asn Ala Arg Phe Thr Ser Arg Glu Glu Ala Ile His Ala Leu
      35      40      45
Thr Gln Arg Leu Ala Ala Leu Gly Lys Ile Ser Ser Thr Glu Gln Phe
      50      55      60
Leu Glu Glu Val Tyr Arg Arg Glu Ser Leu Gly Pro Thr Ala Leu Gly
      65      70      75      80
Glu Gly Leu Ala Val Pro His Gly Lys Thr Ala Ala Val Lys Glu Ala
      85      90      95
Ala Phe Ala Val Ala Thr Leu Ser Glu Pro Leu Gln Trp Glu Gly Val
      100      105      110
Asp Gly Pro Glu Ala Val Asp Leu Val Val Leu Leu Ala Ile Pro Pro

```

|   |                         |                 |
|---|-------------------------|-----------------|
| 115   | 120                     | 125             |
| Asn Glu Ala Gly Thr Thr   | His Met Gln Leu Leu Thr | Ala Leu Thr Thr |
| 130   | 135                     | 140             |
| Arg Leu Ala Asp Asp Glu Ile Arg Ala Arg Ile Gln Ser Ala Thr Thr |                         |                 |
| 145   | 150                     | 155             |
| Pro Asp Glu Leu Leu Ser Ala Leu Asp Asp Lys Gly Gly Thr Gln Pro |                         |                 |
| 165   | 170                     | 175             |
| Ser Ala Ser Phe Ser Asn Ala Pro Thr Ile Val Cys Val Thr Ala Cys |                         |                 |
| 180   | 185                     | 190             |
| Pro Ala Gly Ile Ala His Thr Tyr Met Ala Ala Glu Tyr Leu Glu Lys |                         |                 |
| 195   | 200                     | 205             |
| Ala Gly Arg Lys Leu Gly Val Asn Val Tyr Val Glu Lys Gln Gly Ala |                         |                 |
| 210   | 215                     | 220             |
| Asn Gly Ile Glu Gly Arg Leu Thr Ala Asp Gln Leu Asn Ser Ala Thr |                         |                 |
| 225   | 230                     | 235             |
| Ala Cys Ile Phe Ala Ala Glu Val Ala Ile Lys Glu Ser Glu Arg Phe |                         |                 |
| 245   | 250                     | 255             |
| Asn Gly Ile Pro Ala Leu Ser Val Pro Val Ala Glu Pro Ile Arg His |                         |                 |
| 260   | 265                     | 270             |
| Ala Glu Ala Leu Ile Gln Gln Ala Leu Thr Leu Lys Arg Ser Asp Glu |                         |                 |
| 275   | 280                     | 285             |
| Thr Arg Thr Val Gln Gln Asp Thr Gln Pro Val Lys Ser Val Lys Thr |                         |                 |
| 290   | 295                     | 300             |
| Glu Leu Lys Gln Ala Leu Ser Gly Ile Ser Phe Ala Val Pro Leu     |                         |                 |
| 305   | 310                     | 315             |
| Ile Val Ala Gly Gly Thr Val Leu Ala Val Ala Val Leu Leu Ser Gln |                         |                 |
| 325   | 330                     | 335             |
| Ile Phe Gly Leu Gln Asp Leu Phe Asn Glu Glu Asn Ser Trp Leu Trp |                         |                 |
| 340   | 345                     | 350             |
| Met Tyr Arg Lys Leu Gly Gly Gly Leu Leu Gly Ile Leu Met Val Pro |                         |                 |
| 355   | 360                     | 365             |
| Val Leu Ala Ala Tyr Thr Ala Tyr Ser Leu Ala Asp Lys Pro Ala Leu |                         |                 |
| 370   | 375                     | 380             |
| Ala Pro Gly Phe Ala Ala Gly Leu Ala Ala Asn Met Ile Gly Ser Gly |                         |                 |
| 385   | 390                     | 395             |
| Phe Leu Gly Ala Val Val Gly Gly Leu Ile Ala Gly Tyr Leu Met Arg |                         |                 |
| 405   | 410                     | 415             |
| Trp Val Lys Asn His Leu Arg Leu Ser Ser Lys Phe Asn Gly Phe Leu |                         |                 |
| 420   | 425                     | 430             |
| Thr Phe Tyr Leu Tyr Pro Val Leu Gly Thr Leu Gly Ala Gly Ser Leu |                         |                 |
| 435   | 440                     | 445             |
| Met Leu Phe Val Val Gly Glu Pro Val Ala Trp Ile Asn Asn Ser Leu |                         |                 |
| 450   | 455                     | 460             |
| Thr Ala Trp Leu Asn Gly Leu Ser Gly Ser Asn Ala Leu Leu Leu Gly |                         |                 |
| 465   | 470                     | 475             |
| Ala Ile Leu Gly Phe Met Cys Ser Phe Asp Leu Gly Gly Pro Val Asn |                         |                 |
| 485   | 490                     | 495             |
| Lys Ala Ala Tyr Ala Phe Cys Leu Gly Ala Met Ala Asn Gly Val Tyr |                         |                 |
| 500   | 505                     | 510             |
| Gly Pro Tyr Ala Ile Phe Ala Ser Val Lys Met Val Ser Ala Phe Thr |                         |                 |
| 515   | 520                     | 525             |
| Val Thr Ala Ser Thr Met Leu Ala Pro Arg Leu Phe Lys Glu Phe Glu |                         |                 |
| 530   | 535                     | 540             |
| Ile Glu Thr Gly Lys Ser Thr Trp Leu Leu Gly Leu Ala Gly Ile Thr |                         |                 |
| 545   | 550                     | 555             |
| Glu Gly Ala Ile Pro Met Ala Ile Glu Asp Pro Leu Arg Val Ile Gly |                         |                 |
| 565   | 570                     | 575             |
| Ser Phe Val Leu Gly Ser Met Val Thr Gly Ala Ile Val Gly Ala Met |                         |                 |
| 580   | 585                     | 590             |
| Asn Ile Gly Leu Ser Thr Pro Gly Ala Gly Ile Phe Ser Leu Phe Leu |                         |                 |
| 595   | 600                     | 605             |

Leu His Asp Asn Gly Ala Gly Gly Val Met Ala Ala Ile Gly Trp Phe  
 610 615 620  
 Gly Ala Ala Leu Val Gly Ala Ala Ile Ser Thr Ala Ile Leu Leu Met  
 625 630 635 640  
 Trp Arg Arg His Ala Val Lys His Gly Asn Tyr Leu Thr Asp Gly Val  
 645 650 655  
 Met Pro

<210> 353  
 <211> 877  
 <212> PRT  
 <213> E. Coli

<400> 353  
 Met Lys Ala Val Ser Arg Val His Ile Thr Pro His Met His Trp Asp  
 1 5 10 15  
 Arg Glu Trp Tyr Phe Thr Thr Glu Glu Ser Arg Ile Leu Leu Val Asn  
 20 25 30  
 Asn Met Glu Glu Ile Leu Cys Arg Leu Glu Gln Asp Asn Glu Tyr Lys  
 35 40 45  
 Tyr Tyr Val Leu Asp Gly Gln Thr Ala Ile Leu Glu Asp Tyr Phe Ala  
 50 55 60  
 Val Lys Pro Glu Asn Lys Asp Arg Val Lys Lys Gln Val Glu Ala Gly  
 65 70 75 80  
 Lys Leu Ile Ile Gly Pro Trp Tyr Thr Gln Thr Asp Thr Thr Ile Val  
 85 90 95  
 Ser Ala Glu Ser Ile Val Arg Asn Leu Met Tyr Gly Met Arg Asp Cys  
 100 105 110  
 Leu Ala Phe Gly Glu Pro Met Lys Ile Gly Tyr Leu Pro Asp Ser Phe  
 115 120 125  
 Gly Met Ser Gly Gln Leu Pro His Ile Tyr Asn Gly Phe Gly Ile Thr  
 130 135 140  
 Arg Thr Met Phe Trp Arg Gly Cys Ser Glu Arg His Gly Thr Asp Lys  
 145 150 155 160  
 Thr Glu Phe Leu Trp Gln Ser Ser Asp Gly Ser Glu Val Thr Ala Gln  
 165 170 175  
 Val Leu Pro Leu Gly Tyr Ala Ile Gly Lys Tyr Leu Pro Ala Asp Glu  
 180 185 190  
 Asn Gly Leu Arg Lys Arg Leu Asp Ser Tyr Phe Asp Val Leu Glu Lys  
 195 200 205  
 Ala Ser Val Thr Lys Glu Ile Leu Leu Pro Asn Gly His Asp Gln Met  
 210 215 220  
 Pro Leu Gln Gln Asn Ile Phe Glu Val Met Asp Lys Leu Arg Glu Ile  
 225 230 235 240  
 Tyr Pro Gln Arg Lys Phe Val Met Ser Arg Phe Glu Glu Val Phe Glu  
 245 250 255  
 Lys Ile Glu Ala Gln Arg Asp Asn Leu Ala Thr Leu Lys Gly Glu Phe  
 260 265 270  
 Ile Asp Gly Lys Tyr Met Arg Val His Arg Thr Ile Gly Ser Thr Arg  
 275 280 285  
 Met Asp Ile Lys Ile Ala His Ala Arg Ile Glu Asn Lys Ile Val Asn  
 290 295 300  
 Leu Leu Glu Pro Leu Ala Thr Leu Ala Trp Thr Leu Gly Phe Glu Tyr  
 305 310 315 320  
 His His Gly Leu Leu Glu Lys Met Trp Lys Glu Ile Leu Lys Asn His  
 325 330 335  
 Ala His Asp Ser Ile Gly Cys Cys Ser Asp Lys Val His Arg Glu  
 340 345 350  
 Ile Val Ala Arg Phe Glu Leu Ala Glu Asp Met Ala Asp Asn Leu Ile

```

      355      360      365
Arg Phe Tyr Met Arg Lys Ile Ala Asp Asn Met Pro Gln Ser Asp Ala
370      375      380
Asp Lys Leu Val Leu Phe Asn Leu Met Pro Trp Pro Arg Glu Glu Val
385      390      395      400
Ile Asn Thr Thr Val Arg Leu Arg Ala Ser Gln Phe Asn Leu Arg Asp
405      410      415
Asp Arg Gly Gln Pro Val Pro Tyr Phe Ile Arg His Ala Arg Glu Ile
420      425      430
Asp Pro Gly Leu Ile Asp Arg Gln Ile Val His Tyr Gly Asn Tyr Asp
435      440      445
Pro Phe Met Glu Phe Asp Ile Gln Ile Asn Gln Ile Val Pro Ser Met
450      455      460
Gly Tyr Arg Thr Leu Tyr Ile Glu Ala Asn Gln Pro Gly Asn Val Ile
465      470      475      480
Ala Ala Lys Ser Asp Ala Glu Gly Ile Leu Glu Asn Ala Phe Trp Gln
485      490      495
Ile Ala Leu Asn Glu Asp Gly Ser Leu Gln Leu Val Asp Lys Asp Ser
500      505      510
Gly Val Arg Tyr Asp Arg Val Leu Gln Ile Glu Glu Ser Ser Asp Asp
515      520      525
Gly Asp Glu Tyr Asp Tyr Ser Pro Ala Lys Glu Glu Trp Val Ile Thr
530      535      540
Ala Ala Asn Ala Lys Pro Gln Cys Asp Ile Ile His Glu Ala Trp Gln
545      550      555      560
Ser Arg Ala Val Ile Arg Tyr Asp Met Ala Val Pro Leu Asn Leu Ser
565      570      575
Glu Arg Ser Ala Arg Gln Ser Thr Gly Arg Val Gly Val Val Leu Val
580      585      590
Val Thr Leu Ser His Asn Ser Arg Arg Ile Asp Val Asp Ile Asn Leu
595      600      605
Asp Asn Gln Ala Asp Asp His Arg Leu Arg Val Leu Val Pro Thr Pro
610      615      620
Phe Asn Thr Asp Ser Val Leu Ala Asp Thr Gln Phe Gly Ser Leu Thr
625      630      635      640
Arg Pro Val Asn Asp Ser Ala Met Asn Asn Trp Gln Gln Glu Gly Trp
645      650      655
Lys Glu Ala Pro Val Pro Val Trp Asn Met Leu Asn Tyr Val Ala Leu
660      665      670
Gln Glu Gly Arg Asn Gly Met Ala Val Phe Ser Glu Gly Leu Arg Glu
675      680      685
Phe Glu Val Ile Gly Glu Glu Lys Lys Thr Phe Ala Ile Thr Leu Leu
690      695      700
Arg Gly Val Gly Leu Leu Gly Lys Glu Asp Leu Leu Arg Pro Gly
705      710      715      720
Arg Pro Ser Gly Ile Lys Met Pro Val Pro Asp Ser Gln Leu Arg Gly
725      730      735
Leu Leu Ser Cys Arg Leu Ser Leu Leu Ser Tyr Thr Gly Thr Pro Thr
740      745      750
Ala Ala Gly Val Ala Gln Gln Ala Arg Ala Trp Leu Thr Pro Val Gln
755      760      765
Cys Tyr Asn Lys Ile Pro Trp Asp Val Met Lys Leu Asn Lys Ala Gly
770      775      780
Phe Asn Val Pro Glu Ser Tyr Ser Leu Leu Lys Met Pro Pro Val Gly
785      790      795      800
Cys Leu Ile Ser Ala Leu Lys Lys Ala Glu Asp Arg Gln Glu Val Ile
805      810      815
Leu Arg Leu Phe Asn Pro Ala Glu Ser Ala Thr Cys Asp Ala Thr Val
820      825      830
Ala Phe Ser Arg Glu Val Ile Ser Cys Ser Glu Thr Met Met Asp Glu
835      840      845

```

His Ile Thr Thr Glu Glu Asn Gln Gly Ser Asn Leu Ser Gly Pro Phe  
 850 855 860  
 Leu Pro Gly Gln Ser Arg Thr Phe Ser Tyr Arg Leu Ala  
 865 870 875

<210> 354  
 <211> 523  
 <212> PRT  
 <213> E. Coli

<400> 354

Met Met Leu Asp Ile Val Glu Leu Ser Arg Leu Gln Phe Ala Leu Thr  
 1 5 10 15  
 Ala Met Tyr His Phe Leu Phe Val Pro Leu Thr Leu Gly Met Ala Phe  
 20 25 30  
 Leu Leu Ala Ile Met Glu Thr Val Tyr Val Leu Ser Gly Lys Gln Ile  
 35 40 45  
 Tyr Lys Asp Met Thr Lys Phe Trp Gly Lys Leu Phe Gly Ile Asn Phe  
 50 55 60  
 Ala Leu Gly Val Ala Thr Gly Leu Thr Met Glu Phe Gln Phe Gly Thr  
 65 70 75 80  
 Asn Trp Ser Tyr Tyr Ser His Tyr Val Gly Asp Ile Phe Gly Ala Pro  
 85 90 95  
 Leu Ala Ile Glu Gly Leu Met Ala Phe Phe Leu Glu Ser Thr Phe Val  
 100 105 110  
 Gly Leu Phe Phe Phe Gly Trp Asp Arg Leu Gly Lys Val Gln His Met  
 115 120 125  
 Cys Val Thr Trp Leu Val Ala Leu Gly Ser Asn Leu Ser Ala Leu Trp  
 130 135 140  
 Ile Leu Val Ala Asn Gly Trp Met Gln Asn Pro Ile Ala Ser Asp Phe  
 145 150 155 160  
 Asn Phe Glu Thr Met Arg Met Glu Met Val Ser Phe Ser Glu Leu Val  
 165 170 175  
 Leu Asn Pro Val Ala Gln Val Lys Phe Val His Thr Val Ala Ser Gly  
 180 185 190  
 Tyr Val Thr Gly Ala Met Phe Ile Leu Gly Ile Ser Ala Trp Tyr Met  
 195 200 205  
 Leu Lys Gly Arg Asp Phe Ala Phe Ala Lys Arg Ser Phe Ala Ile Ala  
 210 215 220  
 Ala Ser Phe Gly Met Ala Ala Val Leu Ser Val Ile Val Leu Gly Asp  
 225 230 235 240  
 Glu Ser Gly Tyr Glu Met Gly Asp Val Gln Lys Thr Lys Leu Ala Ala  
 245 250 255  
 Ile Glu Ala Glu Trp Glu Thr Gln Pro Ala Pro Ala Ala Phe Thr Leu  
 260 265 270  
 Phe Gly Ile Pro Asp Gln Glu Glu Thr Asn Lys Phe Ala Ile Gln  
 275 280 285  
 Ile Pro Tyr Ala Leu Gly Ile Ile Ala Thr Arg Ser Val Asp Thr Pro  
 290 295 300  
 Val Ile Gly Leu Lys Glu Leu Met Val Gln His Glu Arg Ile Arg  
 305 310 315 320  
 Asn Gly Met Lys Ala Tyr Ser Leu Leu Glu Gln Leu Arg Ser Gly Ser  
 325 330 335  
 Thr Asp Gln Ala Val Arg Asp Gln Phe Asn Ser Met Lys Lys Asp Leu  
 340 345 350  
 Gly Tyr Gly Leu Leu Lys Arg Tyr Thr Pro Asn Val Ala Asp Ala  
 355 360 365  
 Thr Glu Ala Gln Ile Gln Gln Ala Thr Lys Asp Ser Ile Pro Arg Val  
 370 375 380  
 Ala Pro Leu Tyr Phe Ala Phe Arg Ile Met Val Ala Cys Gly Phe Leu

```

385          390          395          400
Leu Leu Ala Ile Ile Ala Leu Ser Phe Trp Ser Val Ile Arg Asn Arg
          405          410          415
Ile Gly Glu Lys Lys Trp Leu Leu Arg Ala Ala Leu Tyr Gly Ile Pro
          420          425          430
Leu Pro Trp Ile Ala Val Glu Ala Gly Trp Phe Val Ala Glu Tyr Gly
          435          440          445
Arg Gln Pro Trp Ala Ile Gly Glu Val Leu Pro Thr Ala Val Ala Asn
          450          455          460
Ser Ser Leu Thr Ala Gly Asp Leu Ile Phe Ser Met Val Leu Ile Cys
          465          470          475          480
Gly Leu Tyr Thr Leu Phe Leu Val Ala Glu Leu Phe Leu Met Phe Lys
          485          490          495
Phe Ala Arg Leu Gly Pro Ser Ser Leu Lys Thr Gly Arg Tyr His Phe
          500          505          510
Glu Gln Ser Ser Thr Thr Thr Gln Pro Ala Arg
          515          520

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<210> 355
<211> 379
<212> PRT
<213> E. Coli

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```

<400> 355
Met Ile Asp Tyr Glu Val Leu Arg Phe Ile Trp Trp Leu Leu Val Gly
1      5      10      15
Val Leu Leu Ile Gly Phe Ala Val Thr Asp Gly Phe Asp Met Gly Val
20     25     30
Gly Met Leu Thr Arg Phe Leu Gly Arg Asn Asp Thr Glu Arg Arg Ile
35     40     45
Met Ile Asn Ser Ile Ala Pro His Trp Asp Gly Asn Gln Val Trp Leu
50     55     60
Ile Thr Ala Gly Gly Ala Leu Phe Ala Ala Trp Pro Met Val Tyr Ala
65     70     75     80
Ala Ala Phe Ser Gly Phe Tyr Val Ala Met Ile Leu Val Leu Ala Ser
85     90     95
Leu Phe Phe Arg Pro Val Gly Phe Asp Tyr Arg Ser Lys Ile Glu Glu
100    105    110
Thr Arg Trp Arg Asn Met Trp Asp Trp Gly Ile Phe Ile Gly Ser Phe
115    120    125
Val Pro Pro Leu Val Ile Gly Val Ala Phe Gly Asn Leu Leu Gln Gly
130    135    140
Val Pro Phe Asn Val Asp Glu Tyr Leu Arg Leu Tyr Tyr Thr Gly Asn
145    150    155    160
Phe Phe Gln Leu Leu Asn Pro Phe Gly Leu Leu Ala Gly Val Val Ser
165    170    175
Val Gly Met Ile Ile Thr Gln Gly Ala Thr Tyr Leu Gln Met Arg Thr
180    185    190
Val Gly Glu Leu His Leu Arg Thr Arg Ala Thr Ala Gln Val Ala Ala
195    200    205
Leu Val Thr Leu Val Cys Phe Ala Leu Ala Gly Val Trp Val Met Tyr
210    215    220
Gly Ile Asp Gly Tyr Val Val Lys Ser Thr Met Asp His Tyr Ala Ala
225    230    235    240
Ser Asn Pro Leu Asn Lys Glu Val Val Arg Glu Ala Gly Ala Trp Leu
245    250    255
Val Asn Phe Asn Asn Thr Pro Ile Leu Trp Ala Ile Pro Ala Leu Gly
260    265    270
Val Val Leu Pro Leu Leu Thr Ile Leu Thr Ala Arg Met Asp Lys Ala
275    280    285

```

Ala Trp Ala Phe Val Phe Ser Ser Leu Thr Leu Ala Cys Ile Ile Leu  
 290 295 300  
 Thr Ala Gly Ile Ala Met Phe Pro Phe Val Met Pro Ser Ser Thr Met  
 305 310 315 320  
 Met Asn Ala Ser Leu Thr Met Trp Asp Ala Thr Ser Ser Gln Leu Thr  
 325 330 335  
 Leu Asn Val Met Thr Trp Val Ala Val Val Leu Val Pro Ile Ile Leu  
 340 345 350  
 Leu Tyr Thr Ala Trp Cys Tyr Trp Lys Met Phe Gly Arg Ile Thr Lys  
 355 360 365  
 Glu Asp Ile Glu Arg Asn Thr His Ser Leu Tyr  
 370 375

<210> 356  
 <211> 456  
 <212> PRT  
 <213> E. Coli

<400> 356  
 Met Glu Leu Ser Ser Leu Thr Ala Val Ser Pro Val Asp Gly Arg Tyr  
 1 5 10 15  
 Gly Asp Lys Val Ser Ala Leu Arg Gly Ile Phe Ser Glu Tyr Gly Leu  
 20 25 30  
 Leu Lys Phe Arg Val Gln Val Glu Val Arg Trp Leu Gln Lys Leu Ala  
 35 40 45  
 Ala His Ala Ala Ile Lys Glu Val Pro Ala Phe Ala Ala Asp Ala Ile  
 50 55 60  
 Gly Tyr Leu Asp Ala Ile Val Ala Ser Phe Ser Glu Glu Asp Ala Ala  
 65 70 75 80  
 Arg Ile Lys Thr Ile Glu Arg Thr Thr Asn His Asp Val Lys Ala Val  
 85 90 95  
 Glu Tyr Phe Leu Lys Glu Lys Val Ala Glu Ile Pro Glu Leu His Ala  
 100 105 110  
 Val Ser Glu Phe Ile His Phe Ala Cys Thr Ser Glu Asp Ile Asn Asn  
 115 120 125  
 Leu Ser His Ala Leu Met Leu Lys Thr Ala Arg Asp Glu Val Ile Leu  
 130 135 140  
 Pro Tyr Trp Arg Gln Leu Ile Asp Gly Ile Lys Asp Leu Ala Val Gln  
 145 150 155 160  
 Tyr Arg Asp Ile Pro Leu Leu Ser Arg Thr His Gly Gln Pro Ala Thr  
 165 170 175  
 Pro Ser Thr Ile Gly Lys Glu Met Ala Asn Val Ala Tyr Arg Met Glu  
 180 185 190  
 Arg Gln Tyr Arg Gln Leu Asn Gln Val Glu Ile Leu Gly Lys Ile Asn  
 195 200 205  
 Gly Ala Val Gly Asn Tyr Asn Ala His Ile Ala Ala Tyr Pro Glu Val  
 210 215 220  
 Asp Trp His Gln Phe Ser Glu Glu Phe Val Thr Ser Leu Gly Ile Gln  
 225 230 235 240  
 Trp Asn Pro Tyr Thr Thr Gln Ile Glu Pro His Asp Tyr Ile Ala Glu  
 245 250 255  
 Leu Phe Asp Cys Val Ala Arg Phe Asn Thr Ile Leu Ile Asp Phe Asp  
 260 265 270  
 Arg Asp Val Trp Gly Tyr Ile Ala Leu Asn His Phe Lys Gln Lys Thr  
 275 280 285  
 Ile Ala Gly Glu Ile Gly Ser Ser Thr Met Pro His Lys Val Asn Pro  
 290 295 300  
 Ile Asp Phe Glu Asn Ser Glu Gly Asn Leu Gly Leu Ser Asn Ala Val  
 305 310 315 320  
 Leu Gln His Leu Ala Ser Lys Leu Pro Val Ser Arg Trp Gln Arg Asp



```

          325          330          335
Leu Thr Asp Ser Thr Val Leu Arg Asn Leu Gly Val Gly Ile Gly Tyr
          340          345          350
Ala Leu Ile Ala Tyr Gln Ser Thr Leu Lys Gly Val Ser Lys Leu Glu
          355          360          365
Val Asn Arg Asp His Leu Leu Asp Glu Leu Asp His Asn Trp Glu Val
          370          375          380
Leu Ala Glu Pro Ile Gln Thr Val Met Arg Arg Tyr Gly Ile Glu Lys
385          390          395          400
Pro Tyr Glu Lys Leu Lys Glu Leu Thr Arg Gly Lys Arg Val Asp Ala
          405          410          415
Glu Gly Met Lys Gln Phe Ile Asp Gly Leu Ala Leu Pro Glu Glu Glu
          420          425          430
Lys Ala Arg Leu Lys Ala Met Thr Pro Ala Asn Tyr Ile Gly Arg Ala
          435          440          445
Ile Thr Met Val Asp Glu Leu Lys
          450          455

```

<210> 357  
 <211> 61  
 <212> PRT  
 <213> E. Coli

```

          <400> 357
Met Leu Ile Leu Thr Arg Arg Val Gly Glu Thr Leu Met Ile Gly Asp
1          5          10          15
Glu Val Thr Val Thr Val Leu Gly Val Lys Gly Asn Gln Val Arg Ile
          20          25          30
Gly Val Asn Ala Pro Lys Glu Val Ser Val His Arg Glu Glu Ile Tyr
          35          40          45
Gln Arg Ile Gln Ala Glu Lys Ser Gln Gln Ser Ser Tyr
          50          55          60

```

<210> 358  
 <211> 83  
 <212> RNA  
 <213> E. Coli

```

          <400> 358
ggugaggugg ccgagaggcu gaaggcgcuc ccucgcuagg ggaguaugcg gucaaaagcu    60
gcauccgggg uucgaauccc cgccuacccg cca                                83

```

<210> 359  
 <211> 200  
 <212> PRT  
 <213> E. Coli

```

          <400> 359
Met Lys Asn Lys Ala Asp Asn Lys Lys Arg Asn Phe Leu Thr His Ser
1          5          10          15
Glu Ile Glu Ser Leu Leu Lys Ala Ala Asn Thr Gly Pro His Ala Ala
          20          25          30
Arg Asn Tyr Cys Leu Thr Leu Leu Cys Phe Ile His Gly Phe Arg Ala
          35          40          45
Ser Glu Ile Cys Arg Leu Arg Ile Ser Asp Ile Asp Leu Lys Ala Lys
          50          55          60
Cys Ile Tyr Ile His Arg Leu Lys Lys Gly Phe Ser Thr Thr His Pro
65          70          75          80

```

Leu Leu Asn Lys Glu Val Gln Ala Leu Lys Asn Trp Leu Ser Ile Arg  
 85 90 95  
 Thr Ser Tyr Pro His Ala Glu Ser Glu Trp Val Phe Leu Ser Arg Lys  
 100 105 110  
 Gly Asn Pro Leu Ser Arg Gln Gln Phe Tyr His Ile Ile Ser Thr Ser  
 115 120 125  
 Gly Gly Asn Ala Gly Leu Ser Leu Glu Ile His Pro His Met Leu Arg  
 130 135 140  
 His Ser Cys Gly Phe Ala Leu Ala Asn Met Gly Ile Asp Thr Arg Leu  
 145 150 155 160  
 Ile Gln Asp Tyr Leu Gly His Arg Asn Ile Arg His Thr Val Trp Tyr  
 165 170 175  
 Thr Ala Ser Asn Ala Gly Arg Phe Tyr Gly Ile Trp Asp Arg Ala Arg  
 180 185 190  
 Gly Arg Gln Arg His Ala Val Leu  
 195 200

<210> 360  
 <211> 198  
 <212> PRT  
 <213> E. Coli

<400> 360  
 Met Ser Lys Arg Arg Tyr Leu Thr Gly Lys Glu Val Gln Ala Met Met  
 1 5 10 15  
 Gln Ala Val Cys Tyr Gly Ala Thr Gly Ala Arg Asp Tyr Cys Leu Ile  
 20 25 30  
 Leu Leu Ala Tyr Arg His Gly Met Arg Ile Ser Glu Leu Leu Asp Leu  
 35 40 45  
 His Tyr Gln Asp Leu Asp Leu Asn Glu Gly Arg Ile Asn Ile Arg Arg  
 50 55 60  
 Leu Lys Asn Gly Phe Ser Thr Val His Pro Leu Arg Phe Asp Glu Arg  
 65 70 75 80  
 Glu Ala Val Glu Arg Trp Thr Gln Glu Arg Ala Asn Trp Lys Gly Ala  
 85 90 95  
 Asp Arg Thr Asp Ala Ile Phe Ile Ser Arg Arg Gly Ser Arg Leu Ser  
 100 105 110  
 Arg Gln Gln Ala Tyr Arg Ile Ile Arg Asp Ala Gly Ile Glu Ala Gly  
 115 120 125  
 Thr Val Thr Gln Thr His Pro His Met Leu Arg His Ala Cys Gly Tyr  
 130 135 140  
 Glu Leu Ala Glu Arg Gly Ala Asp Thr Arg Leu Ile Gln Asp Tyr Leu  
 145 150 155 160  
 Gly His Arg Asn Ile Arg His Thr Val Arg Tyr Thr Ala Ser Asn Ala  
 165 170 175  
 Ala Arg Phe Ala Gly Leu Trp Glu Arg Asn Asn Leu Ile Asn Glu Lys  
 180 185 190  
 Leu Lys Arg Glu Glu Val  
 195

<210> 361  
 <211> 182  
 <212> PRT  
 <213> E. Coli

<400> 361  
 Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu  
 1 5 10 15

Ser Ser Thr Ala Ala Leu Ala Ala Thr Thr Val Asn Gly Gly Thr  
 20 25 30  
 Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala  
 35 40 45  
 Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser  
 50 55 60  
 Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln  
 65 70 75 80  
 Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe  
 85 90 95  
 Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln  
 100 105 110  
 Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp  
 115 120 125  
 Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu  
 130 135 140  
 Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr  
 145 150 155 160  
 Phe Ala Thr Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr  
 165 170 175  
 Phe Lys Val Gln Tyr Gln  
 180

<210> 362  
 <211> 215  
 <212> PRT  
 <213> E. Coli

<400> 362  
 Met Leu Leu Met Arg Met Arg Pro Ser Arg Phe Ser Ile Asn Asn Leu  
 1 5 10 15  
 Pro Arg Phe Asp Asp Val Ile Thr Gly Arg Asp Ala His Pro Cys Ala  
 20 25 30  
 Ile Lys Ile Thr Met Lys Arg Lys Arg Leu Phe Leu Leu Ala Ser Leu  
 35 40 45  
 Leu Pro Met Phe Ala Leu Ala Gly Asn Lys Trp Asn Thr Thr Leu Pro  
 50 55 60  
 Gly Gly Asn Met Gln Phe Gln Gly Val Ile Ile Ala Glu Thr Cys Arg  
 65 70 75 80  
 Ile Glu Ala Gly Asp Lys Gln Met Thr Val Asn Met Gly Gln Ile Ser  
 85 90 95  
 Ser Asn Arg Phe His Ala Val Gly Glu Asp Ser Ala Pro Val Pro Phe  
 100 105 110  
 Val Ile His Leu Arg Glu Cys Ser Thr Val Val Ser Glu Arg Val Gly  
 115 120 125  
 Val Ala Phe His Gly Val Ala Asp Gly Lys Asn Pro Asp Val Leu Ser  
 130 135 140  
 Val Gly Glu Gly Pro Gly Ile Ala Thr Asn Ile Gly Val Ala Leu Phe  
 145 150 155 160  
 Asp Asp Glu Gly Asn Leu Val Pro Ile Asn Arg Pro Pro Ala Asn Trp  
 165 170 175  
 Lys Arg Leu Tyr Ser Gly Ser Thr Ser Leu His Phe Ile Ala Lys Tyr  
 180 185 190  
 Arg Ala Thr Gly Arg Arg Val Thr Gly Gly Ile Ala Asn Ala Gln Ala  
 195 200 205  
 Trp Phe Ser Leu Thr Tyr Gln  
 210 215

<210> 363  
 <211> 241  
 <212> PRT  
 <213> E. Coli

<400> 363

```

Met Ser Asn Lys Asn Val Asn Val Arg Lys Ser Gln Glu Ile Thr Phe
 1          5          10          15
Cys Leu Leu Ala Gly Ile Leu Met Phe Met Ala Met Met Val Ala Gly
 20          25          30
Arg Ala Glu Ala Gly Val Ala Leu Gly Ala Thr Arg Val Ile Tyr Pro
 35          40          45
Ala Gly Gln Lys Gln Glu Gln Leu Ala Val Thr Asn Asn Asp Glu Asn
 50          55          60
Ser Thr Tyr Leu Ile Gln Ser Trp Val Glu Asn Ala Asp Gly Val Lys
 65          70          75          80
Asp Gly Arg Phe Ile Val Thr Pro Pro Leu Phe Ala Met Lys Gly Lys
 85          90          95
Lys Glu Asn Thr Leu Arg Ile Leu Asp Ala Thr Asn Asn Gln Leu Pro
100          105          110
Gln Asp Arg Glu Ser Leu Phe Trp Met Asn Val Lys Ala Ile Pro Ser
115          120          125
Met Asp Lys Ser Lys Leu Thr Glu Asn Thr Leu Gln Leu Ala Ile Ile
130          135          140
Ser Arg Ile Lys Leu Tyr Tyr Arg Pro Ala Lys Leu Ala Leu Pro Pro
145          150          155          160
Asp Gln Ala Ala Glu Lys Leu Arg Phe Arg Arg Ser Ala Asn Ser Leu
165          170          175
Thr Leu Ile Asn Pro Thr Pro Tyr Tyr Leu Thr Val Thr Glu Leu Asn
180          185          190
Ala Gly Thr Arg Val Leu Glu Asn Ala Leu Val Pro Pro Met Gly Glu
195          200          205
Ser Thr Val Lys Leu Pro Ser Asp Ala Gly Ser Asn Ile Thr Tyr Arg
210          215          220
Thr Ile Asn Asp Tyr Gly Ala Leu Thr Pro Lys Met Thr Gly Val Met
225          230          235          240
Glu

```

<210> 364  
 <211> 878  
 <212> PRT  
 <213> E. Coli

<400> 364

```

Met Ser Tyr Leu Asn Leu Arg Leu Tyr Gln Arg Asn Thr Gln Cys Leu
 1          5          10          15
His Ile Arg Lys His Arg Leu Ala Gly Phe Phe Val Arg Leu Val Val
 20          25          30
Ala Cys Ala Phe Ala Ala Gln Ala Pro Leu Ser Ser Ala Asp Leu Tyr
 35          40          45
Phe Asn Pro Arg Phe Leu Ala Asp Asp Pro Gln Ala Val Ala Asp Leu
 50          55          60
Ser Arg Phe Glu Asn Gly Gln Glu Leu Pro Pro Gly Thr Tyr Arg Val
 65          70          75          80
Asp Ile Tyr Leu Asn Asn Gly Tyr Met Ala Thr Arg Asp Val Thr Phe
 85          90          95
Asn Thr Gly Asp Ser Glu Gln Gly Ile Val Pro Cys Leu Thr Arg Ala
100          105          110
Gln Leu Ala Ser Met Gly Leu Asn Thr Ala Ser Val Ala Gly Met Asn

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|   |     |     |
|---|-----|-----|
| 115   | 120 | 125 |
| Leu Leu Ala Asp Asp Ala Cys Val Pro Leu Thr Thr Met Val Gln Asp |     |     |
| 130   | 135 | 140 |
| Ala Thr Ala His Leu Asp Val Gly Gln Gln Arg Leu Asn Leu Thr Ile |     |     |
| 145   | 150 | 155 |
| Pro Gln Ala Phe Met Ser Asn Arg Ala Arg Gly Tyr Ile Pro Pro Glu |     |     |
| 165   | 170 | 175 |
| Leu Trp Asp Pro Gly Ile Asn Ala Gly Leu Leu Asn Tyr Asn Phe Ser |     |     |
| 180   | 185 | 190 |
| Gly Asn Ser Val Gln Asn Arg Ile Gly Gly Asn Ser His Tyr Ala Tyr |     |     |
| 195   | 200 | 205 |
| Leu Asn Leu Gln Ser Gly Leu Asn Ile Gly Ala Trp Arg Leu Arg Asp |     |     |
| 210   | 215 | 220 |
| Asn Thr Thr Trp Ser Tyr Asn Ser Ser Asp Arg Ser Ser Gly Ser Lys |     |     |
| 225   | 230 | 235 |
| Asn Lys Trp Gln His Ile Asn Thr Trp Leu Glu Arg Asp Ile Ile Pro |     |     |
| 245   | 250 | 255 |
| Leu Arg Ser Arg Leu Thr Leu Gly Asp Gly Tyr Thr Gln Gly Asp Ile |     |     |
| 260   | 265 | 270 |
| Phe Asp Gly Ile Asn Phe Arg Gly Ala Gln Leu Ala Ser Asp Asp Asn |     |     |
| 275   | 280 | 285 |
| Met Leu Pro Asp Ser Gln Arg Gly Phe Ala Pro Val Ile His Gly Ile |     |     |
| 290   | 295 | 300 |
| Ala Arg Gly Thr Ala Gln Val Thr Ile Lys Gln Asn Gly Tyr Asp Ile |     |     |
| 305   | 310 | 315 |
| Tyr Asn Ser Thr Val Pro Pro Gly Pro Phe Thr Ile Asn Asp Ile Tyr |     |     |
| 325   | 330 | 335 |
| Ala Ala Gly Asn Ser Gly Asp Leu Gln Val Thr Ile Lys Glu Ala Asp |     |     |
| 340   | 345 | 350 |
| Gly Ser Thr Gln Ile Phe Thr Val Pro Tyr Ser Ser Val Pro Leu Leu |     |     |
| 355   | 360 | 365 |
| Gln Arg Glu Gly His Thr Arg Tyr Ser Ile Thr Ala Gly Glu Tyr Arg |     |     |
| 370   | 375 | 380 |
| Ser Gly Asn Ala Gln Gln Lys Thr Arg Phe Phe Gln Ser Thr Leu     |     |     |
| 385   | 390 | 395 |
| Leu His Gly Leu Pro Ala Gly Trp Thr Ile Tyr Gly Gly Thr Gln Leu |     |     |
| 405   | 410 | 415 |
| Ala Asp Arg Tyr Arg Ala Phe Asn Phe Gly Ile Gly Lys Asn Met Gly |     |     |
| 420   | 425 | 430 |
| Ala Leu Gly Ala Leu Ser Val Asp Met Thr Gln Ala Asn Ser Thr Leu |     |     |
| 435   | 440 | 445 |
| Pro Asp Asp Ser Gln His Asp Gly Gln Ser Val Arg Phe Leu Tyr Asn |     |     |
| 450   | 455 | 460 |
| Lys Ser Leu Asn Glu Ser Gly Thr Asn Ile Gln Leu Val Gly Tyr Arg |     |     |
| 465   | 470 | 475 |
| Tyr Ser Thr Ser Gly Tyr Phe Asn Phe Ala Asp Thr Thr Tyr Ser Arg |     |     |
| 485   | 490 | 495 |
| Met Asn Gly Tyr Asn Ile Glu Thr Gln Asp Gly Val Ile Gln Val Lys |     |     |
| 500   | 505 | 510 |
| Pro Lys Phe Thr Asp Tyr Tyr Asn Leu Ala Tyr Asn Lys Arg Gly Lys |     |     |
| 515   | 520 | 525 |
| Leu Gln Leu Thr Val Thr Gln Gln Leu Gly Arg Thr Ser Thr Leu Tyr |     |     |
| 530   | 535 | 540 |
| Leu Ser Gly Ser His Gln Thr Tyr Trp Gly Thr Ser Asn Val Asp Glu |     |     |
| 545   | 550 | 555 |
| Gln Phe Gln Ala Gly Leu Asn Thr Ala Phe Glu Asp Ile Asn Trp Thr |     |     |
| 565   | 570 | 575 |
| Leu Ser Tyr Ser Leu Thr Lys Asn Ala Trp Gln Lys Gly Arg Asp Gln |     |     |
| 580   | 585 | 590 |
| Met Leu Ala Leu Asn Val Asn Ile Pro Phe Ser His Trp Leu Arg Ser |     |     |
| 595   | 600 | 605 |

Asp Ser Lys Ser Gln Trp Arg His Ala Ser Ala Ser Tyr Ser Met Ser  
 610 615 620  
 His Asp Leu Asn Gly Arg Met Thr Asn Leu Ala Gly Val Tyr Gly Thr  
 625 630 635 640  
 Leu Leu Glu Asp Asn Asn Leu Ser Tyr Ser Val Gln Thr Gly Tyr Ala  
 645 650 655  
 Gly Gly Gly Asp Gly Asn Ser Gly Ser Thr Gly Tyr Ala Thr Leu Asn  
 660 665 670  
 Tyr Arg Gly Gly Tyr Gly Asn Ala Asn Ile Gly Tyr Ser His Ser Asp  
 675 680 685  
 Asp Ile Lys Gln Leu Tyr Tyr Gly Val Ser Gly Gly Val Leu Ala His  
 690 695 700  
 Ala Asn Gly Val Thr Leu Gly Gln Pro Leu Asn Asp Thr Val Val Leu  
 705 710 715 720  
 Val Lys Ala Pro Gly Ala Lys Asp Ala Lys Val Glu Asn Gln Thr Gly  
 725 730 735  
 Val Arg Thr Asp Trp Arg Gly Tyr Ala Val Leu Pro Tyr Ala Thr Glu  
 740 745 750  
 Tyr Arg Glu Asn Arg Val Ala Leu Asp Thr Asn Thr Leu Ala Asp Asn  
 755 760 765  
 Val Asp Leu Asp Asn Ala Val Ala Asn Val Val Pro Thr Arg Gly Ala  
 770 775 780  
 Ile Val Arg Ala Glu Phe Lys Ala Arg Val Gly Ile Lys Leu Leu Met  
 785 790 795 800  
 Thr Leu Thr His Asn Asn Lys Pro Leu Pro Phe Gly Ala Met Val Thr  
 805 810 815  
 Ser Glu Ser Ser Gln Ser Ser Gly Ile Val Ala Asp Asn Gly Gln Val  
 820 825 830  
 Tyr Leu Ser Gly Met Pro Leu Ala Gly Lys Val Gln Val Lys Trp Gly  
 835 840 845  
 Glu Glu Glu Asn Ala His Cys Val Ala Asn Tyr Gln Leu Pro Pro Glu  
 850 855 860  
 Ser Gln Gln Gln Leu Leu Thr Gln Leu Ser Ala Glu Cys Arg  
 865 870 875

&lt;210&gt; 365

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 365

Met Arg Asn Lys Pro Phe Tyr Leu Leu Cys Ala Phe Leu Trp Leu Ala  
 1 5 10 15  
 Val Ser His Ala Leu Ala Ala Asp Ser Thr Ile Thr Ile Arg Gly Tyr  
 20 25 30  
 Val Arg Asp Asn Gly Cys Ser Val Ala Ala Glu Ser Thr Asn Phe Thr  
 35 40 45  
 Val Asp Leu Met Glu Asn Ala Ala Lys Gln Phe Asn Asn Ile Gly Ala  
 50 55 60  
 Thr Thr Pro Val Val Pro Phe Arg Ile Leu Leu Ser Pro Cys Gly Asn  
 65 70 75 80  
 Ala Val Ser Ala Val Lys Val Gly Phe Thr Gly Val Ala Asp Ser His  
 85 90 95  
 Asn Ala Asn Leu Leu Ala Leu Glu Asn Thr Val Ser Ala Ala Ser Gly  
 100 105 110  
 Leu Gly Ile Gln Leu Leu Asn Glu Gln Gln Asn Gln Ile Pro Leu Asn  
 115 120 125  
 Ala Pro Ser Ser Ala Leu Ser Trp Thr Thr Leu Thr Pro Gly Lys Pro  
 130 135 140  
 Asn Thr Leu Asn Phe Tyr Ala Arg Leu Met Ala Thr Gln Val Pro Val

<210> 366  
<211> 167  
<212> PRT  
<213> E. Coli

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<210> 367
<211> 300
<212> PRT
<213> E. Coli
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-183-

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Ser Leu Ile Ala Val Leu Ile Leu Arg Gln Thr Asn Asn Tyr Asn Ser
145          150          155          160
Asp Asp Phe Gln Phe Val Trp Asn Ile Tyr Ala Asn Asn Asp Val Val
          165          170          175
Val Pro Thr Gly Gly Cys Asp Val Ser Ala Arg Asp Val Thr Val Thr
          180          185          190
Leu Pro Asp Tyr Pro Gly Ser Val Pro Ile Pro Leu Thr Val Tyr Cys
          195          200          205
Ala Lys Ser Gln Asn Leu Gly Tyr Tyr Leu Ser Gly Thr Thr Ala Asp
          210          215          220
Ala Gly Asn Ser Ile Phe Thr Asn Thr Ala Ser Phe Ser Pro Ala Gln
225          230          235          240
Gly Val Gly Val Gln Leu Thr Arg Asn Gly Thr Ile Ile Pro Ala Asn
          245          250          255
Asn Thr Val Ser Leu Gly Ala Val Gly Thr Ser Ala Val Ser Leu Gly
          260          265          270
Leu Thr Ala Asn Tyr Ala Arg Thr Gly Gly Gln Val Thr Ala Gly Asn
          275          280          285
Val Gln Ser Ile Ile Gly Val Thr Phe Val Tyr Gln
          290          295          300

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<210> 368  
 <211> 521  
 <212> PRT  
 <213> E. Coli

<400> 368

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Met Leu Ser Lys Leu Pro Arg Arg Leu Arg Ser Phe Gln Thr Tyr Cys
1          5          10          15
Thr Ile Arg Val His Arg Gly Glu Asp Met Lys Ser Met Asp Lys Leu
          20          25          30
Thr Thr Gly Val Ala Tyr Gly Thr Ser Ala Gly Asn Ala Gly Phe Trp
          35          40          45
Ala Leu Gln Leu Leu Asp Lys Val Thr Pro Ser Gln Trp Ala Ala Ile
          50          55          60
Gly Val Leu Gly Ser Leu Val Phe Gly Leu Leu Thr Tyr Leu Thr Asn
65          70          75          80
Leu Tyr Phe Lys Ile Lys Glu Asp Arg Arg Lys Ala Ala Arg Gly Glu
          85          90          95
Ser Asn Asp Ser Arg Leu Thr Gly Cys Glu Arg Ser Pro Phe Glu Ser
          100          105          110
Tyr Gly Asn Cys Ser Leu Thr Gly Gln Arg Thr Leu Arg Asn Phe Pro
          115          120          125
Gly Cys Arg His Gly Pro Cys Arg Ser Cys Ala Gly Val Leu Gly Ser
          130          135          140
Ser Gln Lys Glu Arg Pro Ala Ser Leu Pro Gly Ser Ser Arg Lys Ile
145          150          155          160
Val Arg Lys Ser Val Leu Ser Ala Ala Ser Val Leu Leu Asp Lys Ser
          165          170          175
Cys Gln Ala Arg Ala Ser Ser Ser Ile Ser Met Asn Thr Lys Ile Arg
          180          185          190
Tyr Gly Leu Ser Ala Ala Val Leu Ala Leu Ile Gly Ala Gly Ala Ser
          195          200          205
Ala Pro Gln Ile Leu Asp Gln Phe Leu Asp Glu Lys Glu Gly Asn His
210          215          220
Thr Met Ala Tyr Arg Asp Gly Ser Gly Ile Trp Thr Ile Cys Arg Gly
225          230          235          240
Ala Thr Val Val Asp Gly Lys Thr Val Phe Pro Asn Met Lys Leu Ser
          245          250          255

```



Lys Glu Lys Cys Asp Gln Val Asn Ala Ile Glu Arg Asp Lys Ala Leu  
 260 265 270  
 Ala Trp Val Glu Arg Asn Ile Lys Val Pro Leu Thr Glu Pro Gln Lys  
 275 280 285  
 Ala Gly Ile Ala Ser Phe Cys Pro Tyr Asn Ile Gly Pro Gly Lys Cys  
 290 295 300  
 Phe Pro Ser Thr Phe Tyr Lys Arg Leu Asn Ala Gly Asp Arg Lys Gly  
 305 310 315 320  
 Ala Cys Glu Ala Ile Arg Trp Trp Ile Lys Asp Gly Gly Arg Asp Cys  
 325 330 335  
 Arg Ile Arg Ser Asn Asn Cys Tyr Gly Gln Val Ile Arg Arg Asp Gln  
 340 345 350  
 Glu Ser Ala Leu Thr Cys Trp Gly Ile Glu Gln Ile Arg Tyr Ser Trp  
 355 360 365  
 Phe Phe Ser Cys Cys Gln Asp Leu Ser Ser Glu Met Ser Gly Ala Thr  
 370 375 380  
 Glu Asp Gly Lys Lys Asn Gly Arg Asn Val Met Leu Pro His Tyr His  
 385 390 395 400  
 Lys Arg Met Leu Asn Leu Leu Glu Leu Asn Arg Gly Glu Leu Pro  
 405 410 415  
 Val Met Arg Leu Leu Lys Met Arg Asn Arg Asn Leu Leu Lys Phe Leu  
 420 425 430  
 Pro Gly Leu Leu Ile Cys Leu Ile Val Leu Thr Ser Cys Val Pro Lys  
 435 440 445  
 Gln Lys Asn Met Pro Tyr Ala Leu Thr Gln Arg Ser Ile Pro Gln Ile  
 450 455 460  
 Leu Pro Leu Pro Ser Glu Ala Lys Gln Pro Lys Pro Pro Lys Glu Cys  
 465 470 475 480  
 Ser Pro Thr Cys Ser Glu Ile Leu Gln Gln Lys Leu Ser Phe Met Leu  
 485 490 495  
 Lys Leu Leu Thr Asn Ala Thr Ser Gln Glu Leu Val Asn Arg Ser Met  
 500 505 510  
 Asn Leu Glu Ile Lys Ser Ile Lys Cys  
 515 520

<210> 369  
 <211> 177  
 <212> PRT  
 <213> E. Coli

<400> 369  
 Met Asn Thr Lys Ile Arg Tyr Gly Leu Ser Ala Ala Val Leu Ala Leu  
 1 5 10 15  
 Ile Gly Ala Gly Ala Ser Ala Pro Gln Ile Leu Asp Gln Phe Leu Asp  
 20 25 30  
 Glu Lys Glu Gly Asn His Thr Met Ala Tyr Arg Asp Gly Ser Gly Ile  
 35 40 45  
 Trp Thr Ile Cys Arg Gly Ala Thr Val Val Asp Gly Lys Thr Val Phe  
 50 55 60  
 Pro Asn Met Lys Leu Ser Lys Glu Lys Cys Asp Gln Val Asn Ala Ile  
 65 70 75 80  
 Glu Arg Asp Lys Ala Leu Ala Trp Val Glu Arg Asn Ile Lys Val Pro  
 85 90 95  
 Leu Thr Glu Pro Gln Lys Ala Gly Ile Ala Ser Phe Cys Pro Tyr Asn  
 100 105 110  
 Ile Gly Pro Gly Lys Cys Phe Pro Ser Thr Phe Tyr Lys Arg Leu Asn  
 115 120 125  
 Ala Gly Asp Arg Lys Gly Ala Cys Glu Ala Ile Arg Trp Trp Ile Lys  
 130 135 140

Asp Gly Gly Arg Asp Cys Arg Ile Arg Ser Asn Asn Cys Tyr Gly Gln  
 145 150 155 160  
 Val Ile Arg Arg Asp Gln Glu Ser Ala Leu Thr Cys Trp Gly Ile Glu  
 165 170 175  
 Gln

<210> 370  
 <211> 103  
 <212> PRT  
 <213> E. Coli

<400> 370  
 Met Thr Gln Asp Tyr Glu Leu Val Val Lys Gly Val Arg Asn Phe Glu  
 1 5 10 15  
 Asn Lys Val Thr Val Thr Val Ala Leu Gln Asp Lys Glu Arg Phe Asp  
 20 25 30  
 Gly Glu Ile Phe Asp Leu Asp Val Ala Met Asp Arg Val Glu Gly Ala  
 35 40 45  
 Ala Leu Glu Phe Tyr Glu Ala Ala Ala Arg Arg Ser Val Arg Gln Val  
 50 55 60  
 Phe Leu Glu Val Ala Glu Lys Leu Ser Glu Lys Val Glu Ser Tyr Leu  
 65 70 75 80  
 Gln His Gln Tyr Ser Phe Lys Ile Glu Asn Pro Ala Asn Lys His Glu  
 85 90 95  
 Arg Pro His His Lys Tyr Leu  
 100

<210> 371  
 <211> 96  
 <212> PRT  
 <213> E. Coli

<400> 371  
 Met Leu Ser Lys Leu Pro Arg Arg Leu Arg Ser Phe Gln Thr Tyr Cys  
 1 5 10 15  
 Thr Ile Arg Val His Arg Gly Glu Asp Met Lys Ser Met Asp Lys Leu  
 20 25 30  
 Thr Thr Gly Val Ala Tyr Gly Thr Ser Ala Gly Asn Ala Gly Phe Trp  
 35 40 45  
 Ala Leu Gln Leu Leu Asp Lys Val Thr Pro Ser Gln Trp Ala Ala Ile  
 50 55 60  
 Gly Val Leu Gly Ser Leu Val Phe Gly Leu Leu Thr Tyr Leu Thr Asn  
 65 70 75 80  
 Leu Tyr Phe Lys Ile Lys Glu Asp Arg Arg Lys Ala Ala Arg Gly Glu  
 85 90 95

<210> 372  
 <211> 71  
 <212> PRT  
 <213> E. Coli

<400> 372  
 Met Ser Asn Lys Met Thr Gly Leu Val Lys Trp Phe Asn Ala Asp Lys  
 1 5 10 15  
 Gly Phe Gly Phe Ile Ser Pro Val Asp Gly Ser Lys Asp Val Phe Val

20 25 30  
 His Phe Ser Ala Ile Gln Asn Asp Asn Tyr Arg Thr Leu Phe Glu Gly  
 35 40 45  
 Gln Lys Val Thr Phe Ser Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala  
 50 55 60  
 Ala Asn Val Ile Ile Thr Asp  
 65 70

<210> 373  
 <211> 338  
 <212> PRT  
 <213> E. Coli

<400> 373  
 Met Phe Val Ile Trp Ser His Arg Thr Gly Phe Ile Met Ser His Gln  
 1 5 10 15  
 Leu Thr Phe Ala Asp Ser Glu Phe Ser Ser Lys Arg Arg Gln Thr Arg  
 20 25 30  
 Lys Glu Ile Phe Leu Ser Arg Met Glu Gln Ile Leu Pro Trp Gln Asn  
 35 40 45  
 Met Val Glu Val Ile Glu Pro Phe Tyr Pro Lys Ala Gly Asn Gly Arg  
 50 55 60  
 Arg Pro Tyr Pro Leu Glu Thr Met Leu Arg Ile His Cys Met Gln His  
 65 70 75 80  
 Trp Tyr Asn Leu Ser Asp Gly Ala Met Glu Asp Ala Leu Tyr Glu Ile  
 85 90 95  
 Ala Ser Met Arg Leu Phe Ala Arg Leu Ser Leu Asp Ser Ala Leu Pro  
 100 105 110  
 Asp Arg Thr Thr Ile Met Asn Phe Arg His Leu Leu Glu Gln His Gln  
 115 120 125  
 Leu Ala Arg Gln Leu Phe Lys Thr Ile Asn Arg Trp Leu Ala Glu Ala  
 130 135 140  
 Gly Val Met Met Thr Gln Gly Thr Leu Val Asp Ala Thr Ile Ile Glu  
 145 150 155 160  
 Ala Pro Ser Ser Thr Lys Asn Lys Glu Gln Gln Arg Asp Pro Glu Met  
 165 170 175  
 His Gln Thr Lys Lys Gly Asn Gln Trp His Phe Gly Met Lys Ala His  
 180 185 190  
 Ile Gly Val Asp Ala Lys Ser Gly Leu Thr His Ser Leu Val Thr Thr  
 195 200 205  
 Ala Ala Asn Glu His Asp Leu Asn Gln Leu Gly Asn Leu Leu His Gly  
 210 215 220  
 Glu Glu Gln Phe Val Ser Ala Asp Ala Gly Tyr Gln Gly Ala Pro Gln  
 225 230 235 240  
 Arg Glu Glu Leu Ala Glu Val Asp Val Asp Trp Leu Ile Ala Glu Arg  
 245 250 255  
 Pro Gly Lys Val Arg Thr Leu Lys Gln His Pro Arg Lys Asn Lys Thr  
 260 265 270  
 Ala Ile Asn Ile Glu Tyr Met Lys Ala Ser Ile Arg Ala Arg Val Glu  
 275 280 285  
 His Pro Phe Arg Ile Ile Lys Arg Gln Phe Gly Phe Val Lys Ala Arg  
 290 295 300  
 Tyr Lys Gly Leu Leu Lys Asn Asp Asn Gln Leu Ala Met Leu Phe Thr  
 305 310 315 320  
 Leu Ala Asn Leu Phe Arg Ala Asp Gln Met Ile Arg Gln Trp Glu Arg  
 325 330 335  
 Ser His

<210> 374  
 <211> 157  
 <212> PRT  
 <213> E. Coli

<400> 374

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Met Val Tyr Ile Ile Ile Val Ser His Gly His Glu Asp Tyr Ile Lys
 1           5           10           15
Lys Leu Leu Glu Asn Leu Asn Ala Asp Asp Glu His Tyr Lys Ile Ile
 20           25           30
Val Arg Asp Asn Lys Asp Ser Leu Leu Leu Lys Gln Ile Cys Gln His
 35           40           45
Tyr Ala Gly Leu Asp Tyr Ile Ser Gly Gly Val Tyr Gly Phe Gly His
 50           55           60
Asn Asn Asn Ile Ala Val Ala Tyr Val Lys Glu Lys Tyr Arg Pro Ala
 65           70           75           80
Asp Asp Asp Tyr Ile Leu Phe Leu Asn Pro Asp Ile Ile Met Lys His
 85           90           95
Asp Asp Leu Leu Thr Tyr Ile Lys Tyr Val Glu Ser Lys Arg Tyr Ala
100           105           110
Phe Ser Thr Leu Cys Leu Phe Arg Asp Glu Ala Lys Ser Leu His Asp
115           120           125
Tyr Ser Val Arg Lys Phe Pro Val Leu Ser Asp Phe Ile Val Ser Phe
130           135           140
Met Leu Gly Ile Lys Glu Gly Ala Asn Lys Ser Leu Ile
145           150           155

```

<210> 375  
 <211> 372  
 <212> PRT  
 <213> E. Coli

<400> 375

```

Met Gly Lys Ser Ile Val Val Val Ser Ala Val Asn Phe Thr Thr Gly
 1           5           10           15
Gly Pro Phe Thr Ile Leu Lys Lys Phe Leu Ala Ala Thr Asn Asn Lys
 20           25           30
Glu Asn Val Ser Phe Ile Ala Leu Val His Ser Ala Lys Glu Leu Lys
 35           40           45
Glu Ser Tyr Pro Trp Val Lys Phe Ile Glu Phe Pro Glu Val Lys Gly
 50           55           60
Ser Trp Leu Lys Arg Leu His Phe Glu Tyr Val Val Cys Lys Lys Leu
 65           70           75           80
Ser Lys Glu Leu Asn Ala Thr His Trp Ile Cys Leu His Asp Ile Thr
 85           90           95
Ala Asn Val Val Thr Lys Lys Arg Tyr Val Tyr Cys His Asn Pro Ala
100           105           110
Pro Phe Tyr Lys Gly Ile Leu Phe Arg Glu Ile Leu Met Glu Pro Ser
115           120           125
Phe Phe Leu Phe Lys Met Leu Tyr Gly Leu Ile Tyr Lys Ile Asn Ile
130           135           140
Lys Lys Asn Thr Ala Val Phe Val Gln Gln Phe Trp Met Lys Glu Lys
145           150           155           160
Phe Ile Lys Lys Tyr Ser Ile Asn Asn Ile Ile Val Ser Arg Pro Glu
165           170           175
Ile Lys Leu Ser Asp Lys Ser Gln Leu Thr Asp Asp Asp Ser Gln Phe
180           185           190
Lys Asn Asn Pro Ser Glu Leu Thr Ile Phe Tyr Pro Ala Val Pro Arg

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      195              200              205
Val Phe Lys Asn Tyr Glu Leu Ile Ile Ser Ala Ala Arg Lys Leu Lys
210              215              220
Glu Gln Ser Asn Ile Lys Phe Leu Leu Thr Ile Ser Gly Thr Glu Asn
225              230              235              240
Ala Tyr Ala Lys Tyr Ile Ile Ser Leu Ala Glu Gly Leu Asp Asn Val
245              250              255
His Phe Leu Gly Tyr Leu Asp Lys Glu Lys Ile Asp His Cys Tyr Asn
260              265              270
Ile Ser Asp Ile Val Cys Phe Pro Ser Arg Leu Glu Thr Trp Gly Leu
275              280              285
Pro Leu Ser Glu Ala Lys Glu Arg Gly Lys Trp Val Leu Ala Ser Asp
290              295              300
Phe Pro Phe Thr Arg Glu Thr Leu Gly Ser Tyr Glu Lys Lys Ala Phe
305              310              315              320
Phe Asp Ser Asn Asn Asp Asp Met Leu Val Lys Leu Ile Ile Asp Phe
325              330              335
Lys Lys Gly Asn Leu Lys Lys Asp Ile Ser Asp Ala Asn Phe Ile Tyr
340              345              350
Arg Asn Glu Asn Val Leu Val Gly Phe Asp Glu Leu Val Asn Phe Ile
355              360              365
Thr Glu Glu His
370

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<210> 376
<211> 196
<212> PRT
<213> E. Coli

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      <400> 376
Met Ile Leu Lys Leu Ala Lys Arg Tyr Gly Leu Cys Gly Phe Ile Arg
1              5              10              15
Leu Val Arg Asp Val Leu Leu Thr Arg Val Phe Tyr Arg Asn Cys Arg
20              25              30
Ile Ile Arg Phe Pro Cys Tyr Ile Arg Asn Asp Gly Ser Ile Asn Phe
35              40              45
Gly Glu Asn Phe Thr Ser Gly Val Gly Leu Arg Leu Asp Ala Phe Gly
50              55              60
Arg Gly Val Ile Phe Phe Ser Asp Asn Val Gln Val Asn Asp Tyr Val
65              70              75              80
His Ile Ala Ser Ile Glu Ser Val Thr Ile Gly Arg Asp Thr Leu Ile
85              90              95
Ala Ser Lys Val Phe Ile Thr Asp His Asn His Gly Ser Phe Lys His
100              105              110
Ser Asp Pro Met Ser Ser Pro Asn Ile Pro Pro Asp Met Arg Thr Leu
115              120              125
Glu Ser Ser Ala Val Val Ile Gly Gln Arg Val Trp Leu Gly Glu Asn
130              135              140
Val Thr Val Leu Pro Gly Thr Ile Ile Gly Asn Gly Val Val Val Gly
145              150              155              160
Ala Asn Ser Val Val Arg Gly Ser Ile Pro Glu Asn Thr Val Ile Ala
165              170              175
Gly Val Pro Ala Lys Ile Ile Lys Lys Tyr Asn His Glu Thr Lys Leu
180              185              190
Trp Glu Lys Ala
195

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<210> 377
<211> 330
<212> PRT

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&lt;213&gt; E. Coli

&lt;400&gt; 377

```

Met Tyr Phe Leu Asn Asp Leu Asn Phe Ser Arg Arg Asp Ala Gly Phe
 1          5          10          15
Lys Ala Arg Lys Asp Ala Leu Asp Ile Ala Ser Asp Tyr Glu Asn Ile
 20          25          30
Ser Val Val Asn Ile Pro Leu Trp Gly Gly Val Val Gln Arg Ile Ile
 35          40          45
Ser Ser Val Lys Leu Ser Thr Phe Leu Cys Gly Leu Glu Asn Lys Asp
 50          55          60
Val Leu Ile Phe Asn Phe Pro Met Ala Lys Pro Phe Trp His Ile Leu
 65          70          75          80
Ser Phe Phe His Arg Leu Leu Lys Phe Arg Ile Val Pro Leu Ile His
 85          90          95
Asp Ile Asp Glu Leu Arg Gly Gly Gly Gly Ser Asp Ser Val Arg Leu
100          105          110
Ala Thr Cys Asp Met Val Ile Ser His Asn Pro Gln Met Thr Lys Tyr
115          120          125
Leu Ser Lys Tyr Met Ser Gln Asp Lys Ile Lys Asp Ile Lys Ile Phe
130          135          140
Asp Tyr Leu Val Ser Ser Asp Val Glu His Arg Asp Val Thr Asp Lys
145          150          155          160
Gln Arg Gly Val Ile Tyr Ala Gly Asn Leu Ser Arg His Lys Cys Ser
165          170          175
Phe Ile Tyr Thr Glu Gly Cys Asp Phe Thr Leu Phe Gly Val Asn Tyr
180          185          190
Glu Asn Lys Asp Asn Pro Lys Tyr Leu Gly Ser Phe Asp Ala Gln Ser
195          200          205
Pro Glu Lys Ile Asn Leu Pro Gly Met Gln Phe Gly Leu Ile Trp Asp
210          215          220
Gly Asp Ser Val Glu Thr Cys Ser Gly Ala Phe Gly Asp Tyr Leu Lys
225          230          235          240
Phe Asn Asn Pro His Lys Thr Ser Leu Tyr Leu Ser Met Glu Leu Pro
245          250          255
Val Phe Ile Trp Asp Lys Ala Ala Leu Ala Asp Phe Ile Val Asp Asn
260          265          270
Arg Ile Gly Tyr Ala Val Gly Ser Ile Lys Glu Met Gln Glu Ile Val
275          280          285
Asp Ser Met Thr Ile Glu Thr Tyr Lys Gln Ile Ser Glu Asn Thr Lys
290          295          300
Ile Ile Ser Gln Lys Ile Arg Thr Gly Ser Tyr Phe Arg Asp Val Leu
305          310          315          320
Glu Glu Val Ile Asp Asp Leu Lys Thr Arg
325          330

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&lt;210&gt; 378

&lt;211&gt; 388

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 378

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Met Ile Tyr Leu Val Ile Ser Val Phe Leu Ile Thr Ala Phe Ile Cys
 1          5          10          15
Leu Tyr Leu Lys Lys Asp Ile Phe Tyr Pro Ala Val Cys Val Asn Ile
 20          25          30
Ile Phe Ala Leu Val Leu Leu Gly Tyr Glu Ile Thr Ser Asp Ile Tyr
 35          40          45
Ala Phe Gln Leu Asn Asp Ala Thr Leu Ile Phe Leu Leu Cys Asn Val
 50          55          60

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Leu Thr Phe Thr Leu Ser Cys Leu Leu Thr Glu Ser Val Leu Asp Leu  
 65 70 75 80  
 Asn Ile Arg Lys Val Asn Asn Ala Ile Tyr Ser Ile Pro Ser Lys Lys  
 85 90 95  
 Val His Asn Val Gly Leu Leu Val Ile Ser Phe Ser Met Ile Tyr Ile  
 100 105 110  
 Cys Met Arg Leu Ser Asn Tyr Gln Phe Gly Thr Ser Leu Leu Ser Tyr  
 115 120 125  
 Met Asn Leu Ile Arg Asp Ala Asp Val Glu Asp Thr Ser Arg Asn Phe  
 130 135 140  
 Ser Ala Tyr Met Gln Pro Ile Ile Leu Thr Thr Phe Ala Leu Phe Ile  
 145 150 155 160  
 Trp Ser Lys Lys Phe Thr Asn Thr Lys Val Ser Lys Thr Phe Thr Leu  
 165 170 175  
 Leu Val Phe Ile Val Phe Ile Phe Ala Ile Ile Leu Asn Thr Gly Lys  
 180 185 190  
 Gln Ile Val Phe Met Val Ile Ile Ser Tyr Ala Phe Ile Val Gly Val  
 195 200 205  
 Asn Arg Val Lys His Tyr Val Tyr Leu Ile Thr Ala Val Gly Val Leu  
 210 215 220  
 Phe Ser Leu Tyr Met Leu Phe Leu Arg Gly Leu Pro Gly Gly Met Ala  
 225 230 235 240  
 Tyr Tyr Leu Ser Met Tyr Leu Val Ser Pro Ile Ile Ala Phe Gln Glu  
 245 250 255  
 Phe Tyr Phe Gln Gln Val Ser Asn Ser Ala Ser Ser His Val Phe Trp  
 260 265 270  
 Phe Phe Glu Arg Leu Met Gly Leu Leu Thr Gly Gly Val Ser Met Ser  
 275 280 285  
 Leu His Lys Glu Phe Val Trp Val Gly Leu Pro Thr Asn Val Tyr Thr  
 290 295 300  
 Ala Phe Ser Asp Tyr Val Tyr Ile Ser Ala Glu Leu Ser Tyr Leu Met  
 305 310 315 320  
 Met Val Ile His Gly Cys Ile Ser Gly Val Leu Trp Arg Leu Ser Arg  
 325 330 335  
 Asn Tyr Ile Ser Val Lys Ile Phe Tyr Ser Tyr Phe Ile Tyr Thr Phe  
 340 345 350  
 Ser Phe Ile Phe Tyr His Glu Ser Phe Met Thr Asn Ile Ser Ser Trp  
 355 360 365  
 Ile Gln Ile Thr Leu Cys Ile Ile Val Phe Ser Gln Phe Leu Lys Ala  
 370 375 380  
 Gln Lys Ile Lys  
 385

<210> 379  
 <211> 367  
 <212> PRT  
 <213> E. Coli

<400> 379  
 Met Tyr Asp Tyr Ile Ile Val Gly Ser Gly Leu Phe Gly Ala Val Cys  
 1 5 10 15  
 Ala Asn Glu Leu Lys Lys Leu Asn Lys Lys Val Leu Val Ile Glu Lys  
 20 25 30  
 Arg Asn His Ile Gly Gly Asn Ala Tyr Thr Glu Asp Cys Glu Gly Ile  
 35 40 45  
 Gln Ile His Lys Tyr Gly Ala His Ile Phe His Thr Asn Asp Lys Tyr  
 50 55 60  
 Ile Trp Asp Tyr Val Asn Asp Leu Val Glu Phe Asn Arg Phe Thr Asn  
 65 70 75 80

Ser Pro Leu Ala Ile Tyr Lys Asp Lys Leu Phe Asn Leu Pro Phe Asn  
 85 90 95  
 Met Asn Thr Phe His Gln Met Trp Gly Val Lys Asp Pro Gln Glu Ala  
 100 105 110  
 Gln Asn Ile Ile Asn Ala Gln Lys Lys Tyr Gly Asp Lys Val Pro  
 115 120 125  
 Glu Asn Leu Glu Glu Gln Ala Ile Ser Leu Val Gly Glu Asp Leu Tyr  
 130 135 140  
 Gln Ala Leu Ile Lys Gly Tyr Thr Glu Lys Gln Trp Gly Arg Ser Ala  
 145 150 155 160  
 Lys Glu Leu Pro Ala Phe Ile Ile Lys Arg Ile Pro Val Arg Phe Thr  
 165 170 175  
 Phe Asp Asn Asn Tyr Phe Ser Asp Arg Tyr Gln Gly Ile Pro Val Gly  
 180 185 190  
 Gly Tyr Thr Lys Leu Ile Glu Lys Met Leu Glu Gly Val Asp Val Lys  
 195 200 205  
 Leu Gly Ile Asp Phe Leu Lys Asp Lys Asp Ser Leu Ala Ser Lys Ala  
 210 215 220  
 His Arg Ile Ile Tyr Thr Gly Pro Ile Asp Gln Tyr Phe Asp Tyr Arg  
 225 230 235 240  
 Phe Gly Ala Leu Glu Tyr Arg Ser Leu Lys Phe Glu Thr Glu Arg His  
 245 250 255  
 Glu Phe Pro Asn Phe Gln Gly Asn Ala Val Ile Asn Phe Thr Asp Ala  
 260 265 270  
 Asn Val Pro Tyr Thr Arg Ile Ile Glu His Lys His Phe Asp Tyr Val  
 275 280 285  
 Glu Thr Lys His Thr Val Val Thr Lys Glu Tyr Pro Leu Glu Trp Lys  
 290 295 300  
 Val Gly Asp Glu Pro Tyr Tyr Pro Val Asn Asp Asn Lys Asn Met Glu  
 305 310 315 320  
 Leu Phe Lys Lys Tyr Arg Glu Leu Ala Ser Arg Glu Asp Lys Val Ile  
 325 330 335  
 Phe Gly Gly Arg Leu Ala Glu Tyr Lys Tyr Tyr Asp Met His Gln Val  
 340 345 350  
 Ile Ser Ala Ala Leu Tyr Gln Val Lys Asn Ile Met Ser Thr Asp  
 355 360 365

<210> 380  
 <211> 371  
 <212> PRT  
 <213> E. Coli

<400> 380  
 Met Phe Pro Lys Ile Met Asn Asp Glu Asn Phe Phe Lys Lys Ala Ala  
 1 5 10 15  
 Ala His Gly Glu Pro Pro Leu Thr Pro Gln Asn Glu His Gln Arg  
 20 25 30  
 Ser Gly Leu Arg Phe Ala Arg Arg Val Arg Leu Pro Arg Ala Val Gly  
 35 40 45  
 Leu Ala Gly Met Phe Leu Pro Ile Ala Ser Thr Leu Val Ser His Pro  
 50 55 60  
 Pro Pro Gly Trp Trp Trp Leu Val Leu Val Gly Trp Ala Phe Val Trp  
 65 70 75 80  
 Pro His Leu Ala Trp Gln Ile Ala Ser Arg Ala Val Asp Pro Leu Ser  
 85 90 95  
 Arg Glu Ile Tyr Asn Leu Lys Thr Asp Ala Val Leu Ala Gly Met Trp  
 100 105 110  
 Val Gly Val Met Gly Val Asn Val Leu Pro Ser Thr Ala Met Leu Met  
 115 120 125  
 Ile Met Cys Leu Asn Leu Met Gly Ala Gly Gly Pro Arg Leu Phe Val



130 135 140  
 Ala Gly Leu Val Leu Met Val Val Ser Cys Leu Val Thr Leu Glu Leu  
 145 150 155 160  
 Thr Gly Ile Thr Val Ser Phe Asn Ser Ala Pro Leu Glu Trp Trp Leu  
 165 170 175  
 Ser Leu Pro Ile Ile Val Ile Tyr Pro Leu Leu Phe Gly Trp Val Ser  
 180 185 190  
 Tyr Gln Thr Ala Thr Lys Leu Ala Glu His Lys Arg Arg Leu Gln Val  
 195 200 205  
 Met Ser Thr Arg Asp Gly Met Thr Gly Val Tyr Asn Arg Arg His Trp  
 210 215 220  
 Glu Thr Met Leu Arg Asn Glu Phe Asp Asn Cys Arg Arg His Asn Arg  
 225 230 235 240  
 Asp Ala Thr Leu Leu Ile Ile Asp Ile Asp His Phe Lys Ser Ile Asn  
 245 250 255  
 Asp Thr Trp Gly His Asp Val Gly Asp Glu Ala Ile Val Ala Leu Thr  
 260 265 270  
 Arg Gln Leu Gln Ile Thr Leu Arg Gly Ser Asp Val Ile Gly Arg Phe  
 275 280 285  
 Gly Gly Asp Glu Phe Ala Val Ile Met Ser Gly Thr Pro Ala Glu Ser  
 290 295 300  
 Ala Ile Thr Ala Met Leu Arg Val His Glu Gly Leu Asn Thr Leu Arg  
 305 310 315 320  
 Leu Pro Asn Thr Pro Gln Val Thr Leu Arg Ile Ser Val Gly Val Ala  
 325 330 335  
 Pro Leu Asn Pro Gln Met Ser His Tyr Arg Glu Trp Leu Lys Ser Ala  
 340 345 350  
 Asp Leu Ala Leu Tyr Lys Ala Lys Lys Ala Gly Arg Asn Arg Thr Glu  
 355 360 365  
 Val Ala Ala  
 370

<210> 381  
 <211> 467  
 <212> PRT  
 <213> E. Coli

<400> 381  
 Met Asp Val Asn Val Asp Gln Phe Asp Thr Glu Ala Phe Arg Thr Asp  
 1 5 10 15  
 Lys Leu Glu Leu Thr Ser Gly Asn Ile Ala Asp His Asn Gly Asn Val  
 20 25 30  
 Val Ser Gly Val Phe Asp Ile His Ser Ser Asp Tyr Val Leu Asn Ala  
 35 40 45  
 Asp Leu Val Asn Asp Arg Thr Trp Asp Thr Ser Lys Ser Asn Tyr Gly  
 50 55 60  
 Tyr Gly Ile Val Ala Met Asn Ser Asp Gly His Leu Thr Ile Asn Gly  
 65 70 75 80  
 Asn Gly Asp Val Asp Asn Gly Thr Glu Leu Asp Asn Ser Ser Val Asp  
 85 90 95  
 Asn Val Val Ala Ala Thr Gly Asn Tyr Lys Val Arg Ile Asp Asn Ala  
 100 105 110  
 Thr Gly Ala Gly Ala Ile Ala Asp Tyr Lys Asp Lys Glu Ile Ile Tyr  
 115 120 125  
 Val Asn Asp Val Asn Ser Asn Ala Thr Phe Ser Ala Ala Asn Lys Ala  
 130 135 140  
 Asp Leu Gly Ala Tyr Thr Tyr Gln Ala Glu Gln Arg Gly Asn Thr Val  
 145 150 155 160  
 Val Leu Gln Gln Met Glu Leu Thr Asp Tyr Ala Asn Met Ala Leu Ser  
 165 170 175  
 Ile Pro Ser Ala Asn Thr Asn Ile Trp Asn Leu Glu Gln Asp Thr Val

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      180      185      190
Gly Thr Arg Leu Thr Asn Ser Arg His Gly Leu Ala Asp Asn Gly Gly
      195      200      205
Ala Trp Val Ser Tyr Phe Gly Gly Asn Phe Asn Gly Asp Asn Gly Thr
      210      215      220
Ile Asn Tyr Asp Gln Asp Val Asn Gly Ile Met Val Gly Val Asp Thr
      225      230      235      240
Lys Ile Asp Gly Asn Asn Ala Lys Trp Ile Val Gly Ala Ala Ala Gly
      245      250      255
Phe Ala Lys Gly Asp Met Asn Asp Arg Ser Gly Gln Val Asp Gln Asp
      260      265      270
Ser Gln Thr Ala Tyr Ile Tyr Ser Ser Ala His Phe Ala Asn Asn Val
      275      280      285
Phe Val Asp Gly Ser Leu Ser Tyr Ser His Phe Asn Asn Asp Leu Ser
      290      295      300
Ala Thr Met Ser Asn Gly Thr Tyr Val Asp Gly Ser Thr Asn Ser Asp
      305      310      315      320
Ala Trp Gly Phe Gly Leu Lys Ala Gly Tyr Asp Phe Lys Leu Gly Asp
      325      330      335
Ala Gly Tyr Val Thr Pro Tyr Gly Ser Val Ser Gly Leu Phe Gln Ser
      340      345      350
Gly Asp Asp Tyr Gln Leu Ser Asn Asp Met Lys Val Asp Gly Gln Ser
      355      360      365
Tyr Asp Ser Met Arg Tyr Glu Leu Gly Val Asp Ala Gly Tyr Thr Phe
      370      375      380
Thr Tyr Ser Glu Asp Gln Ala Leu Thr Pro Tyr Phe Lys Leu Ala Tyr
      385      390      395      400
Val Tyr Asp Asp Ser Asn Asn Asp Asn Asp Val Asn Gly Asp Ser Ile
      405      410      415
Asp Asn Gly Thr Glu Gly Ser Ala' Val Arg Val Gly Leu Gly Thr Gln
      420      425      430
Phe Ser Phe Thr Lys Asn Phe Ser Ala Tyr Thr Asp Ala Asn Tyr Leu
      435      440      445
Gly Gly Gly Asp Val Asp Gln Asp Trp Ser Ala Asn Val Gly Val Lys
      450      455      460
Tyr Thr Trp
      465

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<210> 382
<211> 222
<212> PRT
<213> E. Coli

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      <400> 382
Met Pro Val Lys Asp Leu Thr Gly Ile Thr Ala Lys Asp Ala Gln Met
      1      5      10      15
Leu Ser Val Val Lys Pro Leu Gln Glu Phe Gly Lys Leu Asp Lys Cys
      20      25      30
Leu Ser Arg Tyr Gly Thr Arg Phe Glu Phe Asn Asn Glu Lys Gln Val
      35      40      45
Ile Phe Ser Ser Asp Val Asn Asn Glu Asp Thr Phe Val Ile Leu Glu
      50      55      60
Gly Val Ile Ser Leu Arg Arg Glu Glu Asn Val Leu Ile Gly Ile Thr
      65      70      75      80
Gln Ala Pro Tyr Ile Met Gly Leu Ala Asp Gly Leu Met Lys Asn Asp
      85      90      95
Ile Pro Tyr Lys Leu Ile Ser Glu Gly Asn Cys Thr Gly Tyr His Leu
      100      105      110
Pro Ala Lys Gln Thr Ile Thr Leu Ile Glu Gln Asn Gln Leu Trp Arg
      115      120      125

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Asp Ala Phe Tyr Trp Leu Ala Trp Gln Asn Arg Ile Leu Glu Leu Arg  
 130 135 140  
 Asp Val Gln Leu Ile Gly His Asn Ser Tyr Glu Gln Ile Arg Ala Thr  
 145 150 155 160  
 Leu Leu Ser Met Ile Asp Trp Asn Glu Glu Leu Arg Ser Arg Ile Gly  
 165 170 175  
 Val Met Asn Tyr Ile His Gln Arg Thr Arg Ile Ser Arg Ser Val Val  
 180 185 190  
 Ala Glu Val Leu Ala Ala Leu Arg Lys Gly Gly Tyr Ile Glu Met Asn  
 195 200 205  
 Lys Gly Lys Leu Val Ala Ile Asn Arg Leu Pro Ser Glu Tyr  
 210 215 220

<210> 383  
 <211> 84  
 <212> PRT  
 <213> E. Coli

<400> 383  
 Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys  
 1 5 10 15  
 Met Glu Lys Ser Ile Val Val Ala Ile Glu Arg Phe Val Lys His Pro  
 20 25 30  
 Ile Tyr Gly Lys Phe Ile Lys Arg Thr Thr Lys Leu His Val His Asp  
 35 40 45  
 Glu Asn Asn Glu Cys Gly Ile Gly Asp Val Val Glu Ile Arg Glu Cys  
 50 55 60  
 Arg Pro Leu Ser Lys Thr Lys Ser Trp Thr Leu Val Arg Val Val Glu  
 65 70 75 80  
 Lys Ala Val Leu

<210> 384  
 <211> 63  
 <212> PRT  
 <213> E. Coli

<400> 384  
 Met Lys Ala Lys Glu Leu Arg Glu Lys Ser Val Glu Glu Leu Asn Thr  
 1 5 10 15  
 Glu Leu Leu Asn Leu Leu Arg Glu Gln Phe Asn Leu Arg Met Gln Ala  
 20 25 30  
 Ala Ser Gly Gln Leu Gln Gln Ser His Leu Leu Lys Gln Val Arg Arg  
 35 40 45  
 Asp Val Ala Arg Val Lys Thr Leu Leu Asn Glu Lys Ala Gly Ala  
 50 55 60

<210> 385  
 <211> 136  
 <212> PRT  
 <213> E. Coli

<400> 385  
 Met Leu Gln Pro Lys Arg Thr Lys Phe Arg Lys Met His Lys Gly Arg  
 1 5 10 15  
 Asn Arg Gly Leu Ala Gln Gly Thr Asp Val Ser Phe Gly Ser Phe Gly  
 20 25 30  
 Leu Lys Ala Val Gly Arg Gly Arg Leu Thr Ala Arg Gln Ile Glu Ala

```

      35      40      45
Ala Arg Arg Ala Met Thr Arg Ala Val Lys Arg Gln Gly Lys Ile Trp
  50      55      60
Ile Arg Val Phe Pro Asp Lys Pro Ile Thr Glu Lys Pro Leu Ala Val
  65      70      75      80
Arg Met Gly Lys Gly Lys Gly Asn Val Glu Tyr Trp Val Ala Leu Ile
      85      90      95
Gln Pro Gly Lys Val Leu Tyr Glu Met Asp Gly Val Pro Glu Glu Leu
      100      105      110
Ala Arg Glu Ala Phe Lys Leu Ala Ala Lys Leu Pro Ile Lys Thr
      115      120      125
Thr Phe Val Thr Lys Thr Val Met
      130      135

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<210> 386  
 <211> 233  
 <212> PRT  
 <213> E. Coli

```

      <400> 386
Met Gly Gln Lys Val His Pro Asn Gly Ile Arg Leu Gly Ile Val Lys
  1      5      10
Pro Trp Asn Ser Thr Trp Phe Ala Asn Thr Lys Glu Phe Ala Asp Asn
      20      25      30
Leu Asp Ser Asp Phe Lys Val Arg Gln Tyr Leu Thr Lys Glu Leu Ala
      35      40      45
Lys Ala Ser Val Ser Arg Ile Val Ile Glu Arg Pro Ala Lys Ser Ile
      50      55      60
Arg Val Thr Ile His Thr Ala Arg Pro Gly Ile Val Ile Gly Lys Lys
      65      70      75      80
Gly Glu Asp Val Glu Lys Leu Arg Lys Val Val Ala Asp Ile Ala Gly
      85      90      95
Val Pro Ala Gln Ile Asn Ile Ala Glu Val Arg Lys Pro Glu Leu Asp
      100      105      110
Ala Lys Leu Val Ala Asp Ser Ile Thr Ser Gln Leu Glu Arg Arg Val
      115      120      125
Met Phe Arg Arg Ala Met Lys Arg Ala Val Gln Asn Ala Met Arg Leu
      130      135      140
Gly Ala Lys Gly Ile Lys Val Glu Val Ser Gly Arg Leu Gly Gly Ala
      145      150      155      160
Glu Ile Ala Arg Thr Glu Trp Tyr Arg Glu Gly Arg Val Pro Leu His
      165      170      175
Thr Leu Arg Ala Asp Ile Asp Tyr Asn Thr Ser Glu Ala His Thr Thr
      180      185      190
Tyr Gly Val Ile Gly Val Lys Val Trp Ile Phe Lys Gly Glu Ile Leu
      195      200      205
Gly Gly Met Ala Ala Val Glu Gln Pro Glu Lys Pro Ala Ala Gln Pro
      210      215      220
Lys Lys Gln Gln Arg Lys Gly Arg Lys
      225      230

```

<210> 387  
 <211> 110  
 <212> PRT  
 <213> E. Coli

<400> 387

Met Glu Thr Ile Ala Lys His Arg His Ala Arg Ser Ser Ala Gln Lys  
 1 5 10 15  
 Val Arg Leu Val Ala Asp Leu Ile Arg Gly Lys Lys Val Ser Gln Ala  
 20 25 30  
 Leu Asp Ile Leu Thr Tyr Thr Asn Lys Lys Ala Ala Val Leu Val Lys  
 35 40 45  
 Lys Val Leu Glu Ser Ala Ile Ala Asn Ala Glu His Asn Asp Gly Ala  
 50 55 60  
 Asp Ile Asp Asp Leu Lys Val Thr Lys Ile Phe Val Asp Glu Gly Pro  
 65 70 75 80  
 Ser Met Lys Arg Ile Met Pro Arg Ala Lys Gly Arg Ala Asp Arg Ile  
 85 90 95  
 Leu Lys Arg Thr Ser His Ile Thr Val Val Val Ser Asp Arg  
 100 105 110

<210> 388  
 <211> 92  
 <212> PRT  
 <213> E. Coli

<400> 388  
 Met Pro Arg Ser Leu Lys Lys Gly Pro Phe Ile Asp Leu His Leu Leu  
 1 5 10 15  
 Met Lys Val Glu Lys Ala Val Glu Ser Gly Asp Lys Lys Pro Leu Arg  
 20 25 30  
 Thr Trp Ser Arg Arg Ser Thr Ile Phe Pro Asn Met Ile Gly Leu Thr  
 35 40 45  
 Ile Ala Val His Asn Gly Arg Gln His Val Pro Val Phe Val Thr Asp  
 50 55 60  
 Glu Met Val Gly His Lys Leu Gly Glu Phe Ala Pro Thr Arg Thr Tyr  
 65 70 75 80  
 Arg Gly His Ala Ala Asp Lys Lys Ala Lys Lys  
 85 90

<210> 389  
 <211> 273  
 <212> PRT  
 <213> E. Coli

<400> 389  
 Met Ala Val Val Lys Cys Lys Pro Thr Ser Pro Gly Arg Arg His Val  
 1 5 10 15  
 Val Lys Val Val Asn Pro Glu Leu His Lys Gly Lys Pro Phe Ala Pro  
 20 25 30  
 Leu Leu Glu Lys Asn Ser Lys Ser Gly Gly Arg Asn Asn Asn Gly Arg  
 35 40 45  
 Ile Thr Thr Arg His Ile Gly Gly Gly His Lys Gln Ala Tyr Arg Ile  
 50 55 60  
 Val Asp Phe Lys Arg Asn Lys Asp Gly Ile Pro Ala Val Val Glu Arg  
 65 70 75 80  
 Leu Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Leu Tyr  
 85 90 95  
 Lys Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys Gly Leu Lys Ala  
 100 105 110  
 Gly Asp Gln Ile Gln Ser Gly Val Asp Ala Ala Ile Lys Pro Gly Asn  
 115 120 125  
 Thr Leu Pro Met Arg Asn Ile Pro Val Gly Ser Thr Val His Asn Val

```

      130              135              140
Glu Met Lys Pro Gly Lys Gly Gly Gln Leu Ala Arg Ser Ala Gly Thr
145              150              155              160
Tyr Val Gln Ile Val Ala Arg Asp Gly Ala Tyr Val Thr Leu Arg Leu
      165              170              175
Arg Ser Gly Glu Met Arg Lys Val Glu Ala Asp Cys Arg Ala Thr Leu
      180              185              190
Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Val Leu Gly Lys Ala
      195              200              205
Gly Ala Ala Arg Trp Arg Gly Val Arg Pro Thr Val Arg Gly Thr Ala
      210              215              220
Met Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Arg Asn Phe
225              230              235              240
Gly Lys His Pro Val Thr Pro Trp Gly Val Gln Thr Lys Gly Lys Lys
      245              250              255
Thr Arg Ser Asn Lys Arg Thr Asp Lys Phe Ile Val Arg Arg Arg Ser
      260              265              270
Lys

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```

<210> 390
<211> 100
<212> PRT
<213> E. Coli

```

```

      <400> 390
Met Ile Arg Glu Glu Arg Leu Leu Lys Val Leu Arg Ala Pro His Val
 1              5              10              15
Ser Glu Lys Ala Ser Thr Ala Met Glu Lys Ser Asn Thr Ile Val Leu
      20              25              30
Lys Val Ala Lys Asp Ala Thr Lys Ala Glu Ile Lys Ala Ala Val Gln
      35              40              45
Lys Leu Phe Glu Val Glu Val Glu Val Val Asn Thr Leu Val Val Lys
      50              55              60
Gly Lys Val Lys Arg His Gly Gln Arg Ile Gly Arg Arg Ser Asp Trp
65              70              75              80
Lys Lys Ala Tyr Val Thr Leu Lys Glu Gly Gln Asn Leu Asp Phe Val
      85              90              95
Gly Gly Ala Glu
      100

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<210> 391
<211> 201
<212> PRT
<213> E. Coli

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```

      <400> 391
Met Glu Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu
 1              5              10              15
Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val
      20              25              30
Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr
      35              40              45
Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly
      50              55              60
Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser
65              70              75              80

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Gly Gly Val Thr Phe Ala Ala Arg Pro Gln Asp His Ser Gln Lys Val  
 85 90 95  
 Asn Lys Lys Met Tyr Arg Gly Ala Leu Lys Ser Ile Leu Ser Glu Leu  
 100 105 110  
 Val Arg Gln Asp Arg Leu Ile Val Val Glu Lys Phe Ser Val Glu Ala  
 115 120 125  
 Pro Lys Thr Lys Leu Leu Ala Gln Lys Leu Lys Asp Met Ala Leu Glu  
 130 135 140  
 Asp Val Leu Ile Ile Thr Gly Glu Leu Asp Glu Asn Leu Phe Leu Ala  
 145 150 155 160  
 Ala Arg Asn Leu His Lys Val Asp Val Arg Asp Ala Thr Gly Ile Asp  
 165 170 175  
 Pro Val Ser Leu Ile Ala Phe Asp Lys Val Val Met Thr Ala Asp Ala  
 180 185 190  
 Val Lys Gln Val Glu Glu Met Leu Ala  
 195 200

<210> 392  
 <211> 209  
 <212> PRT  
 <213> E. Coli

<400> 392  
 Met Ile Gly Leu Val Gly Lys Lys Val Gly Met Thr Arg Ile Phe Thr  
 1 5 10 15  
 Glu Asp Gly Val Ser Ile Pro Val Thr Val Ile Glu Val Glu Ala Asn  
 20 25 30  
 Arg Val Thr Gln Val Lys Asp Leu Ala Asn Asp Gly Tyr Arg Ala Ile  
 35 40 45  
 Gln Val Thr Thr Gly Ala Lys Lys Ala Asn Arg Val Thr Lys Pro Glu  
 50 55 60  
 Ala Gly His Phe Ala Lys Ala Gly Val Glu Ala Gly Arg Gly Leu Trp  
 65 70 75 80  
 Glu Phe Arg Leu Ala Glu Gly Glu Glu Phe Thr Val Gly Gln Ser Ile  
 85 90 95  
 Ser Val Glu Leu Phe Ala Asp Val Lys Lys Val Asp Val Thr Gly Thr  
 100 105 110  
 Ser Lys Gly Lys Gly Phe Ala Gly Thr Val Lys Arg Trp Asn Phe Arg  
 115 120 125  
 Thr Gln Asp Ala Thr His Gly Asn Ser Leu Ser His Arg Val Pro Gly  
 130 135 140  
 Ser Ile Gly Gln Asn Gln Thr Pro Gly Lys Val Phe Lys Gly Lys Lys  
 145 150 155 160  
 Met Ala Gly Gln Met Gly Asn Glu Arg Val Thr Val Gln Ser Leu Asp  
 165 170 175  
 Val Val Arg Val Asp Ala Glu Arg Asn Leu Leu Leu Val Lys Gly Ala  
 180 185 190  
 Val Pro Gly Ala Thr Gly Ser Asp Leu Ile Val Lys Pro Ala Val Lys  
 195 200 205  
 Ala

<210> 393  
 <211> 103  
 <212> PRT  
 <213> E. Coli

&lt;400&gt; 393

```

Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg
 1           5           10           15
Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr
           20           25           30
Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg
           35           40           45
Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln
           50           55           60
Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr
65           70           75           80
Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val
           85           90           95
Asp Val Gln Ile Ser Leu Gly
           100

```

&lt;210&gt; 394

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 394

```

Met Ala Arg Val Lys Arg Gly Val Ile Ala Arg Ala Arg His Lys Lys
 1           5           10           15
Ile Leu Lys Gln Ala Lys Gly Tyr Tyr Gly Ala Arg Ser Arg Val Tyr
           20           25           30
Arg Val Ala Phe Gln Ala Val Ile Lys Ala Gly Gln Tyr Ala Tyr Arg
           35           40           45
Asp Arg Arg Gln Arg Lys Arg Gln Phe Arg Gln Leu Trp Ile Ala Arg
           50           55           60
Ile Asn Ala Ala Ala Arg Gln Asn Gly Ile Ser Tyr Ser Lys Phe Ile
65           70           75           80
Asn Gly Leu Lys Lys Ala Ser Val Glu Ile Asp Arg Lys Ile Leu Ala
           85           90           95
Asp Ile Ala Val Phe Asp Lys Val Ala Phe Thr Ala Leu Val Glu Lys
           100           105           110
Ala Lys Ala Ala Leu Ala
           115

```

&lt;210&gt; 395

&lt;211&gt; 65

&lt;212&gt; PRT

&lt;213&gt; E. Coli

&lt;400&gt; 395

```

Met Pro Lys Ile Lys Thr Val Arg Gly Ala Ala Lys Arg Phe Lys Lys
 1           5           10           15
Thr Gly Lys Gly Gly Phe Lys His Lys His Ala Asn Leu Arg His Ile
           20           25           30
Leu Thr Lys Lys Ala Thr Lys Arg Lys Arg His Leu Arg Pro Lys Ala
           35           40           45
Met Val Ser Lys Gly Asp Leu Gly Leu Val Ile Ala Cys Leu Pro Tyr
           50           55           60
Ala
65

```



<210> 396  
 <211> 180  
 <212> PRT  
 <213> E. Coli

<400> 396  
 Met Lys Gly Gly Lys Arg Val Gln Thr Ala Arg Pro Asn Arg Ile Asn  
 1 5 10 15  
 Gly Glu Ile Arg Ala Gln Glu Val Arg Leu Thr Gly Leu Glu Gly Glu  
 20 25 30  
 Gln Leu Gly Ile Val Ser Leu Arg Glu Ala Leu Glu Lys Ala Glu Glu  
 35 40 45  
 Ala Gly Val Asp Leu Val Glu Ile Ser Pro Asn Ala Glu Pro Pro Val  
 50 55 60  
 Cys Arg Ile Met Asp Tyr Gly Lys Phe Leu Tyr Glu Lys Ser Lys Ser  
 65 70 75 80  
 Ser Lys Glu Gln Lys Lys Gln Lys Val Ile Gln Val Lys Glu Ile  
 85 90 95  
 Lys Phe Arg Pro Gly Thr Asp Glu Gly Asp Tyr Gln Val Lys Leu Arg  
 100 105 110  
 Ser Leu Ile Arg Phe Leu Glu Glu Gly Asp Lys Ala Lys Ile Thr Leu  
 115 120 125  
 Arg Phe Arg Gly Arg Glu Met Ala His Gln Gln Ile Gly Met Glu Val  
 130 135 140  
 Leu Asn Arg Val Lys Asp Asp Leu Gln Glu Leu Ala Val Val Glu Ser  
 145 150 155 160  
 Phe Pro Thr Lys Ile Glu Gly Arg Gln Met Ile Met Val Leu Ala Pro  
 165 170 175  
 Lys Lys Lys Gln  
 180

<210> 397  
 <211> 642  
 <212> PRT  
 <213> E. Coli

<400> 397  
 Met Pro Val Ile Thr Leu Pro Asp Gly Ser Gln Arg His Tyr Asp His  
 1 5 10 15  
 Ala Val Ser Pro Met Asp Val Ala Leu Asp Ile Gly Pro Gly Leu Ala  
 20 25 30  
 Lys Ala Cys Ile Ala Gly Arg Val Asn Gly Glu Leu Val Asp Ala Cys  
 35 40 45  
 Asp Leu Ile Glu Asn Asp Ala Gln Leu Ser Ile Ile Thr Ala Lys Asp  
 50 55 60  
 Glu Glu Gly Leu Glu Ile Ile Arg His Ser Cys Ala His Leu Leu Gly  
 65 70 75 80  
 His Ala Ile Lys Gln Leu Trp Pro His Thr Lys Met Ala Ile Gly Pro  
 85 90 95  
 Val Ile Asp Asn Gly Phe Tyr Tyr Asp Val Asp Leu Asp Arg Thr Leu  
 100 105 110  
 Thr Gln Glu Asp Val Glu Ala Leu Glu Lys Arg Met His Glu Leu Ala  
 115 120 125  
 Glu Lys Asn Tyr Asp Val Ile Lys Lys Lys Val Ser Trp His Glu Ala  
 130 135 140  
 Arg Glu Thr Phe Ala Asn Arg Gly Glu Ser Tyr Lys Val Ser Ile Leu  
 145 150 155 160  
 Asp Glu Asn Ile Ala His Asp Asp Lys Pro Gly Leu Tyr Phe His Glu  
 165 170 175

Glu Tyr Val Asp Met Cys Arg Gly Pro His Val Pro Asn Met Arg Phe  
 180 185 190  
 Cys His His Phe Lys Leu Met Lys Thr Ala Gly Ala Tyr Trp Arg Gly  
 195 200 205  
 Asp Ser Asn Asn Lys Met Leu Gln Arg Ile Tyr Gly Thr Ala Trp Ala  
 210 215 220  
 Asp Lys Lys Ala Leu Asn Ala Tyr Leu Gln Arg Leu Glu Glu Ala Ala  
 225 230 235 240  
 Lys Arg Asp His Arg Lys Ile Gly Lys Gln Leu Asp Leu Tyr His Met  
 245 250 255  
 Gln Glu Glu Ala Pro Gly Met Val Phe Thr His Asn Asp Gly Trp Thr  
 260 265 270  
 Ile Phe Arg Glu Leu Glu Val Phe Val Arg Ser Lys Leu Lys Glu Tyr  
 275 280 285  
 Gln Tyr Gln Glu Val Lys Gly Pro Phe Met Met Asp Arg Val Leu Trp  
 290 295 300  
 Glu Lys Thr Gly His Trp Asp Asn Tyr Lys Asp Ala Met Phe Thr Thr  
 305 310 315 320  
 Ser Ser Glu Asn Arg Glu Tyr Cys Ile Lys Pro Met Asn Cys Pro Gly  
 325 330 335  
 His Val Gln Ile Phe Asn Gln Gly Leu Lys Ser Tyr Arg Asp Leu Pro  
 340 345 350  
 Leu Arg Met Ala Glu Phe Gly Ser Cys His Arg Asn Glu Pro Ser Gly  
 355 360 365  
 Ser Leu His Gly Leu Met Arg Val Arg Gly Phe Thr Gln Asp Asp Ala  
 370 375 380  
 His Ile Phe Cys Thr Glu Glu Gln Ile Arg Asp Glu Val Asn Gly Cys  
 385 390 395 400  
 Ile Arg Leu Val Tyr Asp Met Tyr Ser Thr Phe Gly Phe Glu Lys Ile  
 405 410 415  
 Val Val Lys Leu Ser Thr Arg Pro Glu Lys Arg Ile Gly Ser Asp Glu  
 420 425 430  
 Met Trp Asp Arg Ala Glu Ala Asp Leu Ala Val Ala Leu Glu Glu Asn  
 435 440 445  
 Asn Ile Pro Phe Glu Tyr Gln Leu Gly Glu Gly Ala Phe Tyr Gly Pro  
 450 455 460  
 Lys Ile Glu Phe Thr Leu Tyr Asp Cys Leu Asp Arg Ala Trp Gln Cys  
 465 470 475 480  
 Gly Thr Val Gln Leu Asp Phe Ser Leu Pro Ser Arg Leu Ser Ala Ser  
 485 490 495  
 Tyr Val Gly Glu Asp Asn Glu Arg Lys Val Pro Val Met Ile His Arg  
 500 505 510  
 Ala Ile Leu Gly Ser Met Glu Arg Phe Ile Gly Ile Leu Thr Glu Glu  
 515 520 525  
 Phe Ala Gly Phe Phe Pro Thr Trp Leu Ala Pro Val Gln Val Val Ile  
 530 535 540  
 Met Asn Ile Thr Asp Ser Gln Ser Glu Tyr Val Asn Glu Leu Thr Gln  
 545 550 555 560  
 Lys Leu Ser Asn Ala Gly Ile Arg Val Lys Ala Asp Leu Arg Asn Glu  
 565 570 575  
 Lys Ile Gly Phe Lys Ile Arg Glu His Thr Leu Arg Arg Val Pro Tyr  
 580 585 590  
 Met Leu Val Cys Gly Asp Lys Glu Val Glu Ser Gly Lys Val Ala Val  
 595 600 605  
 Arg Thr Arg Arg Gly Lys Asp Leu Gly Ser Met Asp Val Asn Glu Val  
 610 615 620  
 Ile Glu Lys Leu Gln Gln Glu Ile Arg Ser Arg Ser Leu Lys Gln Leu  
 625 630 635 640  
 Glu Glu

<210> 398  
 <211> 450  
 <212> PRT  
 <213> E. Coli

<400> 398

```

Met Thr Lys His Tyr Asp Tyr Ile Ala Ile Gly Gly Gly Ser Gly Gly
 1      5      10      15
Ile Ala Ser Ile Asn Arg Ala Ala Met Tyr Gly Gln Lys Cys Ala Leu
 20      25      30
Ile Glu Ala Lys Glu Leu Gly Gly Thr Cys Val Asn Val Gly Cys Val
 35      40      45
Pro Lys Lys Val Met Trp His Ala Ala Gln Ile Arg Glu Ala Ile His
 50      55      60
Met Tyr Gly Pro Asp Tyr Gly Phe Asp Thr Thr Ile Asn Lys Phe Asn
 65      70      75      80
Trp Glu Thr Leu Ile Ala Ser Arg Thr Ala Tyr Ile Asp Arg Ile His
 85      90      95
Thr Ser Tyr Glu Asn Val Leu Gly Lys Asn Asn Val Asp Val Ile Lys
100      105      110
Gly Phe Ala Arg Phe Val Asp Ala Lys Thr Leu Glu Val Asn Gly Glu
115      120      125
Thr Ile Thr Ala Asp His Ile Leu Ile Ala Thr Gly Gly Arg Pro Ser
130      135      140
His Pro Asp Ile Pro Gly Val Glu Tyr Gly Ile Asp Ser Asp Gly Phe
145      150      155      160
Phe Ala Leu Pro Ala Leu Pro Glu Arg Val Ala Val Val Gly Ala Gly
165      170      175
Tyr Ile Ala Val Glu Leu Ala Gly Val Ile Asn Gly Leu Gly Ala Lys
180      185      190
Thr His Leu Phe Val Arg Lys His Ala Pro Leu Arg Ser Phe Asp Pro
195      200      205
Met Ile Ser Glu Thr Leu Val Glu Val Met Asn Ala Glu Gly Pro Gln
210      215      220
Leu His Thr Asn Ala Ile Pro Lys Ala Val Val Lys Asn Thr Asp Gly
225      230      235      240
Ser Leu Thr Leu Glu Leu Glu Asp Gly Arg Ser Glu Thr Val Asp Cys
245      250      255
Leu Ile Trp Ala Ile Gly Arg Glu Pro Ala Asn Asp Asn Ile Asn Leu
260      265      270
Glu Ala Ala Gly Val Lys Thr Asn Glu Lys Gly Tyr Ile Val Val Asp
275      280      285
Lys Tyr Gln Asn Thr Asn Ile Glu Gly Ile Tyr Ala Val Gly Asp Asn
290      295      300
Thr Gly Ala Val Glu Leu Thr Pro Val Ala Val Ala Ala Gly Arg Arg
305      310      315      320
Leu Ser Glu Arg Leu Phe Asn Asn Lys Pro Asp Glu His Leu Asp Tyr
325      330      335
Ser Asn Ile Pro Thr Val Val Phe Ser His Pro Pro Ile Gly Thr Val
340      345      350
Gly Leu Thr Glu Pro Gln Ala Arg Glu Gln Tyr Gly Asp Asp Gln Val
355      360      365
Lys Val Tyr Lys Ser Ser Phe Thr Ala Met Tyr Thr Ala Val Thr Thr
370      375      380
His Arg Gln Pro Cys Arg Met Lys Leu Val Cys Val Gly Ser Glu Glu
385      390      395      400
Lys Ile Val Gly Ile His Gly Ile Gly Phe Gly Met Asp Glu Met Leu
405      410      415
Gln Gly Phe Ala Val Ala Leu Lys Met Gly Ala Thr Lys Lys Asp Phe
420      425      430

```

Asp Asn Thr Val Ala Ile His Pro Thr Ala Ala Glu Glu Phe Val Thr  
 435 440 445  
 Met Arg  
 450

<210> 399  
 <211> 2894  
 <212> RNA  
 <213> E. Coli

<400> 399

|             |             |            |            |             |             |      |
|-------------|-------------|------------|------------|-------------|-------------|------|
| aagguuaagc  | cucacggguuc | auuaguaccg | guuagcucaa | cgcaucgcug  | cgcuuacaca  | 60   |
| cccgcccuau  | caacgucguc  | gucuucaacg | uuccuucagg | acccuuaaaag | ggucaggagg  | 120  |
| aacucaucuc  | ggggcaaguu  | ucgugcuuag | augcuuucag | cacuuauucuc | uuccgcgauuu | 180  |
| agcuaccggg  | cagugccauu  | ggcaugacaa | cccgaacacc | agugaugcgu  | ccacuccgggu | 240  |
| ccucucguac  | uaggagcagc  | ccccucagu  | ucuccagcgc | ccacggcgaga | uagggaccga  | 300  |
| acugucucac  | gacguucuaa  | acccagcucg | cguaaccacu | uaaaugggcg  | acagccauac  | 360  |
| ccuugggacc  | uacuucagcc  | ccaggauug  | augagccgac | aucgaggugc  | caaacaccgc  | 420  |
| cgucgauaug  | aacucuuagg  | cgguuacagc | cuguuauccc | cgagguaccu  | uuuauccguu  | 480  |
| gagcgauggc  | ccuuccauuc  | agaaccaccg | gaucacuaug | accugcuuuc  | gcaccugcuc  | 540  |
| gcgccguac   | gcucgcaguc  | aagcuggguu | augccauuug | acuaaccucc  | ugauguccga  | 600  |
| ccaggauuag  | ccaaccuucg  | ugcuuccucg | uuaucuuua  | ggaggagacc  | gccccaguca  | 660  |
| aacuaaccac  | cagacacugu  | ccgcaaccgg | gauuacgggu | caacguuaga  | acaucaaa    | 720  |
| uuaaagggu   | guauuucag   | gucggcucca | ugcagacugg | cguccacacu  | ucaaagccuc  | 780  |
| ccaccuaucc  | uacacaucaa  | ggcucaaugu | ucagugucua | gcuauaguaa  | agguuacagg  | 840  |
| ggucuuuccg  | ucuugcccg   | gguaacacug | aucuucacag | cgaguucuuu  | uucacugagu  | 900  |
| cucgggugga  | gacagccugg  | ccaucuuuac | gccauucgug | caggucggaa  | cuuaccggac  | 960  |
| aaaggauuuc  | gcuaccuua   | gaccguuua  | guuacggcg  | ccguuuaccg  | gggcuucgau  | 1020 |
| caagagcuuc  | gcuugcgcu   | accccauca  | uuuaccuucc | ggcaccgggg  | agggcucaca  | 1080 |
| ccguauuacg  | ccacuuucgu  | guuugcacag | ugcuguguuu | uuauuaaaca  | guugcagcca  | 1140 |
| gcuuguauc   | ucgacugauu  | ucagcuccau | ccgcgaggga | ccuaccuac   | auaucagcgu  | 1200 |
| gccuucuccc  | gaaguacagg  | caccauuuug | ccuaguuccu | ucaccccgag  | ucucucaagg  | 1260 |
| gccuugggua  | ucucuaccug  | accaccugug | ucgguuuugg | guacgauuug  | auguuaccug  | 1320 |
| augcuuagag  | gcuuuuccug  | gaagcagggg | auuuguugcu | ucagcaccgu  | agugccucgu  | 1380 |
| caucacgccc  | cagccuugau  | uuuccggauu | ugccuggaaa | accagccuac  | acgcuuaaac  | 1440 |
| cgggacaacc  | gucgcccggc  | caacauagcc | uucuccgucc | ccccuucgca  | guuacacca   | 1500 |
| guacaggaa   | auuaaccugu  | uucccaucga | cuacgcuuu  | cgccucggcc  | uuaggggucg  | 1560 |
| acucaccucg  | ccccgaauaa  | cguuggcag  | gaacccuugg | ucuuccggcg  | agcgggcuuu  | 1620 |
| ucaccccgcu  | uauuguuacu  | uauugcagca | uucgcacuuc | ugauaccucc  | agcaugccuc  | 1680 |
| acagcacacc  | uucgcaggcu  | uacagaacgc | uccccuaccc | aacaacgcgu  | aagcgucgcu  | 1740 |
| gccgcagcuu  | cggugcagug  | uuuagcccc  | uuacauucuc | cgcgagggcc  | gacucgacca  | 1800 |
| gugagcuauu  | acgcuuucuu  | uaaauagugg | cugcuucuaa | gccaaacucc  | uggcugucug  | 1860 |
| ggccuuccca  | caucguuucc  | cacuuuaaca | ugacuauugg | accuuagcug  | gcggucuggg  | 1920 |
| uuuuuuuccu  | cuucacgagc  | gacguuagca | cccgcggugu | gucucccgug  | auaacaauuc  | 1980 |
| ccgguaucg   | caguuugcau  | cggguuggua | agucgggag  | accccccugc  | cgaaacagug  | 2040 |
| cucuaacccc  | ggagaugaa   | ucacgagggc | cuaccuaaa  | agcuuucggg  | gagaaccagc  | 2100 |
| uauucucccg  | uuugauuugc  | cuuucacccc | cagccacaag | ucauccgcua  | auuuuucaac  | 2160 |
| auuagucgg   | ucggguccucc | aguuauguuu | acccaaccuu | caaccugccc  | auggcuaag   | 2220 |
| caccggguuu  | cgggucuaau  | cccugcaacu | uaacgcccag | uuuagacucg  | guuucccuuc  | 2280 |
| ggcuccccua  | uucgguuaac  | cuugcuacag | auuuaaguc  | gcugacccau  | uuuacaaaag  | 2340 |
| guacgcaguc  | acacgcuuua  | gcgugcuccc | acugcuugua | cguaacagggu | uucagguucu  | 2400 |
| uuuuacacucc | ccucgcccgg  | guuucuuucg | ccuuucccuc | acgguacugg  | uucacuaucg  | 2460 |
| gucagucagg  | aguauuuagc  | cuuggaggau | ggucccccca | uuuacagaca  | ggauaccacg  | 2520 |
| ugucccgccc  | uacucaucga  | gcucacagca | ugugcauuuu | uguguaacggg | gcugucacccc | 2580 |
| uguaucggcg  | gccuuuccag  | acgcuuccac | uaacacacac | acugauuucag | gcucugggcu  | 2640 |
| gcuccccguu  | cgcucgcccgc | uacuggggga | aucucggguu | auuucuuuuc  | cucggggguac | 2700 |
| uuagauguuu  | caguuuccccc | gguuucgccc | auuaaccuau | ggauucaguu  | aaugauagug  | 2760 |
| ugucgaaaca  | cacugggguu  | ccccauucgg | aaauccggcg | uuuuaacggg  | ucauauacc   | 2820 |
| uuaccgacgc  | uuauccgaga  | uuagcacguc | cuuacugccc | ucugacugcc  | agggcaucca  | 2880 |

ccguguacgc uuagucgcuu aacc

2894

<210> 400  
 <211> 120  
 <212> RNA  
 <213> E. Coli

&lt;400&gt; 400

|   |     |
|---|-----|
| augccuggca guucccuacu cucgcauggg gagacccac acuaccaucg gcgcuacggc  | 60  |
| guuucacuuu ugaguuaggc auggggucag gugggaccac cgcgcuacgg ccgccaggca | 120 |

<210> 401  
 <211> 76  
 <212> RNA  
 <213> E. Coli

&lt;400&gt; 401

|   |    |
|---|----|
| gucccuuucg ucuagaggcc caggacaccg cccuuucacg gcgguaacag ggguucgaau | 60 |
| cccuagggg acgcca  | 76 |

<210> 402  
 <211> 1549  
 <212> RNA  
 <213> E. Coli

&lt;400&gt; 402

|   |      |
|---|------|
| aaaugaaga guuugaucan ggcucagauu gaacgcuggc ggcaggccua acacaugcaa    | 60   |
| gucgaacggg aacaggaagc agcuugcugc uucgcugacg aguggcggac gggugaguaa   | 120  |
| ugucugggaa gcugccugau gggggggggu aacuaucugga aacgguaagcu aaauaccgau | 180  |
| aaugucgcaa gaccaaagag ggggaccuuc gggccucuuu ccaucggauug ugcccagau   | 240  |
| ggauuagcuu guuggggggg uaacggcuca ccaaggcgac gaucccuagc ugguucugaga  | 300  |
| ggauagaccag ccacacugga acugagacac gguccagacu ccuacgggag gcagcagugg  | 360  |
| ggaaauuugc acaaugggcg caagccugau gcagccaugc cgcguguaug aagaaggccu   | 420  |
| ucggguugua aaguacuuc agcggggagg aagggaguaa aguuauuacc uuugcucauu    | 480  |
| gacguuacc gcagaagaag caccggcuua cuccgugcca gcagcccgcg aaauacggag    | 540  |
| ggugcaagcg uuaaucggaa uuacggggcg uaaagcgac gcagccgggu ugguuaaguc    | 600  |
| agauuguaa uccccggcu caaccuggga acugcaucg auacuggcaa gcuugagucu      | 660  |
| cguagagggg gguagaauuc caggguuagc ggugaaaugc guagagaucg ggaggaauc    | 720  |
| cgguggcgaa ggcggccccc uggaagaaag cugacgcuca ggugcgaaag cguggggagc   | 780  |
| aaacaggauu agauaccucg guaguccacg ccguaaacga ugucgacuug gagguugugc   | 840  |
| ccuugaggcg ugguuucccg agcuuacgcg uuaagucgac cgccugggga guacggccgc   | 900  |
| aaggguaaaa cucaauagaa uugacggggg cccgcacaag cggugggagca ugugguuaa   | 960  |
| uucgaugcaa cgcgaagaac cuuaccuggu cuugacauc accggaaguu ucagagauga    | 1020 |
| gaauugccu ucgggaaccg ugagacaggu gcugcaugc ugucgucagc ucguuugug      | 1080 |
| aaauguuggg uuaagucccg caacgagcgc aaccuuauu cuuuguugcc agcggucccg    | 1140 |
| ccgggaacuc aaaggagacu gccagugaua aacuggaggga agggggggau gacgucaagu  | 1200 |
| caucauggcc cuuacgacca gggcuacaca cgugcuacaa uggcgcuauc aaagagaagc   | 1260 |
| gaccucgcga gagcaagcgg accucauaaa gugcgucgua guccggauug gagucugcaa   | 1320 |
| cucgacucca ugaagucgga aucgcuagua aucguggauc agaaugccac ggugaauacg   | 1380 |
| uucccgggcc uuquacacac cgcccgucac accaugggag ugguuugcaa aagaaguag    | 1440 |
| uagcuuaacc uucgggaggg cgcuuaccac uuugugauuc augacugggg ugaagucgua   | 1500 |
| acaagguaac cguaggggaa ccugcgguug gaucaccucc uuaccuuaa               | 1549 |

<210> 403  
 <211> 17  
 <212> DNA  
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 <220>  
 <223> Primer Oligonucleotide  
  
 <400> 403  
 tgtttatcag accgctt 17  
  
 <210> 404  
 <211> 18  
 <212> DNA  
 <213> Artificial  
 <220>  
 <223> Primer Oligonucleotide  
  
 <400> 404  
 acaatttcac acagcctc 18  
  
 <210> 405  
 <211> 159  
 <212> DNA  
 <213> Escherichia coli  
  
 <400> 405  
 caggtggtat ggaaacccaa aatggagacg ggaagctgaa ccagatagtt actggagggtg 60  
 atcaccagca gatgaaataa cgataaccag aacaacgcct tatagcgttg agtttgcgag 120  
 aaaacgttca tattgtacct ttttgattaa ccattgggg 159  
  
 <210> 406  
 <211> 640  
 <212> DNA  
 <213> Escherichia coli  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(640)  
 <223> n = A,T,C or G  
  
 <400> 406  
 ggggnccaaa gtgtttgggn cgggcaactg gaggccaaacc ttaanttnng ggaaattttt 60  
 aanaaaaggc ggggatttgt nagccacggg ngattanttt anaataaatt aagtgttgcc 120  
 ataaggggac aaagngaagg aagtggntat taanggannc gccaatgcga nttagggcag 180  
 accattcggc cattcgcctt cttgggtatc gaagtccatc cagatagccg ttgccngacc 240  
 gaccagattc gcttcnggca caaagcccca gtaacggctg tccgcgctgt tgcgcgggtt 300  
 gtcgccccatc atgaagtatt gtcccggagg aacaatccag gttgccagtt gttgccctgg 360  
 ctgctggtaa tacatcccca cctgatcctg cgcaatcggc actgtcagaa tgcggtgcgt 420  
 cacatcaccc agtgtctctt tacgctcgga aagacgaatt ccattttctt tggtttcgtt 480  
 tttcggcact tcaaagaatc cgctggtcgc ttccccacca ttacggcgtg agaaggctcg 540  
 aacgaaatcg ctcggttcca cgtttgagta ggtgaccggc agcgcgtttt cacacgcctg 600  
 gccggaactg catcccgggt gaatcgtcag ctcttttgag 640  
  
 <210> 407  
 <211> 682  
 <212> DNA  
 <213> Escherichia coli  
  
 <220>  
 <221> misc\_feature

&lt;222&gt; (1)...(682)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 407

|             |            |             |            |            |             |     |
|-------------|------------|-------------|------------|------------|-------------|-----|
| cctgcagggt  | aatgtcgcca | ttaactggc   | gcaggcagcc | aaagagttgc | tccgcttcta  | 60  |
| cccagtcggc  | agcgacaact | tgcgttaaag  | tcgcaaaatt | atcatctgca | ctcactgcgt  | 120 |
| gacgtaagcg  | gatggagtg  | ccggaaacct  | catagtgaac | gccaccagc  | tggcctgcat  | 180 |
| cgctttgtag  | cgtacgcgc  | gcattggcaa  | taagattcag | atactcagac | tcttccgggg  | 240 |
| ccttcgccag  | cataaaagag | gaggatgctc  | gcgtatgcag | caactgctcc | agcgcaaat   | 300 |
| gcagccggcg  | ttgagtatca | ctgaataaag  | gatcgttttc | gtcaatcaaa | tgtggctgag  | 360 |
| caaataatttc | ctgatagcta | tcggatatcag | gaaccaggtc | acgccatgca | agtttcgtaa  | 420 |
| tggtcaaaagt | tgatgttttt | tagtctgttg  | tcaaagccgc | nattataccn | gtaaccggca  | 480 |
| ctacagcaca  | cgtagaaagc | acccgacaat  | actcctggca | tgggcgttaa | agctcacagg  | 540 |
| atggagatct  | tttcttcact | ggcctaataa  | gctgatattc | tgtaaagagt | tacacngtaa  | 600 |
| cattgagatc  | gctatgaaat | atcaacaact  | tggaaaatct | tgnaaagcng | gttggaaaaat | 660 |
| ggaaagtatc  | tggttaagaa | gc          |            |            |             | 682 |

&lt;210&gt; 408

&lt;211&gt; 309

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 408

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ggggatccgg  | cagaatttta | cgctgaccaa | tgacgcgacg | acgtggcatg | gaaatactcc | 60  |
| gttggttaatt | caggattgtc | caaaactcta | cgagtttagt | ttgacattta | agttaaaacg | 120 |
| tttggcctta  | cttaacggag | aaccattaag | ccttaggacg | cttcacgcca | tacttggaac | 180 |
| gagcctgctt  | acggtcttta | acgccggagc | agtcaagcgc | accacgtacg | gtgtggtaac | 240 |
| gaacaccggg  | gaggtcttta | acacgaccgc | cacggatcag | gatcacggag | tgctcctgca | 300 |
| gccaaagctt  |            |            |            |            |            | 309 |

&lt;210&gt; 409

&lt;211&gt; 1167

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 409

|            |            |            |            |            |             |      |
|------------|------------|------------|------------|------------|-------------|------|
| gtcgacccat | ctgtccattg | agcggacagt | ttgtgcaaca | ctattttgtt | gaccggaaaa  | 60   |
| tggaacactt | tccgcaatgc | ctgttgctat | cacgcttaaa | ccatttcatt | gcgatttaca  | 120  |
| cagaacggac | gtcctgtcgc | agtatattaa | gtcgtcgata | gaaacaagca | ttgaaaggca  | 180  |
| cagcagtagt | caaacagtgt | gaaacgctac | tggcgcctta | cagcgcaaaa | aggctgggtga | 240  |
| ctaaaaagtc | accagccatc | agcctgattt | ctcaggctgc | aaccggaaag | gttggcttat  | 300  |
| ttaacttcaa | cttcagcgcc | agcttcttcc | agagcttttt | tcagtgcctc | tgctgcgtct  | 360  |
| ttgctcacgc | cttctttcag | agcagccggt | gcagattcta | ccaggctctt | agcttctttc  | 420  |
| agaccagggc | cagttgcgcc | acgtactgct | ttgataacag | caactttgtt | agcgccagca  | 480  |
| gctttcagaa | ttacgtcgaa | ttcagttttt | tcttcagcag | cttcaaccgg | gccagcagct  | 540  |
| acagctacag | cagcagcagc | ggaacaccgc | aatttttctt | ycattgcaga | gatcaagttc  | 600  |
| tacaacgtcc | attacagaca | tagctgcaac | tgcttcaatg | awttgatctt | tagtgataga  | 660  |
| cattttaaak | gttcttgaat | atcagaataa | gtttatacgt | aagcgaatgc | gttaaaaaga  | 720  |
| taactgcgaw | taagcagctt | ytttcgcac  | gcgtacagma | gccagagtac | gaaccagttt  | 780  |
| gccagccgaa | gcttctttca | tggttgccat | caggcgtgca | attgcttctt | cgtaggtcgg  | 840  |
| cagagttgcc | aggcggtcga | tctgagacgc | cgggatcagc | tcaccttcaa | aggcagcggc  | 900  |
| tttgacctca | aattttgcat | tcgctttcgc | gaactctttg | aacagacgag | cagcagcgcc  | 960  |
| cgggtgttcc | atagagtatg | caatcagggt | cggaccaaca | aacgcgtctt | tcaggcactc  | 1020 |
| gaacggagta | ccttcaacag | cacggcgccg | cagggtgtta | cgaacaacac | gcatgtatac  | 1080 |
| gccagcttcg | cgacctgctt | tacgcagttc | agtcatttta | tctacagtta | cgcccacggg  | 1140 |
| aatccgcaac | tactgcaagc | caagctt    |            |            |             | 1167 |

&lt;210&gt; 410

&lt;211&gt; 404

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

<400> 410  
 caacmctatt ttgktggacc ggaaaakgga acactttccg cawkgcctgt tgctatcacg 60  
 cttaaaccat ttcattgcga ttacacaga acggacgtcc tgctgcagta tattaagtcg 120  
 tcgatagaaa caagcattga aaggcacagc agtagtcaaa cagtgtgaaa cgctactggc 180  
 gccttacagc gcaaaaaggc tggtagctaa aaagtcacca gccatcagcc tgatttctca 240  
 ggctgcaacc ggaagggttg gcttatttaa cttcaacttc agcgccagct tcttccagag 300  
 cttttttcag tgcttctgcg tcgtctttgc tcacgccttc tttcagagca gccggtgcag 360  
 attctaccag gtcttttagct tctttcagac ccaggccagt tgcg 404

<210> 411  
 <211> 152  
 <212> DNA  
 <213> Escherichia coli

<400> 411  
 agagcttttt tcagtgtctc tgcgtcgtct ttgctcacgc cttctttcaa gaggagcccg 60  
 gtgcagattc taccaggtct ttagcttctt tcagaccag gccagttgag ccaagtactg 120  
 ctttgataac agcaactttg tttagcgccag ca 152

<210> 412  
 <211> 825  
 <212> DNA  
 <213> Escherichia coli

<220>  
 <221> misc\_feature  
 <222> (1)...(825)  
 <223> n = A,T,C or G

<400> 412  
 gatccgtcga cccatctgtc cattgagcgg acagtttgtg caacactatt ttgttgaccg 60  
 gaaaatggaa cactttccgc aatgcctgtt gctatcacgc ttaamccatt tcattgcat 120  
 ttacacagaa cggacgtcct gtcgcagtat attaatgctt cgatagaaaac aagcattgaa 180  
 aggcacagca gtagtcaaac agtgtgaaac gctactggcg ccttacagcg caaaaaggct 240  
 ggtgactaaa aagtcaccag ccatcagcct gatttctcag gctgcaaccg gaagggttgg 300  
 cttatttaac ttcaacttca gcgccagctt cttccagagc ttttttcagt gcttctgcgt 360  
 cgtctttgct cagccttctt ttcagagcag ccgggtgcag attctaccag gtcttttagct 420  
 tctttcagac ccaggccagt tgcgccacgt actgctttga taacagcaac ttgttttagcg 480  
 ccagcagctt tcagaattac gtcgaattca agttttttct tcagcagctt caaccggggc 540  
 agcagctaca gctacagcag cagcagcggg aacaccgaat ttttcttyca ttggcagaga 600  
 tcaagttcta caacgtccat tacagacata gctgcaactg cttcaatgat tkgatcttwa 660  
 gtgatagaca tttaaattgt tcctgaatat cagaataagt ttatacgtaa gcgaatgcgt 720  
 taaaaagata actgcgatta agcagcttct ttcgcacgcg gtacagcagc cagaggtcga 780  
 accagtttgc cagccgaagg ttggtcttcc agcctnnnnn natta 825

<210> 413  
 <211> 425  
 <212> DNA  
 <213> Escherichia coli

<400> 413  
 agtagtcaaa cagggtgkgra acgctactgg cgccttacag cgcaaaaagg ctggtgacta 60  
 aaaagtcacc agccatcacc ctgattttctc aggctgcaac ccggaagggt tggcttattt 120  
 aacttcaact tcagcgccag cttcttccag agcttttttc agtgcttctg cgtcgtcttt 180  
 gctcacgcct tctttcagag cagccggtgc agattctacc aggtcttttag cttctttcag 240  
 acccaggcca gttgcgccac gtactgcttt gataacagca actttgttag cgccagcagc 300  
 tttcagaatt acgtcgcaatt cagttttttc ttcagcagct tcaaccgggc cagcagctac 360  
 agctacagca gcagcagcgg aaacaccgga atttttcttc cattgcagag atcaagttct 420  
 acaac 425



<210> 414  
 <211> 126  
 <212> DNA  
 <213> Escherichia coli

<400> 414  
 agagcttttt tcagtgtctt tgcgtcgtct ttgctcacgc cttctttcag agcagccggg 60  
 gcagattcta ccagggtttt agcttctttc agaccaggc cagttgcgcc acgtactgct 120  
 ttrata 126

<210> 415  
 <211> 264  
 <212> DNA  
 <213> Escherichia coli

<400> 415  
 ctgcmaccgg garggggtgg cttatttaac ttcaacttca gcgccagctt cttcagagc 60  
 ttttttcaag tgcttctgcg tcgtctttgc tcacgccttc tttcagagca gccgggtgcag 120  
 attctaccag gtcttttagct tctttcagac ccaggccagt tgcgccacgt actgctttga 180  
 taacagcaac tttgttagcg ccagcagctt tcagaattac gtcgaattca gttttttctt 240  
 cagcagcttc aaccgggcca gcag 264

<210> 416  
 <211> 201  
 <212> DNA  
 <213> Escherichia coli

<400> 416  
 cgcataccct gcagcatcgg cccgatggag atcagggtcgg cagaacgctg taccgctttg 60  
 taggtgggtg taccgggtgt cagatccggg aagatgaaca cggtagcgcg acctgcaacc 120  
 ggagagttcg gcgctttgga tttcgcaacg tcagccatta ccgcagcgtc gtactgcage 180  
 ggaccgtcga tcatcaggtc a 201

<210> 417  
 <211> 239  
 <212> DNA  
 <213> Escherichia coli

<400> 417  
 aattcagcag ttgacagtgg cataaacgta actggtgact ttgcccggc atgacgccgg 60  
 gcttttttta ttattccgtg acttccagcg tagtgaaggc aaactttctg ccatcaaata 120  
 gcccttgact ggttagtttt agcgcgggga tctctggcag agaaagaaac gccatctgaa 180  
 taaacggctc atcgggtaac ggaccgcatt cacgggcggc ggctttcaag gcgtcaatt 239

<210> 418  
 <211> 223  
 <212> DNA  
 <213> Escherichia coli

<400> 418  
 ttcttttttt cgtcaacggt gtccagaatc attttattta cctcgggtac ttatgctgat 60  
 ttttattatt atggggaagg tgttatttat gagtttcatt tatgccgtaa cgacaatgaa 120  
 ctcgggaatt agtataagca gcgcgagaat aataatcatt gtgcaaatgc taattttaatt 180  
 aatactattt aaatattatt ttgagcatat gcacataagg ttg 223

<210> 419  
 <211> 223  
 <212> DNA  
 <213> Escherichia coli

<400> 419

```

ttcttttttt cgtcaacggt gtccagaatc attttattta cctcgggtac ttatgctgat 60
ttttattatt atggggaagg tggtatttat gagtttcatt tatgccgtaa cgacaatgaa 120
ctcgggaatt agtataagca gcgcgagaat aataatcatt gtgcaaatgc taatttaatt 180
aatactattt aaatattatt ttgagcatat gcacataagg ttg 223

```

<210> 420  
 <211> 212  
 <212> DNA  
 <213> Escherichia coli

```

<400> 420
aatagcgggt atgcacgcct ttcttttttt cgtcaacggt gtccagaatc attttattta 60
cctcgggtac ttatgctgat ttttattatt atggggaagg tggtatttat gagtttcatt 120
tatgccgtaa cgmcaatgaa ctcgggaatt agtataagca gcgcgagaat aataatcatt 180
gtgcaaatgc taatttaatt aatactattt aa 212

```

<210> 421  
 <211> 438  
 <212> DNA  
 <213> Escherichia coli

```

<400> 421
cctcgttaaat tatcgcccgt ggcataaaaa ctgcgtccaa acgccgtctt tgccagcagc 60
caggccataa atgccaccag aattatcgtc aaccaaccaa ttgctgaaac gccaaagcagc 120
agcggggcgg agagctggtt cagttcggcg ggtaaccctt caatccattt gccgccagtc 180
cacagcaaca tgatgcctct gtacaaccct aacgtgccaa ggggtggcaac aatggcaggg 240
atcttttagcc acgcgaccag gacaccgttg aaaaatcccg cgagcaaac aagcagtaaa 300
gtcgcgacac aagcaacagg tagtgaatat cctgcgttca gtaacatccc caacagcacc 360
gcgcacattc cgggtaatcg aaccccactt gaaacatcaa tattgsgsgt aagcattwcc 420
aagcgttcgs gcccatkg 438

```

<210> 422  
 <211> 682  
 <212> DNA  
 <213> Escherichia coli

```

<400> 422
aatcccggt gatccgtcga ccgtgcgtt ccggttggtg caaccgcgca aatggcgcgg 60
cggttaagtat gccggggtta ttcttcccc gttgaggaca ccgggttgct aggttgacca 120
tacgcttaag tgacaacccc gctgcaacgc cctctgttat caattttctg gtgacgtttg 180
gcggtatcag ttttactccg tgactgctct gccgcccttt ttaaagtga ttttgtgatg 240
tggtgaatgc ggctgagcgc acgcggaaca gttaaaacca aaaacagtgt tatgggtgga 300
ttctctgcat ccggcggtta ttgttaactg gttaacgtca cctggaggca ccaggcactg 360
catcacaaaa ttcatgtttg aggacgcgat aatgaaaaag ttattacca acgttaatac 420
gtctgaaggt tgttttgaaa ttggtgtcac tatcagtaac ccagtattta ctgaagatgc 480
cattaacaag agaaaaaag aacgggagct attaaataa atatgcattg tttcaatgct 540
ggctcgttta cgtctgatgc caaaaggatg tgcacaatga attcagcatt tgtgcttgtt 600
ctgacagttt ttcttgtttc cggagagcca gttgatattg cagtcagtgt tcacaggaca 660
atgcaggagt gatgactgca gc 682

```

<210> 423  
 <211> 600  
 <212> DNA  
 <213> Escherichia coli

```

<400> 423
ggggatccga ttgtgactgc tctgccgccc tttttaagt gaattttgtg atgtggtgaa 60
tgcggtgag cgcacgcgga acagttaaaa caaaaaacag tggtatgggt ggattctctg 120
tatccggcgt taattgttaa ctggttaacg tcacctggag gcaccaggca ctgcatcaca 180
aaattcattg ttgaggacgc gataatgaaa acgttattac caaacgttaa tacgtctgaa 240
ggttgctttg aaattggtgt cactatcagt aaccagtat ttactgaaga tgccattaac 300

```

```

aagagaaaac aagaacggga gctattaaat aaaatatgca ttgtttcaat gctggctcgt 360
ttacgtctga tgccaaaagg atgtgcacaa tgaattcagc atttgtgctt gttctgacag 420
tttttctgt ttccggagag ccagttgata ttgcagtcag tgttcacagg acaatgcagg 480
agtgtatgac tgcagcaacc gaacagaaaa ttcccggtaa ctgttaccgc gtcgataaag 540
ttattcacca ggataatata gaaatcccgg caggtcttta aacagttccg taataaataa 600

```

<210> 424  
 <211> 100  
 <212> DNA  
 <213> Escherichia coli

```

<400> 424
gggatccagc aagaagatgc ggtgtgaccg tcctcacgca gatgcgcaaa gctactcagc 60
aactgacctt tcttcgcaat aagcacgcca ttacggtcat 100

```

<210> 425  
 <211> 465  
 <212> DNA  
 <213> Escherichia coli

```

<400> 425
tcgcgtgttt accttcaaca tcggttaactt tctggcggat agtttcacgg taagcaacct 60
gcggtttacc tacgttcgct tcaacgttga attcacgctt catacggta acgatgatgt 120
cgagggtcag ttccgccata ccgcgatga tggctcgtt agattcttcg tcagtcata 180
cacggaaga cgggtcttct tttagccagac ggcccagagc cagaccatt tttcctggt 240
cagctttggt ttccggttca actgcgatgg agattaccgg ctccagggaat tccatacgtt 300
ccagaatgat cggcgcatcc gggtcacaca ggggtgcacc agtgggtacg tctttcagac 360
cgatagcagc agcgatgtcg cccgcgcgaa cttctttgat ctcttcacgt ttgttagcgt 420
gcatctgaac gatacgaccg aaacgctcac gtgcagcttt cacgg 465

```

<210> 426  
 <211> 653  
 <212> DNA  
 <213> Escherichia coli

<220>  
 <221> misc\_feature  
 <222> (1)...(653)  
 <223> n = A,T,C or G

```

<400> 426
tgatcggtc aagcagaact ggtttcgctt tcttaaagcc ttctttaaag gcgatagaag 60
cagccagttt aaacgccagt tcagaggagt caacgtcatg gtaagaaccg aagtgcagac 120
gaatacccat gtctactacc gggtagcctg ccagcggacc tgctttcagc tgttcctgga 180
tacctttatc aacggccggg atgtattcgc cagggattac accaccttta atgtcgttga 240
tgaactcgta gcctttcggg tttgaacccg gtcacagcgg gtacatgtcg ataacaacat 300
gaccatactg accacgacca ccagactgtt tcgcgtgttt accttcaaca tcggttaactt 360
tctggcggat agtttcacgg taagcaacct gcggtttacc tacgttcgct tcaacgttga 420
attcacgctt catacggta acgatgatgt cgagggtcag ttccgccata ccgcgatgat 480
ggctgggtag attcttcgct agtccataca cggnaagacg ggtcttnttt agccagacgg 540
gccagagnca gacctttt tttctggcag ctttgnttc ggtcaactgc gatggaaata 600
cccggctcaa ggaattcata cgtttcanaa tgatcggggc attccgggtc aca 653

```

<210> 427  
 <211> 268  
 <212> DNA  
 <213> Escherichia coli

```

<400> 427
ctttcttaaa gccttcttta aaggcgaatg aagcagccag tttaaaccgc agttcagagg 60
agtcaacgtc atggtaaaga ccgaagtgcg gacgaatacc catgtctact accgggtagc 120

```

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ctgccagcgg | acctgctttc | agctgttcct | ggataccttt | atcaacggcc | gggatgtatt | 180 |
| cgccagggat | tacaccacct | ttaatgtcgt | tgatgaactc | gtagcctttc | gggtttgaac | 240 |
| ccggctccag | cggttacatg | tcgataac   |            |            |            | 268 |

<210> 428  
 <211> 330  
 <212> DNA  
 <213> Escherichia coli

|            |            |             |
|------------|------------|-------------|
| <400> 428  |            |             |
| gttttgggga | gatgtaagg  | ctaactctgaa |
| atgactgatt | gccgatacct | gattaaacgg  |
| ctgatccttc | tggtcttata | acacaaggaa  |
| cggaacgacc | tttaataact | ataaataagt  |
| gtgaatgatt | atgctaagt  | catcaattaa  |
| aatataatta | atactctact | tccagagtag  |
|            |            | 60          |
|            |            | 120         |
|            |            | 180         |
|            |            | 240         |
|            |            | 300         |
|            |            | 330         |

<210> 429  
 <211> 465  
 <212> DNA  
 <213> Escherichia coli

|            |            |             |
|------------|------------|-------------|
| <400> 429  |            |             |
| gttttgggga | gatgtaagg  | ctaactctgaa |
| atgactgatt | gccgatacct | gattaaacgg  |
| ctgatccttc | tggtcttata | acacaaggaa  |
| cggaacgacc | tttaataact | ataaataagt  |
| gtgaatgatt | atgctaagt  | catcaattaa  |
| aatataatta | atactctact | tccagagtag  |
| gcacaaat   | atcccacac  | tggtcttctg  |
| tattggggat | cgggcacacc | ttctggcagg  |
|            |            | 60          |
|            |            | 120         |
|            |            | 180         |
|            |            | 240         |
|            |            | 300         |
|            |            | 360         |
|            |            | 420         |
|            |            | 465         |

<210> 430  
 <211> 379  
 <212> DNA  
 <213> Escherichia coli

|             |            |            |
|-------------|------------|------------|
| <400> 430   |            |            |
| aactctgaatg | gctgcattcc | ttgtttaagg |
| ttaaacgggt  | catcaaaatc | atcattgctg |
| acaaggaaac  | gtacttaagg | tgctccggg  |
| aaataagtgt  | ctgggcagat | actatataaa |
| tcaattaaat  | aaatataatg | gcgttaaggc |
| cagagtagaa  | tattaaat   | tatccgcgtg |
| ttcttctgtc  | tcgacatgc  |            |
|             |            | 60         |
|             |            | 120        |
|             |            | 180        |
|             |            | 240        |
|             |            | 300        |
|             |            | 360        |
|             |            | 379        |

<210> 431  
 <211> 443  
 <212> DNA  
 <213> Escherichia coli

|            |            |             |
|------------|------------|-------------|
| <400> 431  |            |             |
| aagatgatgt | gatgagaaag | tcaatttgaa  |
| aaaaaacact | aatcaaaaa  | ataatggcat  |
| attagtttat | ttcaaatgag | gaaaaatctcc |
| tggtgatcaa | ataaacaaca | gaggagaaat  |
| aatcccat   | ctggcggat  | aagtgcggc   |
| aaaccaatat | cacgcagcag | tttttcgcc   |
| ccctgcatac | cagccagcat | caacgccgca  |
| agataaatgt | actgcccgat | gtc         |
|            |            | 60          |
|            |            | 120         |
|            |            | 180         |
|            |            | 240         |
|            |            | 300         |
|            |            | 360         |
|            |            | 420         |
|            |            | 443         |

<210> 432  
 <211> 638  
 <212> DNA  
 <213> Escherichia coli

<400> 432  
 caggggggttt gttgtgggca atgatgcatt taagttatcg tctgcagata gaggagatat 60  
 tacaataaac aacgaatcag ggcatttgat agtcaatacc gcaattctat caggagatat 120  
 agtcactcta agaggaggag aaattagggt ggtattatag cttgtgcgcg ccatgattgg 180  
 cgcgcaattt aaacttagtg ctttacatcg ctattgtctt gatttctttg aattatttta 240  
 taaattaaaa aaacgactgt tatgtataag caaagggtccg aacgaaaaat acattccaaa 300  
 taaatgcttg cttaaatctc tatatccttc cccgaaaaat gacacataaa attgagatat 360  
 tccaaaaaga gatactacaa ataaagatgc ctttatttta ttatttctaa taaaaataga 420  
 agcaataaaa aataataaca atgatataaa tctaattgtt ttaaatatat tgtcttttat 480  
 gttagttaata gtcgttagta tgtttgatcc tccatatatt acgtgtagtt ttttatatac 540  
 atggaaataa ttttctttat actgagacat cacaccatca tcaaatggaa gtttgaagat 600  
 ggtgcttggt ttgctaacca ataaaaagag tgcattcg 638

<210> 433  
 <211> 299  
 <212> DNA  
 <213> Escherichia coli

<400> 433  
 ctttacctgg catgatccac ttcgccagaa taccggcaat aagcccaaaa ataatccatg 60  
 acagaatgcc cattgtttcc tcacttatct gttttgcatt agcggggttag tcgctgataa 120  
 aaagcatagc acaacatcgg gagggcaaga tttgtgacga gcatcacgga ggtttttttg 180  
 cgatggcgca gaaattgccc catcaacgat cagtataat taccacccac aaacatcatg 240  
 ttcgttttcc gtgtcataag aacgtacggt attcaccaga tcttttatca cttcagcgg 299

<210> 434  
 <211> 388  
 <212> DNA  
 <213> Escherichia coli

<400> 434  
 gaaaaaggag gcaatatcgg gtaaaggcat tagcccgacg aatacgtcgg gctacaaata 60  
 ttattgtgct gcaggtgttt tagcgggttg ttgatccaca ggttctaact ggaagaccac 120  
 atcgacctga tcatcaaaact gaatagcggc ctgctcgtaa gtttctctgg cgacaccgg 180  
 cgcgccatcg gctttcatca tccgcaccat tgggctgggc tgatagtgtg aaacatggta 240  
 gcgcacgcta tataccggcc ccagtttacg atgaaagccg ttgccagtt cctgcgcctg 300  
 atgaatcggc ttatcaatcg ctgccttacg cgctttgtct ttataggcat ccggctgcgc 360  
 caccgccagc gacacagaac gaattccc 388

<210> 435  
 <211> 351  
 <212> DNA  
 <213> Escherichia coli

<400> 435  
 ctatccttga tgaaccgcg agcaaagata ggtgattacg tcatggtttt acagaaaatt 60  
 acagaaaaag gaggaatat cgggtaaagg cattagcccg acgaatacgt cgggctacaa 120  
 atattattgt gctgcagggt ttttagcggg ttgttgatcc acaggttcta actggaagac 180  
 cacatcgacc tgatcatcaa actgaatagc ggcttgctcg taagtttctt gggcgacac 240  
 cggcgcgga tcggttttca tcatccgcac cattgggctg ggctgatagt tggaaacatg 300  
 gttagcgacg ctatataccg gcccagttt acgatgaaag ccgttcgcca g 351

<210> 436  
 <211> 762  
 <212> DNA  
 <213> Escherichia coli

<220>  
 <221> misc\_feature  
 <222> (1)...(762)  
 <223> n = A,T,C or G

<400> 436  
 aattatgaaa cactgtctgg aatcgtctga atgacgggca catttgcgag cacgcaccca 60  
 gtaataaacac aggaaactat tttatctacg cgttagcgat agactgcttg catggcgaaa 120  
 ggaggtgaagc cgacgatttc agcgggacgc tgaaacggga aagcccctcc cgaggaaggg 180  
 gccataaata aggaaagggg catgatgaag ctactcatca tcgtggtgct cttagtcata 240  
 agcttccccc cttactaaga ctaccagggc gggggaaaacc ccgctctacc ctcaactctg 300  
 aaagtatgcc ttcacgataa gattgtcaat ccgcaggcct ttagtctctgc gatcctgcca 360  
 gcaaatattc tttgcgagtc gttacgcaat aatcacagag gaaactattt tattcacgcg 420  
 ttagcgatag actgcattca gggcgaaaagg aggttaagccg atgatttcag cgggacgctg 480  
 aaacgggaaa gcctctcccc gagaagaggg cttttaataa ggaaaggggt atgatgaagc 540  
 acgtcatcat actggtgata ctcttagtga ttagcttcca ggcttactaa gaacaccagg 600  
 gggaggggga aacctcttcc taacctcac ttctgaaatt ggggtgctatg acgctggcgt 660  
 tactgcttan cgctaccagt ttgtctgcc ttgctggtgt aacgccagat cggtagccgt 720  
 ttggatattt taatgaaagc cgacaaatca atcancgtga cg 762

<210> 437  
 <211> 292  
 <212> DNA  
 <213> Escherichia coli

<400> 437  
 cacatttgcg agcacgcac cagtaataac acaggaaact attttatcta cgcgttagcg 60  
 atagactgct tgcattggcg aaggaggtta gccgacgatt tcagcgggac gctgaaacgg 120  
 gaaagcccct cccgaggaag gggccataaa taaggaaagg gtcatgatga agctactcat 180  
 catcgttggtg ctcttagtca taagcttccc cgcttactaa gactaccagg gcgggggaaa 240  
 ccccgctcta ccctcactcc tgaaagtatg ccttcacgat aagattgtca at 292

<210> 438  
 <211> 631  
 <212> DNA  
 <213> Escherichia coli

<400> 438  
 atttacactt tttacgaaat catgggatca ctaacaaaat atcgcttgct agttatattg 60  
 tatggcagga aagatatgag actgatatta cagatcccca aagtggagag tttatgacca 120  
 ttaaaaaata gatgttgctg ggtgcgcttt tgctggttac cagtgcgcgc tgggccgcac 180  
 cagccaccgc gggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 240  
 ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 300  
 agtacaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcact 360  
 ggacctatat ggggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag 420  
 cctacgacgg tgagattttt tatcatcgct aaaaaagcc ccctcatcat gagggggaaa 480  
 tgcagacacc ttgttatttt ttattattag ccacttgctc gtcttgcttg ttattagtgc 540  
 tatttcacgt tgattaatgc ggttgccctc agtgcgccag atttaacttt gtttgatgcg 600  
 tagacgtagt aactggctgt tatcggaatt g 631

<210> 439  
 <211> 566  
 <212> DNA  
 <213> Escherichia coli

<400> 439  
 tatggcagga aagatatgag actgatatta cagatcccca aagtggagag tttatgacca 60  
 ttaaaaaata gatgttgctg ggtgcgcttt tgctggttac cagtgcgcgc tgggccgcac 120  
 cagccaccgc gggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 180  
 ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 240

```

agtacaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcact    300
ggacctatat ggggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaaag    360
cctacgacgg tgagattttt tatcatcgct aaaaaaagcc ccctcatcat gagggggaaa    420
tgcagacacc ttgttatttt ttattattag ccacttgctc gtcttgcttg ttattagtcg    480
tatttcacgt tgattaatgc ggttgccctc agtgcgccag atttaacttt gtttgatatc    540
tagacgtagt aactggctgt atcgaa                                     566

```

<210> 440  
 <211> 339  
 <212> DNA  
 <213> *Escherichia coli*

```

<400> 440
cgtattcaca tccttttgat tgggtgatac atgcgaatcg gtattatttt tccggttgta    60
atcttcatta cagcggtcgt attttttagc tgggttttta ttggcggcta tgcgtgccccg    120
ggagcataaa gatgaaaaaa acaacgatta ttatgatggg tgtggcgatt attgtcgtac    180
tcggcactga gctgggatgg tggtaacgct acctctaaaa aatagcaaa gctgcctgtg    240
tgacgccttt gtgcaattta agcgtttaact tttaatcttc ctgtagataa atagcacgac    300
aatcgacca ataacggcaa ccacgaagct gccaaaatt                                     339

```

<210> 441  
 <211> 376  
 <212> DNA  
 <213> *Escherichia coli*

```

<400> 441
catgaatatt taaaaaggaa aacgacatga aaccgaagca cagaatcaac attctccaat    60
cataaaatat ttccgtggag catttttatta ttgaatatag aggtttaact ccggtaaaaa    120
acaaagaagc attgaatgca gggaaaaata atatggccat aaaaaacatc gaaagaaact    180
cttttaattt aacatgtaaa cgcattggtta atcctcatat cacgggtgga gtgttaagaa    240
catacataaa tggagtcatg ttttcctttt tccatttate aagttcctgt tgccgtttta    300
gtccatctct aattgcatac tttaattttt ctgataaatg gcattgagca tcgatttcac    360
ttaaacaac tgtaca                                     376

```

<210> 442  
 <211> 446  
 <212> DNA  
 <213> *Escherichia coli*

```

<400> 442
ttacgatagc tattagtaaa aatataagag ttagctgtat tggtatgtct gtggcgaaat    60
tgactacctt cgtttttttg attaagaatg attttattat cgtaagtaaa attacatgaa    120
tatttaaaaa ggaacacgac atgaaaccga agcacagaat caacattctc caatcataaa    180
atatttcctg ggagcatttt attattgaat atagagggtt aactccggtg aaaaaacaaag    240
aagcattgaa tgcagggaaa aataatatgg ccataaaaaa catcgaaaag aactctttta    300
atttaacatg taaacgcatg gttaatcctc atatcacggg tggagtgtta agaacataca    360
taaattggag catgttttcc cttttccatt tatcaagttc ctggtgccgt tttagtccat    420
ctctaattgc atattttaat ttttct                                     446

```

<210> 443  
 <211> 388  
 <212> DNA  
 <213> *Escherichia coli*

<220>  
 <221> misc\_feature  
 <222> (1)...(388)  
 <223> n = A,T,C or G

```

<400> 443
tcaccccggt gccgattttc aggcatactg atttaactta gcacccgcaa ctttaactaca    60

```

|  |     |
|--|-----|
| ggaaaacaaa gagataaatg tctaatactg atgcaaatacg agccgatttt ttaatcttta | 120 |
| cggaacttta cccgcctggg ttattaattg cactgtatc cgggcggtcg cccgctttaa   | 180 |
| tcacaatagg ctgtgtagcc tgggcctgtt tctctttcac ccgcgccaga gcggcagcaa  | 240 |
| tcgcattctt atctttggct gcagggtgaa cggctgcgt cttatgtcgt tcaaggcgag   | 300 |
| ccgctttttc gcgctccaga cgagcctggc gcgcttcgaa acgcgctttg gcttctgcgg  | 360 |
| cncgcttttc ttcctgacga atagccgc                                     | 388 |

&lt;210&gt; 444

&lt;211&gt; 209

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 444

|   |     |
|---|-----|
| aattttaata acgctatctg cggataaagc agaataagtg gttaaaccca gacataaacc | 60  |
| gaggaaaata atgttattgt atttcataat ctattgttcc ttagcgacag attgctgtct | 120 |
| gctgtttcag taaggtagca ggagaaactt caggaagctt gtactcgaca atacagtgtg | 180 |
| agttttttatc ttgccccat gaaacctgt                                   | 209 |

&lt;210&gt; 445

&lt;211&gt; 341

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 445

|   |     |
|---|-----|
| catctcaat accgttaaat gcaaccgaa ccccgctgt cctttgtctg cattcactta    | 60  |
| acgtaatctg aaaagggagc gctggacttg tgctaccggt cgttggaat tgtctggcac  | 120 |
| tggttttttg gagatctacg gtaaaattaa gcgaatccga tgagactgtg cagccataat | 180 |
| cgaggacgag cccgctaatt ttaataacgc tatctgcgga taaagcagaa taggtgtgta | 240 |
| acccagacaa taaaccgagg aaaataatgt tattgtattt cataatctat tgttccttag | 300 |
| cgacagattg ctgtctgtctg gttcagtaag gtaccaggag a                    | 341 |

&lt;210&gt; 446

&lt;211&gt; 697

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 446

|   |     |
|---|-----|
| agattttactg ccaattttcgg gcagatcgga aagggttaam ccatattgat ccataagggg | 60  |
| acgaatcmcg ggetataccg ccaggcatgg cttagagccat ggcattaaat tccgcaaatt  | 120 |
| cgggcgctga ttcttccac gcggttattt tggcacacac cagatccagc aagggtttt     | 180 |
| caggatcggt gagcagcaga tgatctacca gtccagcgc ctgggtgtat tgttcctcgt    | 240 |
| tctgaatacc cgccagaaaa ggtgccacag cagttagctt ttctctgtct tgcaagatgt   | 300 |
| cggaatcgc aatcattttt tccccttagt acgatgaaca gcggtaaaga aatcgtattc    | 360 |
| tttatgcgtc ataaacttcac gtatgtagca cttttgcgat tcaaaaaaga ccattgctac  | 420 |
| aacacgtaat tcattgcccc caacattgaa aacataatgc ttatccagat atttgaagtt   | 480 |
| atccagagat gggaaatactg cttttaatga ctcaggtttt ttgaaatatt ccttagcaat  | 540 |
| cgtgktcccc agagccacca actccgtttt atgttgcggg tatttttcgg cagcatcttt   | 600 |
| caatgctttt tgagttatca ggtgcattct tcatcacgtc cgtkgmcaaa ttggcaatat   | 660 |
| gataacatcc gttgccagat tggcacggat gaattat                            | 697 |

&lt;210&gt; 447

&lt;211&gt; 215

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 447

|   |     |
|---|-----|
| aattaataac ttttcgttag gcagttttgg gtgtgagttg caagagggga gactactgaa | 60  |
| taactcaagt ttataatcg aggggaaaaa ggtgatggcg ttcatagcaa aacgccctca  | 120 |
| accataaagg tcgagggcgc ttaagatgtt aaaaaccgc tatccgttaa aaaacaatgt  | 180 |
| tcaactaagg tcagtacat tgcgctaaaa aagcg                             | 215 |



<210> 448  
<211> 395  
<212> DNA  
<213> Escherichia coli

<400> 448  
gcattattca tgagaaatgt gtatcgtaaa tcaactgaaa ttaacgcaac catttggtat 60  
ttaagggtta attatctgtg tgtgatattt tattgaatgt tttaaatatt gtttttattg 120  
gcattgctat aatattgggt atcatttgct gaatggattc agtccttaag agtgggtttt 180  
taagggacag gcatagagta atgatacgtg tgcataacca acatctttac tcattatgtc 240  
attgaatgtt gacgctatgt gtttatgagg gagaggtatt ttcagttgat ctggattgtt 300  
aaattcatat aatgcgcctt tgctcatgaa tggatgccag tatgtagtgg gaaattataa 360  
atattgaaat agtccaacta cttctttatt accaa 395

<210> 449  
<211> 641  
<212> DNA  
<213> Escherichia coli

<220>  
<221> misc\_feature  
<222> (1)...(641)  
<223> n = A,T,C or G

<400> 449  
ataatcagggt aagaaaaggt gcgcggagat taccgtgtgt tgcgatatat tttttagttt 60  
cgcggtggcaa tacatcagtg gcaataaaac gacatatcca gaaaaatata cactaagtga 120  
atgatattctt ccgattttatc ttaatcggtt atggataacg gcaaagggct tcgttttttc 180  
ctatacttat tcagcactca caaataaagg aacgccaatg aaaattatac tctgggctgt 240  
attgattatt ttcctgattg ggctactggt ggtgactggc gtatttaaga tgatatttta 300  
aaatttaatta atgtcatcag gtccgaaaaat aacgagaata tttcagtcctc tcacccctgt 360  
gcgcctcctgt catgtgcatt gcttcatata atcactggcg caaggagcgc cgcaggcgna 420  
gnntgcnecn cgncccacct naccccatgc cgaacttcag aantgaaaac nccntaacnc 480  
cgatngtcgg cggnggcctc cccatgcnan agtangggaa ntgccangcg ncnntataaa 540  
cgaaaggctn attncaaaga ctgggccttn cntttatctg atgtttgtcg gagaacgctc 600  
tcctgagnan gacaaatncc gccgggagcg gatttgaacn t 641

<210> 450  
<211> 314  
<212> DNA  
<213> Escherichia coli

<220>  
<221> misc\_feature  
<222> (1)...(314)  
<223> n = A,T,C or G

<400> 450  
gaactacgag taagaatagc tncgaattcc cgtttatgga taacggcaaa gggcttcggt 60  
ttttcctata cttattcagc actcacaat aaaggaacgc caatgaaaat tatactctgg 120  
gctgtattga ttattttcct gattgggcta ctggtggtga ctggcgattt taagatgata 180  
ttttaaaatt aattaatgtc atcagggtccg aaaataacga gaattttca gtctctcatc 240  
ctgttgcgct cctgtcatgt gcattgcttc atataatcac tggcgcaagg agcgcgcagg 300  
ggntntnnt cttt 314

<210> 451  
<211> 236  
<212> DNA  
<213> Escherichia coli

<400> 451

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| atatacacta | agtgaatgat | atcttccgat | ttatcttaat | cgtttatgga  | taacggcaaa | 60  |
| gggcttcggt | ttttcctata | cttattcagc | actcacaaat | aaaggaacgc  | caatgaaaat | 120 |
| tatactctgg | gctgtattga | ttattttcct | gattgggcta | ctgggtggtga | ctggcgtatt | 180 |
| taagatgata | ttttaaaatt | aattaatgtc | atcaggtccg | aaaataacga  | gaatat     | 236 |

&lt;210&gt; 452

&lt;211&gt; 418

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 452

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| cggagattac | cgtgtgttgc | gatataat   | ttagtctcgc | gtggcaatac  | atcagtggca | 60  |
| ataaaacgac | atatccagaa | aaatatacac | taagtgaatg | atatcttccg  | atttatctta | 120 |
| atcggttatg | gataacggca | aagggcttcg | tttttccta  | tacttattca  | gactcaciaa | 180 |
| ataaaggaa  | gccaatgaaa | attatactct | gggctgtatt | gattattttc  | ctgattgggc | 240 |
| tactggtggt | gactggcgta | tttaagatga | tattttaaaa | tttaattaatg | tcatcaggtc | 300 |
| cgaaaataac | gagaatat   | ctgtctctca | tcctgttgcg | ctcctgtcat  | gtgcattgct | 360 |
| tcatataatc | actggcgcaa | ggagcgcgca | gggggcggcc | aatcgccgcc  | gccccctg   | 418 |

&lt;210&gt; 453

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 453

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aacaatttgc | ccatgcgctc | ggtcatgcgc | tgcacgcgcc | ggccattttg | sgcgtccccc | 60  |
| cgaccgcat  | tgcactgtta | atgggcgaat | cttcagtact | ggtattaggt | ggacaacgcg | 120 |
| cgctgcctaa | acggctggaa | gaagcgggtt | ttgcgtttcg | ctggtagcat | ttagaagagg | 180 |
| cgctggcgga | tgtcgttcgc | tgatgtggtt | tacagcaaac | atccgccagt | taactcccg  | 240 |
| tgttacagga | ttagtggctt | tgcgcgataa | gatcgtctgg | tgaagtcgg  | gtcaccatca | 300 |
| taactaactc | tctgtctaaa | cctctatcca | gcacctcctg | agcaatacgc | agggtctctt | 360 |
| cgtgtttgcc | ctgcattgcg | ccttcttcac | gtaatctgtc | agcaatggtc | atcaagtctt | 420 |
| tccttttctt | gtggtgcgcg | ttccgctatc | tcaccaataa | atgcacgaaa | acgctgggca | 480 |
| tcccctgttt | gtaatacgtg | attaaacagg | gcttttagct | gtctgtcatt | agtgtccct  | 540 |
| gtaactagca | g          |            |            |            |            | 551 |

&lt;210&gt; 454

&lt;211&gt; 93

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 454

|            |            |            |            |            |            |    |
|------------|------------|------------|------------|------------|------------|----|
| tggcatctcg | gtgttgccga | tcttcatgat | atccagcccg | ccgaaaactt | cttcccaaac | 60 |
| ggttttgctg | ttatccattg | agtcacggaa | ctg        |            |            | 93 |

&lt;210&gt; 455

&lt;211&gt; 232

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 455

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cgtgccgaga | tgatcctgta | accatcatca | gttgtgaagt | agtgattcac | gacttcaagg | 60  |
| cgcttttcaa | aagggatatt | tggctttgac | atattagggg | ctattccatt | tcatcgtcca | 120 |
| acaaaatggg | tgcatgacat | actcgttgga | aatcaacaca | ggaggctggg | aatgccgcag | 180 |
| aaatatagat | tactttcttt | aatagtatt  | tgtttcacgc | ttttattttt | ca         | 232 |

&lt;210&gt; 456

&lt;211&gt; 713

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(713)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 456

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ttagnggatn  | naangccac  | ancctcgang | gatctaggag | gtagaatagc | ttcgaattcc | 60  |
| ccagcagagc  | gcggccttct | tcgtcagatt | tcgcagtagt | ggtaatggta | atatccaaac | 120 |
| cacgaacgcg  | gtcgacttta | tcgtagtcga | tttctgggaa | gatgatctgc | tcacggacac | 180 |
| ccatgctgta  | gttaccacga | ccgtcgaaag | acttagcgga | caggccacgg | aagtcacgga | 240 |
| tacgaggtac  | agcaatagt  | atcaggcgct | caaagaactc | ccacatgcgt | tcgccacgca | 300 |
| gaqgttacttt | acagccgac  | ggatagccct | gacggatttt | gaagcctgca | acagatttgc | 360 |
| gtgctttggt  | gatcagcggt | ttttgaccgg | agattgctgc | caggtctgct | gctgcgttat | 420 |
| ccagcagttt  | tttgtcagcg | atcgcttcac | caacacccat | gttcagggtg | atcttctcga | 480 |
| cccgagggac  | ttgcatgaca | gaattgtagt | taaactcagt | catgagtttt | ttaactactt | 540 |
| cgtctttgta  | gtaatcatgc | agtttcgcca | tcgtactact | ccatgtcggg | gaacgctctc | 600 |
| ctgagtagga  | caaatccgcc | ggagccggat | ttaacgttgc | gaacaaccgn | cccggagggg | 660 |
| tggnngcagg  | accccgccat | aactggcagc | attaaattaa | gcagaaggcc | atc        | 713 |

&lt;210&gt; 457

&lt;211&gt; 292

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 457

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| tgaacagcag  | agatacggcc | agtgcgccca | atgttttttg | tcctttaaac | ataacagagt | 60  |
| cctttaagga  | tatagaatag | gggtatagct | acgccagaat | atcgattttg | attattgcta | 120 |
| gttttttagtt | ttgcttaaaa | atattgttag | ttttattaaa | tgcaaaacta | aattattggt | 180 |
| atcatgaatt  | tggtgtatga | tgaataaaat | ataggggggt | atagatagac | gtcattttca | 240 |
| tagggttata  | aatgcgacta | ccatgaagtt | tttaattgaa | agtattgggt | tg         | 292 |

&lt;210&gt; 458

&lt;211&gt; 282

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 458

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| ttattaaatg | caaaaactaaa | ttattggtat | catgaatttg | ttgtatgatg | aataaaatat | 60  |
| aggggggtat | agatagacgt  | cattttcata | gggttataaa | tgcgactacc | atgaagtttt | 120 |
| taattgaaag | tattgggttg  | ctgataat   | gagctgttct | attcttttta | aatatctata | 180 |
| taggtctgtt | aatggatttt  | atttttacaa | ttttttgtgt | ttaggcatat | aaaaatcaac | 240 |
| ccgccatatg | aacggcgggt  | taaaatat   | acaacttagc | aa         |            | 282 |

&lt;210&gt; 459

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 459

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| tctgcgttcc  | gctaaaaggt | gcaaagtctc | aggacgttgc | agcgttttgc | gtgaccgctc  | 60  |
| ggggaaaggca | aaattgcctc | tgggaaagca | ttgcgcgggg | tccggcgctc | atcaacaatc  | 120 |
| ggggggcagc  | aaggggctga | aacgggaaag | cccctccgga | agaaggggce | ttgtataagg  | 180 |
| aaagggttat  | gatgaagctc | gtcatcatat | tggttgtgtt | gttactgtta | agtttcccgga | 240 |
| cttactaaca  | actcatcaga | ggggggagaa | atcctccctt | acccttggtc | ctttactcta  | 300 |

&lt;210&gt; 460

&lt;211&gt; 293

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 460

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| cgggggtccgg | cgctcatcaa | caatcggggg | gcagcaaggg | gctgaaacgg | gaaagcccct | 60  |
| cccgaagaag  | gggccttgta | taaggaaagg | gttatgatga | agctcgtcat | catactgggt | 120 |
| gtgtgtgtac  | tgtaagttt  | cccgacttac | taacaactca | tcagaggggg | gagaaatcct | 180 |
| cccttaccct  | tgttccctta | ctctaggttg | aaaaaacaac | agcgtcaata | ggcctgccat | 240 |
| gtacgaagcg  | agatctgtga | accgctttcc | ggttagcctt | ttttatcctg | ttg        | 293 |

&lt;210&gt; 461

&lt;211&gt; 359

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 461

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| caacacagga | ggctgggaat | gccgcagaaa | tatagattac | tttctttaat | agtgatttgt | 60  |
| ttcacgcttt | tatttttcac | ctggatgata | agagattcac | tggtggaatt | gcatattaaa | 120 |
| caggagagtt | atgagctggc | ggcgttttta | gcctgcaaat | tgaaagagta | agagtcttcg | 180 |
| gcgggaaatt | attccccgct | tacttacggc | gttgcgcatt | ctcattgcac | ccaaatttat | 240 |
| tcttcacaaa | aataataata | gattttatta | cgcgatcgat | tattttattc | ctgaaaacaa | 300 |
| ataaaaaaat | ccccgccaaa | tggcagggat | cttagattct | gtgcttttaa | gcagagatt  | 359 |

&lt;210&gt; 462

&lt;211&gt; 673

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 462

|             |            |             |            |             |            |     |
|-------------|------------|-------------|------------|-------------|------------|-----|
| gcaacccatg  | tcttgacctg | ggttcggggg  | acacaaaaac | gtgccgagat  | gatcctgtaa | 60  |
| ccatcatcag  | ttgtgaagta | gtgattcacg  | acttcaaggc | gcttttcaaa  | agggattttt | 120 |
| ggcttttgaca | tattaggggc | tattccattt  | catcgtccaa | caaaatgggt  | gcagtacata | 180 |
| ctcgttgga   | atcaacacag | gaggctggga  | atgccgcaga | aataatagatt | actttcttta | 240 |
| atagtatttt  | gtttcacgct | tttatttttc  | acctggatga | taagagattc  | actgtgtgaa | 300 |
| ttgcatatta  | aacaggagag | ttatgagctg  | gcggcggttt | tagcctgcaa  | attgaaagag | 360 |
| taagagtctt  | cggcgggaaa | ttattcccgc  | cttacttacg | gcgttgcgca  | ttctcattgc | 420 |
| acccaaattt  | attcttcaca | aaaataataa  | tagattttat | tacgcgatcg  | attattttat | 480 |
| tcttgaanaac | aaataaaaaa | atccccgccca | aatggcaggg | atcttagatt  | ctgtgctttt | 540 |
| aagcagagaa  | tacaggctgg | ttacgttacc  | agctgccggg | cctttagcgc  | cgctttcgat | 600 |
| ggtgaaggac  | actttctgac | cttcgtccag  | agatttgtaa | ccatcgttct  | ggatagcaga | 660 |
| gaagtgtacg  | aac        |             |            |             |            | 673 |

&lt;210&gt; 463

&lt;211&gt; 630

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 463

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| tggtggcatt  | ggttgctgga | gagagaaaac | ccccgcacgt  | tgagggtatg | cacctgacaa | 60  |
| caccacgggg  | gctaactctg | actctagacc | actcaagaat  | agccgcgaaa | cgttgtcatt | 120 |
| acaacacagg  | cggtatatg  | acgttcgcag | agctgggcat  | ggccttcttg | catgatttag | 180 |
| cggtcccggt  | cattgctggc | attcttgcca | gtatgatcgt  | gaactggctg | aacaagcgga | 240 |
| agtaacgtgt  | catgcgggcg | tcaggctgcc | gtaatggcaa  | tttgcgcccg | gaccaggccg | 300 |
| caggggggaa  | actctgcggc | ctttttcggt | cttactgcgg  | gtaaggcacc | cagtcgccgc | 360 |
| cgttcaggcg  | aacgtacggt | ttatcctggt | attgaataac  | tactgcattt | gagttctcgg | 420 |
| agaccggtgc  | tgtttggtgc | aaccactggg | tgagtttttt  | ccagtcaaca | ttgtcttcgg | 480 |
| tgaaaatctt  | gccatcgaga | acgcgaacca | ccagatcgga  | gatagccagg | aagctgctcg | 540 |
| gttggttcgat | gacaatcggt | gccccctgat | gcgggtgcctt | catgccgaag | aatttcaccc | 600 |
| caacggggac  | gtcggtgata | gacgggctag |             |            |            | 630 |

&lt;210&gt; 464

&lt;211&gt; 391

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

<400> 464  
 ctcaggctgc tgattgtttt tttgtgcaat ggcgcgggtat tagcgtcgtt gctgtcgtg 60  
 gagagaatca taaacgtggt gaatgatgat tgttagcaag gaaaactgtc aaaaatcttc 120  
 aaaaaatttg agggataagg ccggaatggc tccggccaga ggaaggttaa ccgcgaagct 180  
 gttgctgctt gaggtcgctt ttaaccagac gccaggcgct ccatacgcca aaaccgcgtc 240  
 tggccagcg gaccagcata ttaggatggc gaatcgtcca gatcgccatc acgctactgc 300  
 caaccagcgc ccaggagcgc agacttagca gcatattcca gcgacgatcg taagcgccctg 360  
 ttgtctccag ccattcacga cgactggcgg a 391

<210> 465  
 <211> 625  
 <212> DNA  
 <213> Escherichia coli

<400> 465  
 aacacaccac accataaacg gaggcaata atgctgggta atatgaatgt tttaatggcc 60  
 gtactgggaa taattttatt ttctggtttt ctggccgcgt atttcagcca caaatgggat 120  
 gactaatgaa cggagataat ccctcaccta accggcccct tggtacagtt gtgtacaagg 180  
 ggcctgattt ttatgacggc gaaaaaaac cgccagtaaa ccggcgggtga atgcttgcac 240  
 ggatagattt gtgttttgc tttacgctaa caggcatctt cctgcactga taacgaatcg 300  
 ttgacacagt agcatcagtt ttctcaatga atgttaaagc gagcttaaac tcggttaatc 360  
 acattttgtt cgtcaataaa catgcagcga tttcttccgg tttgcttacc ctcatcatt 420  
 gccgggtccg ctcttccaat gaccacatcc agaggctctt caggaaatgc gcgactcaca 480  
 cctgctgtca cggtaatgtt gatatgccct tcagaatgtg tgatggcatg gttatcgact 540  
 aactggcaaa ttctgacacc tgcacgacat gcttcttcat cattagccgc ttgacaata 600  
 atgataaatt cttcgccccc gtagc 625

<210> 466  
 <211> 623  
 <212> DNA  
 <213> Escherichia coli

<400> 466  
 tgcttttgaa tatgtgctcg caatcttgag aaggaaatgg cgaccacgaa agaaaaggca 60  
 aaaacgataa tctgaaagag ccaaggtatt tcagtataag cattgaatgc gacagtaaac 120  
 tctttcggtg tcagccagag agtgagacca aaaatgataa tcgtatacat aagtctttcg 180  
 agtggctcgt tagcaaaaag tttcaacaat ggagtaataa catccaacat atcaataact 240  
 ctcaactgta agggatttga aatgttaaca caagctctcg ctgtaggggt atagccgaga 300  
 ccaccgaagc ccggaggtgg tgaataaaaa ccgggcacaa cacgaagcgc catttccgat 360  
 atccataaag agtcgggtctt gtctgttaaa tttaaatggt gggagtgcgc ctccggttgt 420  
 aaataacgac attgctgtgt gtagtcctgg cggcatcagt tttttcttg aagttcggct 480  
 gatgtccgcc ctttttaaa tgaattttgt gatgcgggtga atgcggctaa gcgcacgtgg 540  
 cacagttaaa agtcatgtta gtccttattg gtttgggtgg gaaagccgac tgtaattgtt 600  
 aactggttgc agtcaacctgg agg 623

<210> 467  
 <211> 234  
 <212> DNA  
 <213> Escherichia coli

<400> 467  
 tgtttactta caagagattc atctttgtat aaataaagat aagtaattac gcataaaaca 60  
 acaatgatta taatagcaaa aataaatatt atcatctttg atagattact tgagatagcc 120  
 agcatcttgt aaagccttta tcgttttttt atgctctgga ttaatatata cactacatct 180  
 atctgagcaa tctgttggtg atggacatgt caacccatgg tcatttacag ccaa 234

<210> 468  
 <211> 529  
 <212> DNA  
 <213> Escherichia coli

<400> 468  
 attagctatt tcggctaaaa tagagactac atgtcttcgg tccatctcac ttaaggagtg 60  
 tagttccggt gtaagttttt ccatagcttg cactgctaaa tttcgaacaa ggaattttct 120  
 gctggtaatc tctaaaaaga tggcatgggt tacaatgatt tttgtttcct tttgattatt 180  
 atgaacaact gtccatgatt tcgtttaaga atgaagagaa atcactaaac gaactgaata 240  
 tatttctgt gccaatatta tctctaattt caaaaaagtt acttttaatg tcggtaatga 300  
 ctccaactta ttgatagtgt tttatgttca gataatgcc gatgactttg tcatgcagct 360  
 ccaccgattt tgagaacgac agcgacttcc gtcccagcgg tgccagggtc tgcctcagat 420  
 tcagggtatg ccgctcaatt cgctgcgtat atcgcttttc cttatcagtt cgttgatgtc 480  
 agtgggtttg accacgaggg agcttcacgc gagttattga aaaccctga 529

<210> 469  
 <211> 261  
 <212> DNA  
 <213> Escherichia coli

<400> 469  
 caaagaacct tcaacatgaa aaatatccat ttgtttgcaa aaaaagatta ttaggaagga 60  
 aattaatgca attatcgaaa attcaaaaaa tatccaaaaa tagtatactt tattccagaa 120  
 gagttcaata taatgtttgt cttcaatttt tcttacttca gggtaatata gattgctcat 180  
 tacattgtga gcttcatctt tatttaattt tctgttgact ccagctctcc gtgataacgg 240  
 ttttataatt agatgcttat c 261

<210> 470  
 <211> 98  
 <212> DNA  
 <213> Escherichia coli

<400> 470  
 agatgattgc cgggaacttg ttagcggcac gcaggcggcg gctcgcaccc ttaccctgct 60  
 ctttacgtac ttctgcgttg atagtaaaaca tttctttc 98

<210> 471  
 <211> 259  
 <212> DNA  
 <213> Escherichia coli

<400> 471  
 agcgcgaacg aagtcgatgt gctgcagctt cggttgtac gggtagcgt gtacgtcctg 60  
 agctttaact ttgatttctt taccgtcaac aacgatggtc agaacttcgc ttagaattc 120  
 agctttagct tgcattgtca tgactttgtc gtgatccagc tcgatagcca gcggcgcttc 180  
 tttgccaccg tagatgattg ccgggaactt gttagcggca cgcaggcggc ggctcgcacc 240  
 cttaccctgc tctttacgt 259

<210> 472  
 <211> 94  
 <212> DNA  
 <213> Escherichia coli

<400> 472  
 aaaaacggcg taaagaaagg atgcaaacat gttaataaaa actcaaattg atcccacgta 60  
 tatattacgc cgcaaaatcc ttacaataaa cagg 94

<210> 473  
 <211> 174  
 <212> DNA  
 <213> Escherichia coli

<400> 473  
 ttaattatta aaatagtgt acgcgattat gtggttatgg gggtaaacat taaataaacc 60  
 agcggggagg ggaggtaag tgaaaaata aaaagcgat aatcttaata agcaggccgg 120

acagcatcgc catccggcac tgatacgagg tttatttcag ctcatcaacc atcg 174

<210> 474  
<211> 138  
<212> DNA  
<213> Escherichia coli

<400> 474  
ctgtaaaaac gtcaaaaaga gtgttttatac aacagaagaa tggagggtctg acagatagta 60  
gtaatgcaaa aaaatggaga cttaagtga atgaacggga gtaaagcgaa aagactatag 120  
agtgaaggag aaattccc 138

<210> 475  
<211> 191  
<212> DNA  
<213> Escherichia coli

<400> 475  
tttgttggct taatattcta ttgttatctt tatttataga tgtttatatt gcatgagggtg 60  
gtttttggag agaagaatga ggaagatgag tcgagccaca gaaacgttag ctttacatat 120  
agcggagggtg atgtgaaatt aatttacaat agaaataatt tacatatcaa acagttagat 180  
gtttttgtgc g 191

<210> 476  
<211> 245  
<212> DNA  
<213> Escherichia coli

<400> 476  
cggccattta tacaggaaaa gcctatgtca gaacgtaaaa actcaaaatc acgccgtaat 60  
tatctcggtta aatgttcctg cccaaactgc acccaagagt cagaacacag tttttcaaga 120  
gtacaaaaag gtgccctttt gatctgccct cattgcaaca aagtattcca gacaaatctt 180  
aaagctgtag cctgattgat tttattagta acaagtattt ttatatattt aataatatat 240  
ttaa 245

<210> 477  
<211> 319  
<212> DNA  
<213> Escherichia coli

<400> 477  
aaattttcag gtaccttgtc accatacttt tttttctgag cattaatgat attttgagct 60  
tcttgaggat ctttaactcc ccacatttgg tggaaagtat tcatattaaa aggaagggtg 120  
aataaattgt ctttataaat cgccagtgga gaattagtaa aacgattaaa ttctactaaa 180  
tcattaacgt aatcccatat atatttatca ttggtatgaa aaatatgtgc accatattta 240  
tgaatctgga taccctcaca gtcctctgtg tacgcatttc caccgatatg atttcttttc 300  
tcaatcacta aaacttttt 319

<210> 478  
<211> 149  
<212> DNA  
<213> Escherichia coli

<400> 478  
gcagtgtatc aagcgatgac gaagtgtatg gaaaaatcag aaaaactcag caaatcctga 60  
tgactttcgc cggacgtcag gccgccactt cgggtcgggt acgtccgggt ttctttgctt 120  
tgtaaacgcg caaatctgcc gatttcaac 149

<210> 479  
<211> 330  
<212> DNA

## &lt;213&gt; Escherichia coli

&lt;400&gt; 479

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| gaaagtatct | tcgttattga | catcactgga | aaatataact | tgcttttcat | tattaaactc  | 60  |
| gaagcgcgta | ccgtatctgg | acaaacattt | atcgagctta | ccaaattcct | gaagagggtt  | 120 |
| aactacagat | aacatttgcg | cgctctttgc | agtaatgccc | gtcaaatcct | tgacggggcat | 180 |
| tatttagatt | aaattaccag | tatttcttcg | gagtgaagaa | tattaccagg | tatatttaac  | 240 |
| acccacgttc | gcggaccagt | cttgatctac | gtcaccacca | ccgaggtagt | tagcatcggt  | 300 |
| ataggcgctg | aagttcttgg | tgaagctaaa |            |            |             | 330 |

&lt;210&gt; 480

&lt;211&gt; 191

&lt;212&gt; DNA

## &lt;213&gt; Escherichia coli

&lt;400&gt; 480

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tttttttcca | gcaacggagc | aaaaggtttg | cccttggtga | gttcagggtt | aaccacttta | 60  |
| actacgtggc | gacgacccgg | agatgtcggt | ttacatttaa | caactgccat | tgtattactc | 120 |
| ctccgactta | ctcagcgccg | ccaacgaagt | ccagattctg | gccttctttc | agggtgacgt | 180 |
| aagctttttt | c          |            |            |            |            | 191 |

&lt;210&gt; 481

&lt;211&gt; 188

&lt;212&gt; DNA

## &lt;213&gt; Escherichia coli

&lt;400&gt; 481

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tccctttaac | taccagggtg | ttaacgactt | cgacttcgac | ttcaaacagt | ttctgcacag | 60  |
| cagctttgat | ttctgctttg | gtcgcgtctt | tagcaacttt | gagtacgatg | gtgttggtt  | 120 |
| tttccatcgc | agtagacgct | ttttcagaaa | cgtgcggtgc | acgcagcacc | ttcagcagac | 180 |
| gttctttca  |            |            |            |            |            | 188 |

&lt;210&gt; 482

&lt;211&gt; 172

&lt;212&gt; DNA

## &lt;213&gt; Escherichia coli

&lt;400&gt; 482

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| caaaggcgaa | caaagcctgt | gaagcccgaa | ggctccacag | acagtgtctac | ttgaaggcct  | 60  |
| tactgtttct | tcttaggagc | gagcaccatg | atcatctggc | ggccttcgat  | cttcggttggg | 120 |
| aaggattcga | ccactgccag | ttcttgcaaa | tcgtctttca | cgcgattaag  | ca          | 172 |

&lt;210&gt; 483

&lt;211&gt; 266

&lt;212&gt; DNA

## &lt;213&gt; Escherichia coli

&lt;400&gt; 483

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| tggagaaaaac | gggtgattga | taaagcaatc | atcgttctag | gggcgttaat | tgcgctgctg | 60  |
| gaactgatcc  | gctttctgct | tcagcttctg | aactgatagc | ggaaacgtaa | ttaggggcta | 120 |
| agagcacact  | actcttagcc | ctttaacatt | taacgcattg | tcacgaactc | ttctgccgcc | 180 |
| gttgggtgaa  | tgcgacgggt | attgtcgaag | tcttttttgg | ttgcccccat | cttcagcgcc | 240 |
| accgcgaagc  | cctgcaacat | ttcgtc     |            |            |            | 266 |

&lt;210&gt; 484

&lt;211&gt; 259

&lt;212&gt; DNA

## &lt;213&gt; Escherichia coli

&lt;400&gt; 484

|            |            |            |            |            |            |    |
|------------|------------|------------|------------|------------|------------|----|
| cgcaggcagc | tgatggtcaa | caggatgaga | gaaacccaga | gacaggttaa | tcacattgcc | 60 |
|------------|------------|------------|------------|------------|------------|----|



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|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ttaaccgct  | gcacggtaac | ctacaccaac | cagctgcagc | ttcttagtga | agccttcggt | 120 |
| aacaccgata | accattgagt | tcagcagggc | acgcgcggta | ccagcctgtg | cccaaccgtc | 180 |
| tgcgtaacca | tcacgcggac | cgaaggtcag | ggtattatct | gcatgtttaa | cttcaacagc | 240 |
| atcgttgaga | gtacgagtc  |            |            |            |            | 259 |

<210> 485

<211> 73

<212> DNA

<213> Escherichia coli

<400> 485

|            |            |            |            |            |            |    |
|------------|------------|------------|------------|------------|------------|----|
| caggtcggaa | cttaccgcac | aaggaatttc | gctaccttag | gaccgttata | gttacggccg | 60 |
| ccgtttaccg | ggg        |            |            |            |            | 73 |